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Patents Act 1990

BIOMOLECULAR RESEARCH INSTITUTE LTD

PROVISIONAL SPECIFICATION

Invention Title:

EGF RECEPTOR AGONISTS AND ANTAGONISTS

The invention is described in the following statement:

EGF RECEPTOR AGONISTS AND ANTAGONISTS

Field of the Invention

This invention relates to the field of epidermal growth factor (EGF) receptor structure and EGF receptor/ligand interactions. In particular, it relates to the field of using the EGF receptor structure to select and screen for agonists and antagonists of the polypeptide ligands.

Background of the Invention

Epidermal growth factor is a small polypeptide cytokine that stimulates marked proliferation of epithelial tissues and is a member of a larger family of structurally related cytokines such as transforming growth factor α (TGFα), amphiregulin, betacellulin, heparin-binding EGF and some viral gene products. Abnormal EGF family signalling is a characteristic of certain cancers (Soler, C. & Carpenter, G., 1994 In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197; Walker, F. & Burgess, A. W., 1994, In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp198-201).

The epidermal growth factor receptor (EGFR) is the cell membrane receptor for EGF (Ullrich, A., and Schlessinger, J. (1990) *Cell* 61, 203-212). The EGFR also binds other ligands that contain amino acid sequences classified as the EGF-like motif. Among these ligands, the three-dimensional structures of EGF and TGFα have been determined by NMR (Montelione, G.T.; Wuthrich, K.; Nice, E.C., Burgess, A.W. and Scheraga, H.A. (1986) *PNAS* 83(22): 8594-8; Campbell, I.D., Cooke, R.M., Baron, M., Harvey, T.S., and Tappin, M.J. (1989) *Prog. Growth Factor Res.* 1, 13-22). Upon binding of the ligand to the extracellular domain, the EGFR undergoes dimerization, which eventually leads to the activation of its cytoplasmic protein tyrosine kinase (Ullrich, A., and Schlessinger, J. (1990) *Cell* 61, 203-212). The EGFR is also known as the ErbB-1 receptor and belongs to the type I family of receptor tyrosine kinases (Ullrich, A., and Schlessinger, J. (1990) *Cell* 61, 203-212). This group also includes the ErbB-2, ErbB-3 and ErbB-4 receptors. The ligand of ErbB-2 is still unknown but it is clear that heregulin is binding to ErbB-3 and ErbB-4 (Plowman, G.D., Green, J.M., Calouscou, J.M., Carlton, G.W., Rothwell, V.M., and Buckley, S. (1993) *Nature* 366, 473-475). One of the heregulins is known as neuregulin or NDF and contains an EGF-like sequence that was found to fold into an EGF-like fold by NMR (Nagata, K., Kohda, D., Hatanska, H., Ichikawa, S., Matsuda, S., Yamamoto, T., Suzuki,

A., and Inagaki, F. (1994) *EMBO J.* 13, 3517-3523 and Jacobson, N.E., Abadl, N., Sliwkowski, M.X., Reilly, D., Skelton, N.J., and Fairbrother, W.J. (1996) *Biochemistry* 36, 3402-3417).

The type II family of receptor tyrosine kinases consists of the insulin receptor (INSR), the insulin-like growth factor I receptor, and the insulin receptor-related receptor (Ullrich, A., and Schlessinger, J. (1990) *Cell* 61, 203-212). Although the type II receptors consist of four chains ($\alpha_2\beta_2$), both the extracellular portions of the receptors from the two families, as well as the tyrosine kinase portions, share significant sequence homology, suggesting a common evolutionary origin (Ullrich, A., and Schlessinger, J. (1990) *Cell* 61, 203-212, and Bajaj, M., Waterfield, M.D., Schlessinger, J., Taylor, W.R., and Blundell, T. (1987) *Biochim. Biophys. Acta* 916, 220-226).

The 621 amino acid residues of the extracellular domain of the human EGFR (sEGFR) can be subdivided into four domains as follows: L1, S1, L2 and S2, where L and S stand for "large" and "small" domains, respectively (Bajaj, M., Waterfield, M.D., Schlessinger, J., Taylor, W.R., and Blundell, T. (1987) *Biochim. Biophys. Acta* 916, 220-226, see Fig. 2). The L1 and L2 domains are homologous, as are the S1 and S2 domains.

Ligand-induced dimerization was first reported for the EGF receptor (Schlessinger, J. (1980) *Trends Biochem Sci* 13, 443-447) and now is widely accepted as a general mechanism for the transmission of growth stimulatory signals across the cell membrane. Although many biochemical experiments have been performed to reveal the molecular mechanism of receptor dimerization (Lemmon, M.A., Bu, Z., Ladbury, J.E., Zhou, M., Pinchasi, D., Lax, L., Engelman, D.M., and Schlessinger, J. (1997) *EMBO J.* 16, 281-294 and Tzabar, E., Pinkas-Kramarski, R., Moyer, J.D., Klapper, D.N., Alroy, L., Levkowitz, G., Shelly, M., Henis, S., Eisenstein, M., Ratzkin, B.J., Sela, M., Andrews, G.C., and Yarden, Y. (1997) *EMBO J.* 16, 4938-4950 and Lax, L., Mitra, A.K., Ravern, C., Hurwitz, D.R., Rubinstein, M., Ullrich, A., Stroud, R.M., and Schlessinger, J. (1991), *J. Biol. Chem.* 266, 13828-13833), the molecular mechanism by which monomeric ligands induce dimerization is still unknown for members of the EGFR family. Single particle averaging of electron microscopic images suggests that the overall shape of the sEGFR is four-lobed and doughnut-like (Lax, L., Mitra, A.K., Ravern, C., Hurwitz, D.R., Rubinstein, M., Ullrich, A., Stroud, R.M., and Schlessinger, J. (1991), *J. Biol. Chem.* 266, 13828-13833). Small angle x-ray scattering also indicate that the

sEGFR is a flattened sphere with long diameters of 110 Å and a short diameter of 20 Å (Lemmon, M.A., Bu, Z., Ladbury, J.E., Zhou, M., Pinchasi, D., Lax, L., Engelman, D.M., and Schlessinger, J. (1997) *EMBO J.* 16, 281-294). The crystallization of sEGFR in complex with EGF has been published (Günther, N., Betzel, C., .and Weber, W. (1990) *J. Biol. Chem.* 265, 22082-22085), but the structure has not yet been reported, despite a decade of effort by many groups.

The EGF receptor ligand, TGF-α has been observed to be overproduced in keratinocyte cells which are subject to psoriasis (Turbitt, M.L. et al., 1990, *J. Invest. Dermatol.* 95(2), 229-232; Higashimyama, M. et al., 1991, *J. Dermatol.*, 18(2), 117-119; Elder, J.T. et al, 1990, 94(1), 19-25). The overproduction of at least one other EGF receptor ligand, amphiregulin, has also been implicated in psoriasis. (Piepkorn, M. 1996, *Am. J. Dermatopath.*, 18(2), 165-171). Molecules that inhibit the EGF receptor have been shown to inhibit the proliferation of both normal keratinocytes (Dvir, A. et al, 1991, *J. Cell Biol.*, 113(4), 857-865) and psoriatic keratinocytes. (Ben-Bassat, H. et al., 1995, *Exp. Dermatol.*, 4(2), 82-88). These findings indicate that EGF receptor antagonists may be useful in the treatment of psoriasis.

Many cancer cells express constitutively active EGFR (Sandgreen, E. P., et al., 1990, Cell, 61:1121-135; Karnes, W. E. J., et al., 1992, Gastroenterology, 102:474-485) or other EGFR family members (Hynes, N. E.,1993, Semin. Cancer Biol. 4:19-26). Elevated levels of activated EGFR occur in bladder, breast, lung and brain tumours (Harris, A. L., et al., 1989, In Furth & Greaves (eds) The Molecular Diagnostics of human cancer. Cold Spring Harbor Lab. Press, CSH, NY, pp353-357). Antibodies to EGFR can inhibit ligand activation of EGFR (Sato, J. D., et al., 1983 Mol. Biol. Med. 1:511-529) and the growth of many epithelial cell lines (Aboud-Pirak E., et al., 1988, J. Natl Cancer Inst. 85:1327-1331). Patients receiving repeated doses of a humanised chimeric anti-EGFR monoclonal antibody (Mab) showed signs of disease stabilization. The large doses required and the cost of production of humanised Mab is likely to limit the application of this type of therapy. These findings indicate that the development of EGF receptor antagonists will be attractive anticancer agents.

Summary of the Invention

The present inventors have now obtained 3-dimensional structural information concerning the epidermal growth factor receptor (EGFR). This structural information was obtained by comparative modelling based on the 3D structure of the IGF-1 receptor as described in PP0585 and PP2598 (a copy of which is annexed hereto as Annexure A). The information presented in the present application provides the opportunity for the development of specific antagonists and agonists of EGFR for therapeutic applications.

Accordingly, in a first aspect the present invention provides a method of screening for, or designing, an agonist of the EGF receptor which method includes

(i) selecting or designing a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by

(a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figure 6 and 7 or a subset thereof; and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a second aspect the present invention provides a method of screening for, or designing, an antagonist of the EGF receptor which method includes

(i) selecting or designing a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by

(a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof; and

(ii) testing the substance for the ability to act as an antagonist of the EGF receptor.

The EGF receptor site defined in the first and second aspects of the present invention comprises the L1, S1 and L2 domains (residues 1-474) of the ectodomain of EGFR. At the centre of this structure is a cavity, bounded by all three domains, of sufficient size to accommodate a ligand molecule. By "stereochemical complementarity" we mean that the substance or a portion thereof correlates, in the manner of the classic "lock-and-key" visualisation of ligand-receptor interaction, with the cavity in the receptor site. Preferably, the stereochemical complementarity is such that the

substance has a K_I for the receptor site of less than 10^{-6}M. More preferably, the K_I value is less than 10^{-8}M and more preferably less than 10^{-9}M.

In preferred embodiments of the first and second aspects of the present invention, the method further involves selecting or designing a substance which has portions that match residues positioned on the surface of the receptor site which faces the cavity. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions which promote desolvation of the biologically active substance within the site, in such a way that retention of the substance within the cavity is favoured energetically.

In a preferred embodiment of the first aspect of the present invention, the method includes screening for, or designing, a substance which possesses a stereochemistry and/or geometry which allows it to interact with both the L1 and L2 domains of the EGF receptor site. It is believed that EGFR monomers dimerise in nature in such a manner that the cavities of each monomer may face each other. Accordingly, the method of the first aspect of the present invention may involve screening for, or designing, a biologically active substance which interacts with the L1 domain of one monomer and the L2 domain of the other monomer.

In a third aspect the present invention provides a method of selecting or designing an agonist of the EGF receptor which method includes

(i) selecting or designing a substance which interacts with

(a) a fragment of the EGF receptor characterised by amino acids 1-474 positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof;

wherein the interaction of the substance with the fragment alters the position of at least one of the L1, L2 or S1 domains of the fragment relative to the position of at least one of the other domains; and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a preferred embodiment of the third aspect of the present invention the substance interacts with the fragment in the region of the L1 domain-S1 domain interface, causing the L1 and S1 domains to move away from each other. In a further preferred embodiment the substance interacts with the hinge region between the L2 domain and the S1 domain causing an alteration in the positions of the domains relative to each other. In a further preferred

embodiment the substance interacts with the β sheet of the L1 domain causing an alteration in the position of the L1 domain relative to the position of the S1 domain or L2 domain.

In a fourth aspect the present invention provides an agonist of the EGF receptor obtained by a method according to the first or third aspects of the present invention.

In a fifth aspect the present invention provides an antagonist of the EGF receptor obtained by a method according to the second aspect of the present invention.

The agonists or antagonists of the fourth and fifth aspects of the present invention may be mutant EGFR ligands where at least one mutation occurs in the region of the ligand which interacts with residues on the surface of the receptor site facing toward the cavity. For example, the residues Arg 41 and Tyr 13 in EGF are conserved in other members of the EGF receptor family of ligands (a Phe residue may be substituted for Tyr 13). Structures of several EGF family members show the two residues to be in close proximity. This portion of EGF may interact with a hydrophobic portion of the EGF receptor which contains one or more negatively charged residues such as the lower β sheet of the L1 domain. Mutants of EGF which show altered activity may be generated by introducing modifications to Arg 41 or Tyr 13 or other nearby residues. Alternatively, mutants of EGF may be generated by introducing modifications to residues on the opposite side of the ligand which may interact with a second receptor molecule in the unmodified ligand.

In a sixth aspect the present invention provides a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by

(a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof;

with the proviso that the substance is not a naturally occurring ligand of the EGF receptor or a mutant thereof.

By "mutant" we mean a ligand which has been modified by one or more point mutations, insertions of amino acids or deletions of amino acids.

In a preferred embodiment of the sixth aspect of the present invention, the stereochemical complementarity is such that the compound has a K_i for

the receptor site of less than 10^{-6}M. More preferably, the K_I value is less than 10^{-8}M and more preferably less than 10^{-9}M.

The 3 dimensional structure of the EGF receptor elucidated by the present inventors also shows that the L2 and S2 domains are positioned such that they form a "corner" structure. It is envisaged that this corner structure provides a further binding site for ligands of the EGF receptor.

Accordingly, in a seventh aspect the present invention provides a method of screening for, or designing, an agonist of the EGF receptor which method includes

(i) selecting or designing a substance which binds simultaneously to the L2 and S2 domains of the EGF receptor, wherein the L2 and S2 domains are positioned substantially according to the atomic coordinates of amino acids 313-621 as shown in Figure 7, and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In an eighth aspect the present invention provides a method of screening for, or designing, an antagonist of the EGF receptor which method includes

(i) selecting or designing a substance which binds simultaneously to the L2 and S2 domains of the EGF receptor, wherein the L2 and S2 domains are positioned substantially according to the atomic coordinates of amino acids 313-621 as shown in Figure 7, and

(ii) testing the substance for the ability to act as an antagonist of the EGF receptor.

In preferred embodiments of the seventh and eighth aspects of the present invention, the method involves selecting or designing a substance which has portions that match residues positioned on the inner surface of the corner structure. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions in such a way that retention of the substance within the corner structure is favoured energetically.

Preferably, the substance matches the residues positioned on the inner surface such that the substance has a K_I for the corner structure of less than 10^{-6}M. More preferably, the K_I value is less than 10^{-8}M and more preferably less than 10^{-9}M.

In a ninth aspect the present invention provides a method of selecting or designing an agonist of the EGF receptor which method includes

(i) selecting or designing a substance which interacts with

(a) a fragment of the EGF receptor characterised by amino acids 313-621 positioned at atomic coordinates substantially as shown in Figure 7 or a subset thereof;

wherein the interaction of the substance with the fragment alters the relative positions of the L2 and S2 domains of the fragment with respect to each other; and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a tenth aspect the present invention provides an agonist of the EGF receptor obtained by a method according to the seventh or ninth aspects of the present invention.

In an eleventh aspect the present invention provides an antagonist of the EGF receptor obtained by a method according to the eighth aspect of the present invention.

In a twelfth aspect the present invention provides a pharmaceutical composition for preventing or treating a disease which would benefit from increased signalling by the EGF receptor, which includes an agonist obtained by a method according to the first, third, seventh or ninth aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In an thirteenth aspect the present invention provides a pharmaceutical composition for preventing or treating a disease associated with signalling by the EGF receptor which includes an antagonist obtained by a method according to the second or eighth aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In a fourteenth aspect the present invention provides a method of preventing or treating a disease which would benefit from increased signalling by the EGF receptor which method includes administering to a subject in need thereof an agonist obtained by a method according to the first, third, seventh or ninth aspects of the present invention.

Diseases which may be treated by administration of EGFR agonists include wound healing and gastric ulcers.

In a fifteenth aspect the present invention provides a method of preventing or treating a disease associated with signalling by the EGF

receptor which method includes administering to a subject in need thereof an antagonist obtained by a method according to the second or eighth aspects of the present invention.

Diseases associated with signalling by the EGF receptor include psoriasis and many types of tumour states including but not restricted to cancer of the breast, brain, ovary, cervix, pancreas, lung, head and neck, and melanoma, rhabdomyosarcoma, mesothelioma and glioblastoma.

Brief Description of the Drawings

Figure 1: Sequence alignment of human EGF receptor family proteins with IGF-1 receptor sequences and insulin receptor sequence for the first two domains of the EGF receptor. The alignment of EGF receptor and the various IGF-1 receptor sequences were used by the MODELLER program to create a model of the EGF receptor domains L1 and S1. Residues which are underlined were used to create additional Cα-Cα restraints for the construction of the EGF receptor model. IGF-1 receptor residues colored in magenta form part of helical secondary structures. Residues colored in light blue, light green and dark yellow reside in one of the three β-sheets (colored light blue, light green and dark yellow respectively) which make up part of the L1 β-helix. Residues colored in dark blue and dark green form part of a β-strand in the β-fingers. The residues in red are also in β-strands. Each cysteine residue in the S1 domain are numbered according to the module that it is a part of.

Figure 2: Sequence alignment of human EGF receptor family proteins with IGF-1 receptor sequences and insulin receptor sequence for the third and fourth domains of the EGF receptor. The labelling scheme of the residues is the same as for Figure 1.

Figure 3: Model polypeptide fold of the L1 and S1 domains of the EGF receptor. The L1 domain is at the left hand side of the structure with the N-terminus facing the front. The secondary structure elements are coloured in the same manner as in Figure 1.

Figure 4: Model polypeptide fold of the L2 and S2 domains of the EGF receptor. The L2 domain is at the bottom with its N-terminus facing the front. The secondary structure elements are coloured in the same manner as in Figure 1.

Figure 5: Superpostion of the two models (of L1 and S1 domains and of L2 and S2 domains) onto structure of first three domains of IGF-1 receptor. The residues have been colored according to an estimate of the accuracy of the model cooridinates. Residues colored in yellow are judged to be well-modelled. Residues colored in orange are judged to have a moderate possibility of error. The coordinates or residues colored in red are believed to be inaccurate.

Figure 6: Coordinates of the model of the EGF receptor domains L1 and S1. The coordinates are in relation to a Cartesian set of orthogonal axes. The final column contains the number 20, 40 or 60 depending on whether the residue containing the atom is judged to be well modelled, have a moderate possibility of error or is believed to be inaccurate respectively.

Figure 7: Coordinates of the model of the EGF receptor domains L2 and S2. The coordinates are in relation to a Cartesian set of orthogonal axes which are independent of the coordinate frame used for the EGF receptor model for L1 and S1 domains. The number in the final column is assigned in the same manner as for Figure 6.

Detailed description of the Invention

Comparative modelling

The comparative modelling method exploits the observation that proteins with more than 25% amino acid identity will almost always have a similar protein backbone (Sander, C. And Schneider, R., 1991, Proteins: Structure Function and Genetics, 9, 56-68). In some cases, proteins will have similar backbone structures with a lower proportion of identical amino acids. By aligning the sequence of a (target) protein which is to be modelled with the sequences with known structures (the templates), a model of the protein can be obtained. Where a region of the target sequence follows the sequences

of a template, the backbone of the target is built to follow that of the template. Where the target sequence can not be aligned to a target sequence, the so-called insertion must be constructed by other means (Greer, J., 1991, Meth. Enzym. pp 239-252).

The MODELLER program (Šali, A and Blundell, T.L., 1993, J. Mol. Biol. 234, 779-815) is a semi-automated approach to building models of proteins given the structures of one or more template structures and an alignment between the sequences of the target protein and the templates. Based on the sequence alignment and a set of rules derived from the analysis of sets of aligned structure, the program generates a series of restraints for variables such as Cα-Cα distances, main chain and side chain dihedral angles for the target structure. The restraints are expressed in terms of probability density functions (PDFs). The PDFs are combined to yield an expression for the most probable structure as a function of the variables (Cα-Cα distances etc). The program then attempts to find structures to maximise the value of this function. In effect, the program attempts to minimise a transformed version of this function.

While some comparative modelling approaches involve the explicit building of regions of the model for which there is no sequence alignment with a template, the MODELLER program constructs PDFs for these regions, thus including them in the consideration of constructing a comparative model. It is conceivable that once a comparative model has been constructed using MODELLER that an algorithm to build the structures of these regions is applied.

The MODELLER program was used to build the structures of the extracellular portion of the EGF receptor using the 3D structure of the IGF-1 receptor (as described in PP0585 and PP2598) as a template. The description of the generation of these models is outlined below.

Construction of the alignment

The sequence of the EGF receptor extracellular domain can be divided into four domains, L1, S1, L2 and S2 on the basis of internal homology and homology with the insulin receptor family (Ward, C.W. et al., 1995, Proteins: Structure Function and Genetics 22: 141-153; Bajaj, M. et al., 1987, Biochim. Biophys. Acta 916: 220-226). At least two important sequence motifs are found in the EGF receptor sequence which are conserved in other EGF receptor homologues. The first motif is the sequence CXXXXXXW which is

found towards the end of both L1 and L2 of EGFR (C is cysteine, W is tryptophan and X is any residue). The second motif is the sequence CW where C is the third cysteine of both S1 and S2 (using the assignment of domain boundaries from Ward, C.W. et al., 1995, Proteins: Structure Function and Genetics 22: 141-153). The first motif is found in L1 but not L2 of the insulin receptor family. The second motif is found in the cysteine-rich domain of the insulin receptor family. These motifs are found in L1 and the cysteine-rich domain of the insulin receptor family. Structurally, the first motif corresponds to part of the L1 domain which allows penetration of the tryptophan residue of the second motif into the β-helix. As the first sequence motif is absent from L2 of the IGF-1 receptor, only the L1 and cysteine rich domains of the IGF-1 receptor were used as templates for the building of the EGF receptor extracellular domain models.

Construction of the alignment of L1 and S1

There are two loops in the structure of the L1 domain which emerge from the breadloaf structure. The second loop (residues 86-93 in EGFR L1, 79-85 in IGF-1R L1) is structurally conserved in the L2 domain and differs by one amino acid residue in length. A region of the L2 domain corresponding to the loop was used as an additional template for this region. The sequence of the EGF receptor which corresponds to the first loop is of a different length and does not seem to be consistent with the loop of the IGF-1 receptor. The latter half of the region of EGF receptor sequence can be aligned to a region of sequence in the IGF-1 receptor's L2 domain. A portion of the IGF-1 receptor structure corresponding to this region of sequence plus the structure of flanking sequences was used as an additional template.

The alignment of the S1 domain of the EGF receptor to the IGF-1 receptor used the same combination of modules but involved the use of other modules from the cysteine-rich domain as additional templates. The first and second modules of the EGF module used the third module of the IGF-1 receptor cysteine-rich domain as additional templates. (This module contains two cysteines in disulfide bonds in a 1-3, 2-4 arrangement.) The sixth module of the EGF receptor can be modelled by the fifth module of the IGF-1 receptor, a β-finger.

Construction of the alignment of L2 and S2

The alignment of the EGF receptor sequence for the L2 domain to the L1 domain of the IGF-1 receptor sequence was similar to that of the L1

alignment. There is a 16 amino acid region which occurs roughly in the same region as the first loop in the IGF-1 receptor L1 domain. This region of sequence, which exhibits sequence homology amongst the EGF receptor family of proteins, can not be aligned with any region of the IGF-1 receptor sequence.

The sequence of the S2 domain was found to differ significantly from the S1 domain and suggested that the pattern of disulfide bonds may be different.

An analysis of the β-finger structures in the IGF-1 receptor, TNF receptor and laminin-γ structures revealed that the β-fingers could be classed into three types exhibiting some structural and sequence conservation. Two of the structural types are relevent to the IGF-1 and EGF receptors. The first type of β-finger is characterised by structural conservation of the C-terminal portion of the module and also of the linker region after the module. The sequence signature is C...CXXC where the third cysteine residue is the start of another β-finger module. The second type of β-finger is characterised by structural conservation of the N-terminal portion of the module and also of the linker region after the module. The sequence signature is C...CXXXC where the third cysteine is the start of a module whose disufide bonding pattern is 1-3,2-4. The fifth module of the IGF-1 receptor cysteine-rich domain has some structural conservation with both types of β-finger.

The regions of the IGF receptor structure which were used as templates were identified as follows. The structure of IGF-1 receptor from the start of the L1 domain to the end of the first module of the cysteine-rich domain (which contains the conserved tryptophan residue which intercalates into the L1 β-helix) was used to model the corresponding regions of L2 and the start of S2 of the EGF receptor. Additional templates were used and "joined" to other templates by virtue of overlap in the sequence alignment.

The fourth and fifth modules of the IGF-1 receptor cysteine-rich domain were found to align with the sequences of the first and second and also the fourth and fifth putative modules of the S2 domain. The seventh module is the second last module of the S2 domain. The eighth module is neither a β-finger nor a module with the 1-3, 2-4 pattern of disulfide bonds. By elimination and use of the information described in the preceding paragraph, the third and sixth modules were assigned to be β-fingers of the second type. Two parts of the IGF-1 receptor structure were used to model

these two β-fingers. The fifth and seventh modules were used to model the β-finger modules. The linker region after the seventh module was also used. Additional residues after the linker were included to guide the placement of the next module. The positioning of the next module (modules 4 and 7 in S2) is essentially arbitrary and the use the extra residues offers a way of obtaining a plausible placement of the module.

Construction of the model

Version 3 of the MODELLER program (Modeler User Guide, October 1996, San Diego Molecular Simulations Inc) was used to build models of the EGF receptor. Models of the L1 and S1 domains were constructed from the alignment shown in Figure 1 using the IGF-1 receptor templates shown and the EGF receptor sequence. Additional distance restraints were generated between Cα atoms of selected residues. The restraints were generated as follows. The small IGF-1 receptor templates were superimposed into the structure of the first two domains of the IGF-1 receptor using the Cα atoms of the residues which are aligned in Figure 1. Using the Homology module of the Insight II program (Homology User Guide, October 1995, San Diego BIOSYM/MSI) coordinates were built for the EGF receptor residues which are aligned to the IGF-1 receptor coordinates which are in bold typeface. From these coordinates, distance restraints in the form of Gaussian curves were constructed for pairs of Cα atoms with a distance less than 50Å. The sigma value of the Gaussian curves was set to be 2Å. A MODELLER run was submitted using the alignment in Figure 1. The built models of proteins attempt to satisfy these restraints in addition to the restraints the program derives from the alignment.

To build models of the L2 and S2 domains, a similar process to that described in the preceding paragraph was used. The alignment used to build the models is shown in Figure 2. Two separate sets of additional restraints were used. The first set of restraints were derived from the IGF-1 receptor templates which are aligned with the first, second and third modules of the EGF receptor S2 domain. The second set of restraints were derived from the IGF-1 receptor templates which were aligned with the fourth, fifith and sixth modules of the EGF receptor S2 domain. Only those residues which are underlined in Figure 2 were used to generate the restraints. The sigma value of the Gaussian curves used to construct the additional restraints was 1Å.

For both sets of models, the MODELLER program constructed 20 models whose coordinates were perturbed from an initial structure by a random value of maximum distance 4Å. The refinement level used was the 'refine1' option in the MODELLER program.

Structure of the EGF receptor model

The structure of the L1 and S1 domains of the EGF receptor as determined by the modelling described above is shown in Figure 3, while the structure of the L2 and S2 domains is shown in Figure 4. The superposition of these two models onto the structure of the extracellular domains of the IGF-1 receptor is shown in Figure 5.

The coordinates of the EGF receptor domains L1 and S1 are shown in Figure 6. The coordinates of the EGF receptor domains L2 and S2 are shown in Figure 7.

The structures of the L1 and S1 domains are similar to those of the IGF-1 receptor structure, as expected. There are two major differences in the S1 domain from the structure of the cysteine-rich region of the IGF-1 receptor structure. The sixth module of S2 is smaller that of the IGF-1 receptor and occupies less of the region between the two L domains. The fifth module, another β-finger, contains a large insertion which points away from the L1 domain. The structure of the end of the EGF receptor S1 domain is similar to that of the IGF-1 receptor cysteine-rich domain and is postulated to contain a hinge region between the last module of the S1 domain and the L2 domain.

A region of EGF receptor in L2 which could not be aligned with the IGF-1 receptor sequence includes the amino acids Trp-Pro which are conserved in the EGF receptor family of structure. This sequence motif is not found in the insulin receptor family and may represent a region of novel structure. This region of sequence could not be modelled on the corresponding region of the IGF-1 structure since none of the amino acids of the sequence Glu-Asn-Arg could be placed such that their side chains are in the interior of the β-helix. The asparagine has been observed to be glycosylated (Smith, K.D. et al, 1996, Growth.Factors, 13(1-2), 121-132) and therefore must point out of the structure. The charged residues glutamate and arginine are also expected to point out from the β-helix.

The amino acids 352-367 correspond to a large insertion in the third domain of the EGF receptor. The amino acids 351-364 have been identified as the epitope for several antibodies against the EGF receptor (Wu, D.G et al,

J. Biol. Chem. 1989 264(29):17469-17475). That this region forms a loop which sticks out of the structure is consistent with this region being accessible to the antibodies. The structure itself is difficult to model accurately since its sequence does not correspond to any part of the IGF-1 receptor sequence. The position of this insertion is in approximately the same region where the structures of IGF-1 receptor L1 and L2 domain differ.

The S2 domain adopts a different shape to the S1 domain. The S2 domain adopts a rod-like shape similar to that of the laminin γ-chain (Stetefeld, J. et al., 1996, J. Mol. Biol., 257(3): 644-657). Like the first half of the receptor model, the S2 domain contacts the L2 domain with the first module (this module contains the conserved tryptophan which intercalates into the breadloaf). Unlike S1, the rest of the S2 domain does not make any more contact with the L2 domain. The S2 domain points out from the L2 domain with a different geometry to the manner in which the S1 domain points out from L1.

Putative binding sites of the EGF receptor

From the IGF-1 receptor structure and a number of insulin receptor mutants, one of the regions of insulin binding was proposed to be the lower β sheet of the L1 domain. This surface is characterised by a number of hydrophobic residues which point out of the structure and also the presence of a structurally conserved loop. By analogy, we propose that the analogous β sheets of the L1 and L2 are potential binding sites. These sheets contain a number of hydrophobic residues, conserved amongst EGF receptor family members, which point away from the core of the β-helix structure. Residue 45 of a mutant EGF has been cross-linked to the residue Lysine 465 which is in the last strand of the lower β sheet of the L2 domain. (Summerfield, AE et al, J Biol Chem, 1996, 271(33), 19656-19659). Tyrosine 101 has been cross-linked to the N-terminus of EGF (Woltjer, RL et al, PNAS, 1992, 89(16), 7801-7805). This residue is in the portion of sequence which immediately follows a strand in the lower β sheet of L1.

The side chain of asparagine 1 of EGF has been cross-linked to lysine 336 of the EGF receptor (Wu, DG et al, PNAS, 1990, 87(8), 3151-3155). The latter residue is in the N-terminal helix of the L2 domain and points towards the cavity which is formed when the two halves of the EGF receptor are postioned in a similar arrangement to the first three domains of the IGF-1 receptor. Two nearby residues, Asn 328 and Asn 337 are glycosylated. This

mutation is in a similar position to the insulin receptor mutant S323L which has aberrent insulin binding.

Several insertional mutants of the EGF receptor extracellular domain have been constructed to probe the role of several regions of the receptor (Harte, M.T. and Gentry, L.E., 1995, Arch. Biochem. Biophys. 322(2), 387-389). EGF receptor mutants with insertions at residues 162, 169, 174 and 220 bound EGF with a similar affinity to wild-type EGF receptor but bound TGF-α with a lower affinity than wild-type receptor. The first insertion was located in the region near the end of the L1 domain and the first cysteine of the first module in S1. The second and third insertions were present in the first module of S1 and the fourth insertion was present in the third module of S1. EGF receptor mutants with insertions at postions at 251 and 574 (both in large β-finger modules, the first in S1 and the second in S2) bound twice as much EGF as the wild type receptor. Two insertional mutants which showed reduced EGF receptor binding contained insertions at postions 291 and 474. The former insertion is contained in the seventh module of S1 which is a β-finger. The latter insertion is near the end of the L2 domain.

Another EGF receptor mutant which shows altered ligand binding behaviour is the R497K mutant. The site of this mutation in the first module of the S2 domain and faces the side of the L2 domain opposite to that containing residue 465. This mutant binds EGF in a similar fashion as wild-type receptor but abolishes the high affinity binding site for TGF-α (Moriai, T. et al, 1994, PNAS 91(21), 10217-10221).

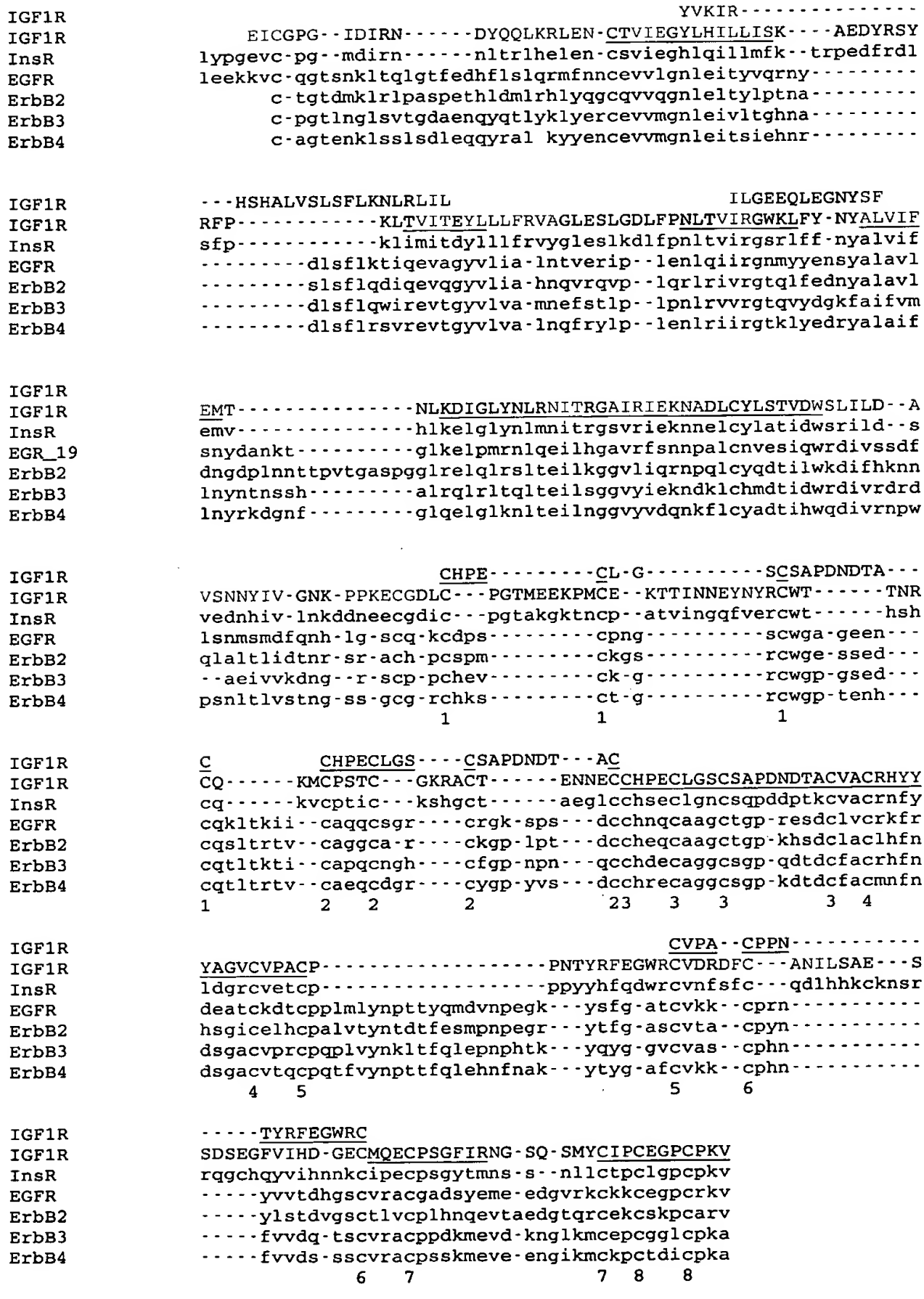
It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this twenty ninth day of May 1998

BIOMOLECULAR RESEARCH
INSTITUTE LTD
Patent Attorneys for the Applicant:

F B RICE & CO

Figure 1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InsR lypgevc-pg--mdirn------nltrlhelen-csvieghlqillmfk--trpedfrdl
EGFR leekkvc-qgtsnkltqlgtfedhflslqrmfnncevvlgnleityvqrny---------
ErbB2 c-tgtdmklrlpaspethldmlrhlyqgcqvvqgnleltylptna---------
ErbB3 c-pgtlnglsvtgdaenqyqtlyklyercevvmgnleivltghna---------
ErbB4 c-agtenklsslsdleqqyral kyyencevvmgnleitsiehnr---------
IGF1R ---HSHALVSLSFLKNLRLIL ILGEEQLEGNYSF
IGF1R RFP-----------KLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFY-NYALVIF
InsR sfp-----------klimitdyllfrvygleslkdlfpnltvirgsrlff-nyalvif
EGFR ---------dlsflktiqevagyvlia-lntverip--lenlqiirgnmyyensyalavl
ErbB2 ---------slsflqdiqevqgyvlia-hnqvrqvp--lqrlrivrgtqlfednyalavl
ErbB3 ---------dlsflqwirevtgyvlva-mnefstlp--lpnlrvvrgtqvydgkfaifvm
ErbB4 ---------dlsflrsvrevtgyvlva-lnqfrylp--lenlriirgtklyedryalaif
IGF1R
IGF1R EMT--------------NLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLILD--A
InsR emv--------------hlkelglynlmnitrgsvrieknnelcylatidwsrild--s
EGR_19 snydankt----------glkelpmrnlqeilhgavrfsnnpalcnvesiqwrdivssdf
ErbB2 dngdplnnttpvtgaspgglrelqlrslteilkggvliqrnpqlcyqdtilwkdifhknn
ErbB3 lnyntnssh---------alrqlrltqlteilsggvyiekndklchmdtidwrdivrdrd
ErbB4 lnyrkdgnf---------glqelglknlteilnggvyvdqnkflcyadtihwqdivrnpw
IGF1R CHPE---------CL-G----------SCSAPDNDTA---
IGF1R VSNNYIV-GNK-PPKECGDLC---PGTMEEKPMCE--KTTINNEYNYRCWT------TNR
InsR vednhiv-lnkddneecgdic---pgtakgktncp--atvingqfvercwt------hsh
EGFR lsnmsmdfqnh-lg-scq-kcdps---------cpng----------scwga-geen---
ErbB2 qlaltlidtnr-sr-ach-pcspm---------ckgs----------rcwge-ssed---
ErbB3 --aeivvkdng--r-scp-pchev---------ck-g----------rcwgp-gsed---
ErbB4 psnltlvstng-ss-gcg-rchks---------ct-g----------rcwgp-tenh---
1 1 1
IGF1R C CHPECLGS----CSAPDNDT---AC
IGF1R CQ------KMCPSTC---GKRACT------ENNECCHPECLGSCSAPDNDTACVACRHYY
InsR cq------kvcptic---kshgct------aeglcchseclgncsqpddptkcvacrnfy
EGFR cqkltkii--caqqcsgr----crgk-sps---dcchnqcaagctgp-resdclvcrkfr
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1 2 2 2 23 3 3 3 4
IGF1R CVPA--CPPN----------
IGF1R YAGVCVPACP----------PNTYRFEGWRCVDRDFC---ANILSAE---S
InsR ldgrcvetcp----------ppyyhfqdwrcvnfsfc---qdlhhkcknsr
EGFR deatckdtcpplmlynpttyqmdvnpegk---ysfg-atcvkk--cprn----------
ErbB2 hsgicelhcpalvtyntdtfesmpnpegr---ytfg-ascvta--cpyn----------
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4 5 5 6
IGF1R -----TYRFEGWRC
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InsR rqgchqyvihnnkcipecpsgytmns-s--nllctpclgpcpkv
EGFR -----yvvtdhgscvracgadsyeme-edgvrkckkcegpcrkv
ErbB2 -----ylstdvgsctlvcplhnqevtaedgtqrcekcskpcarv
ErbB3 -----fvvdq-tscvracppdkmevd-knglkmcepcgglcpka
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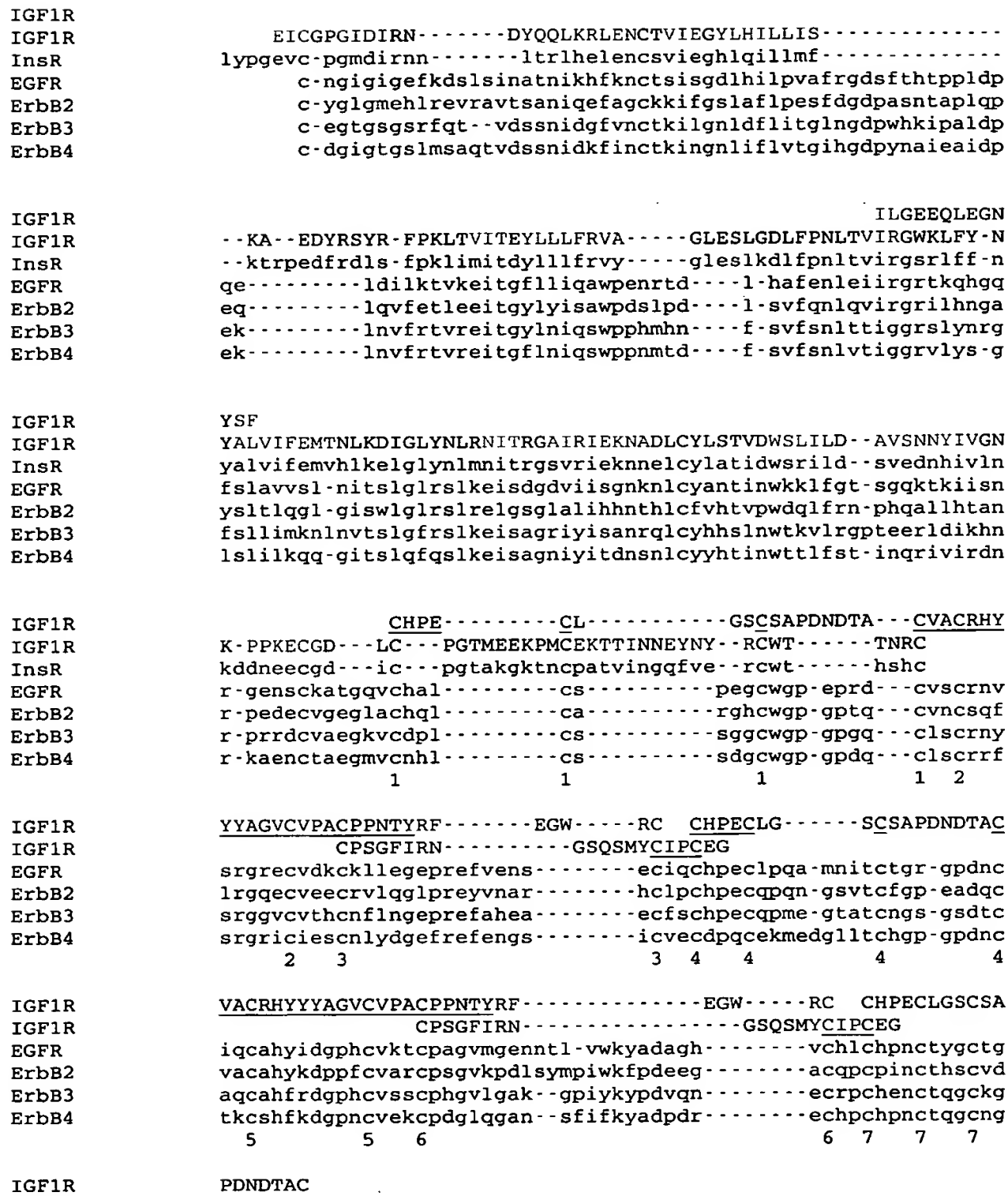
6 7 7 8 8

Figure 2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ErbB3 ek---------lnvfrtvreitgylniqswpphmhn----f-svfsnlttiggrslynrg
ErbB4 ek---------lnvfrtvreitgflniqswppnmtd----f-svfsnlvtiggrvlys-g
IGF1R YSF
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InsR yalvifemvhlkelglynlmnitrgsvrieknnelcylatidwsrild--svednhivln
EGFR fslavvsl-nitslglrslkeisdgdviisgnknlcyantinwkklfgt-sgqktkiisn
ErbB2 ysltlqgl-giswlglrslrelgsglalihhnthlcfvhtvpwdqlfrn-phqallhtan
ErbB3 fsllimknlnvtslgfrslkeisagriyisanrqlcyhhslnwtkvlrgpteerldikhn
ErbB4 lslilkqq-gitslqfqslkeisagniyitdnsnlcyyhtinwttlfst-inqrivirdn
IGF1R CHPE---------CL-----------GSCSAPDNDTA---CVACRHY
IGF1R K-PPKECGD---LC---PGTMEEKPMCEKTTINNEYNY--RCWT------TNRC
InsR kddneecgd---ic---pgtakgktncpatvingqfve--rcwt------hshc
EGFR r-gensckatgqvchal---------cs----------pegcwgp-eprd---cvscrnv
ErbB2 r-pedecvgeglachql---------ca----------rghcwgp-gptq---cvncsqf
ErbB3 r-prrdcvaegkvcdpl---------cs----------sggcwgp-gpgq---clscrny
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1 1 1 1 2
IGF1R YYAGVCVPACPPNTYRF-------EGW-----RC CHPECLG------SCSAPDNDTAC
IGF1R CPSGFIRN----------GSQSMYCIPCEG
EGFR srgrecvdkcklegeprefvens--------eciqchpeclpqa-mnitctgr-gpdnc
ErbB2 lrgqecveecrvlqglpreyvnar--------hclpchpecqpqn-gsvtcfgp-eadqc
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2 3 3 4 4 4 4
IGF1R VACRHYYYAGVCVPACPPNTYRF-------------EGW-----RC CHPECLGSCSA
IGF1R CPSGFIRN----------------GSQSMYCIPCEG
EGFR iqcahyidgphcvktcpagvmgenntl-vwkyadagh--------vchlchpnctygctg
ErbB2 vacahykdppfcvarcpsgvkpdlsympiwkfpdeeg--------acqpcpincthscvd
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ErbB4 tkcshfkdgpncvekcpdglqgan--sfifkyadpdr--------echpchpnctqgcng
5 5 6 6 7 7 7
IGF1R PDNDTAC
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7

Figure 3

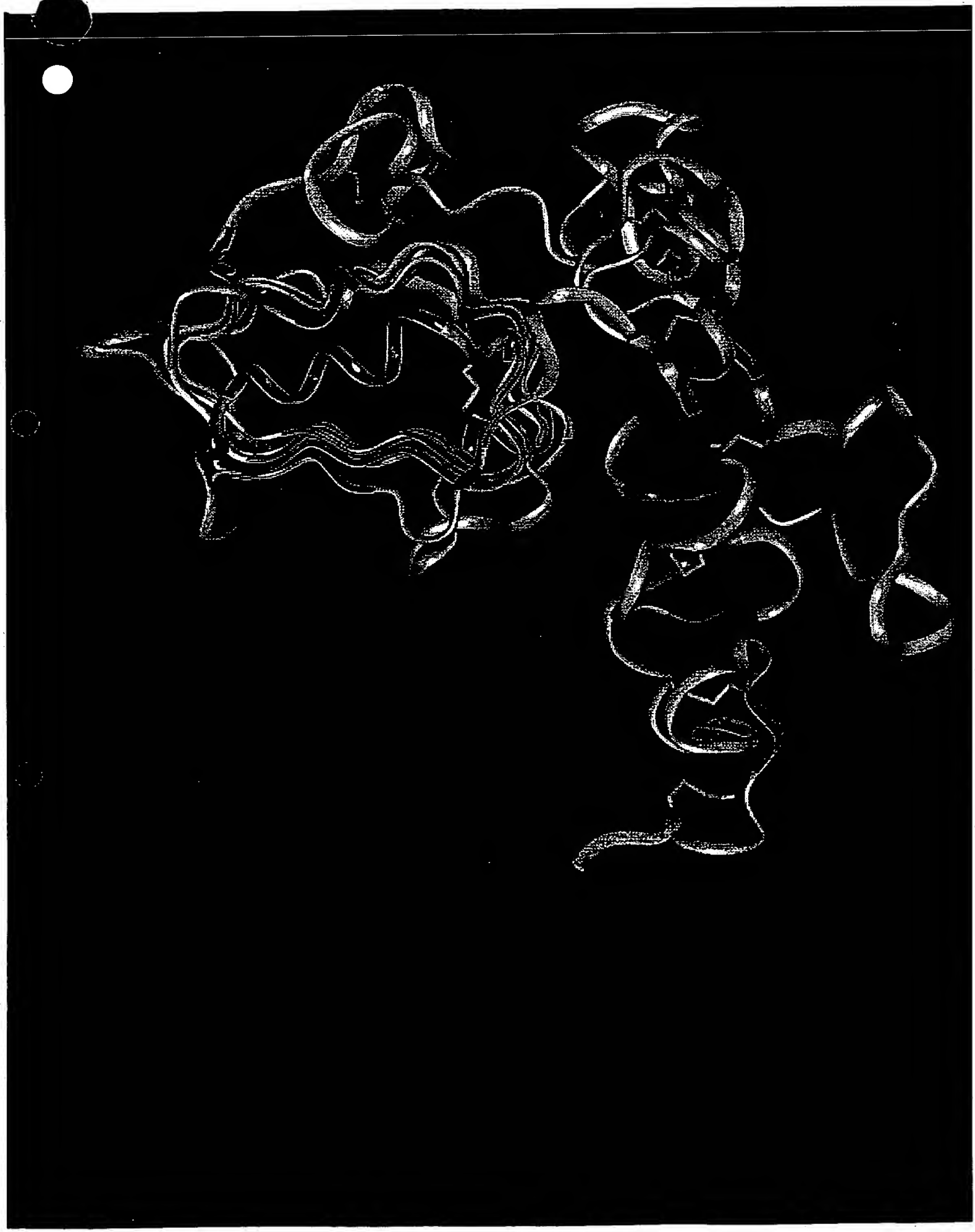

Figure 4

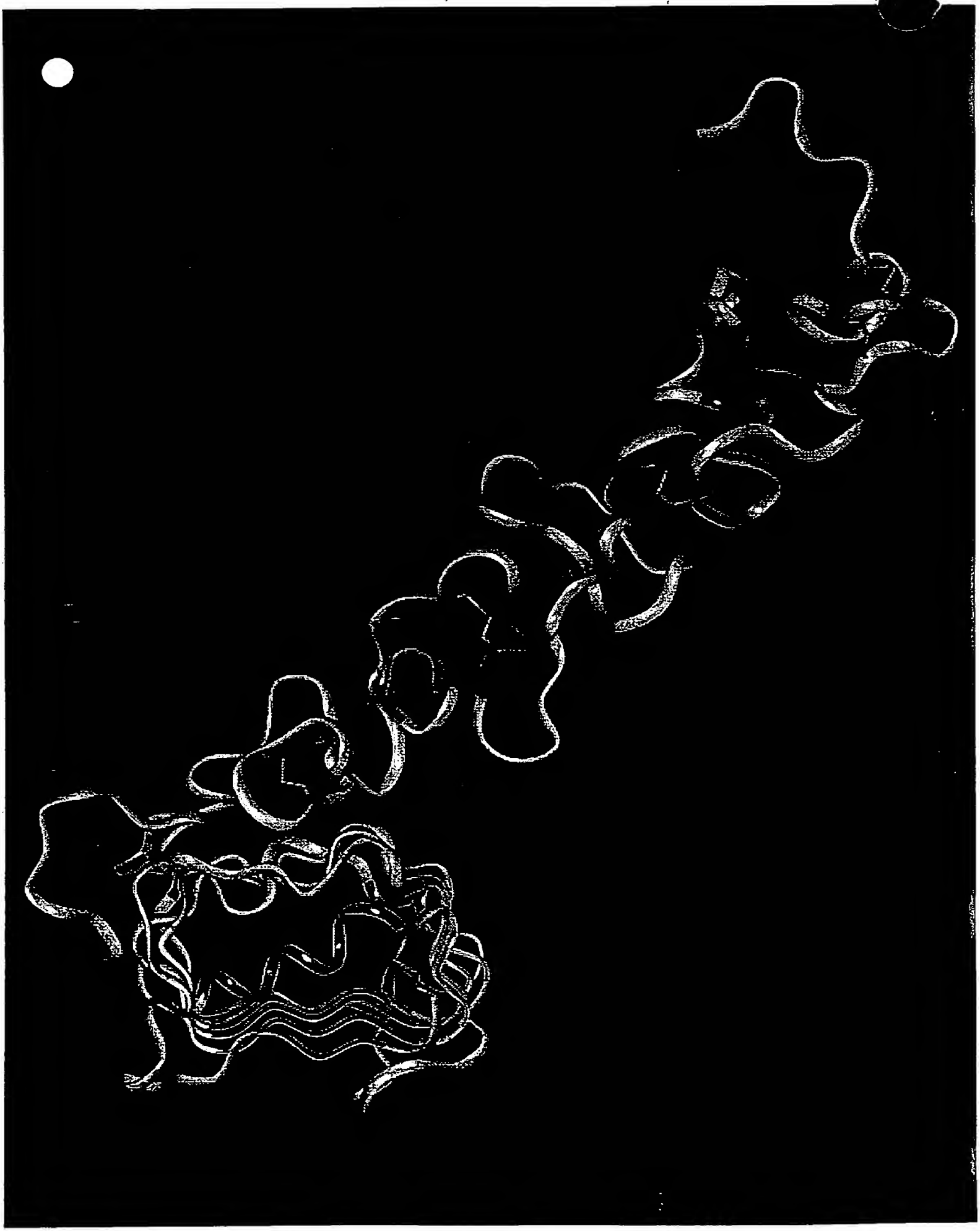

Figure 5

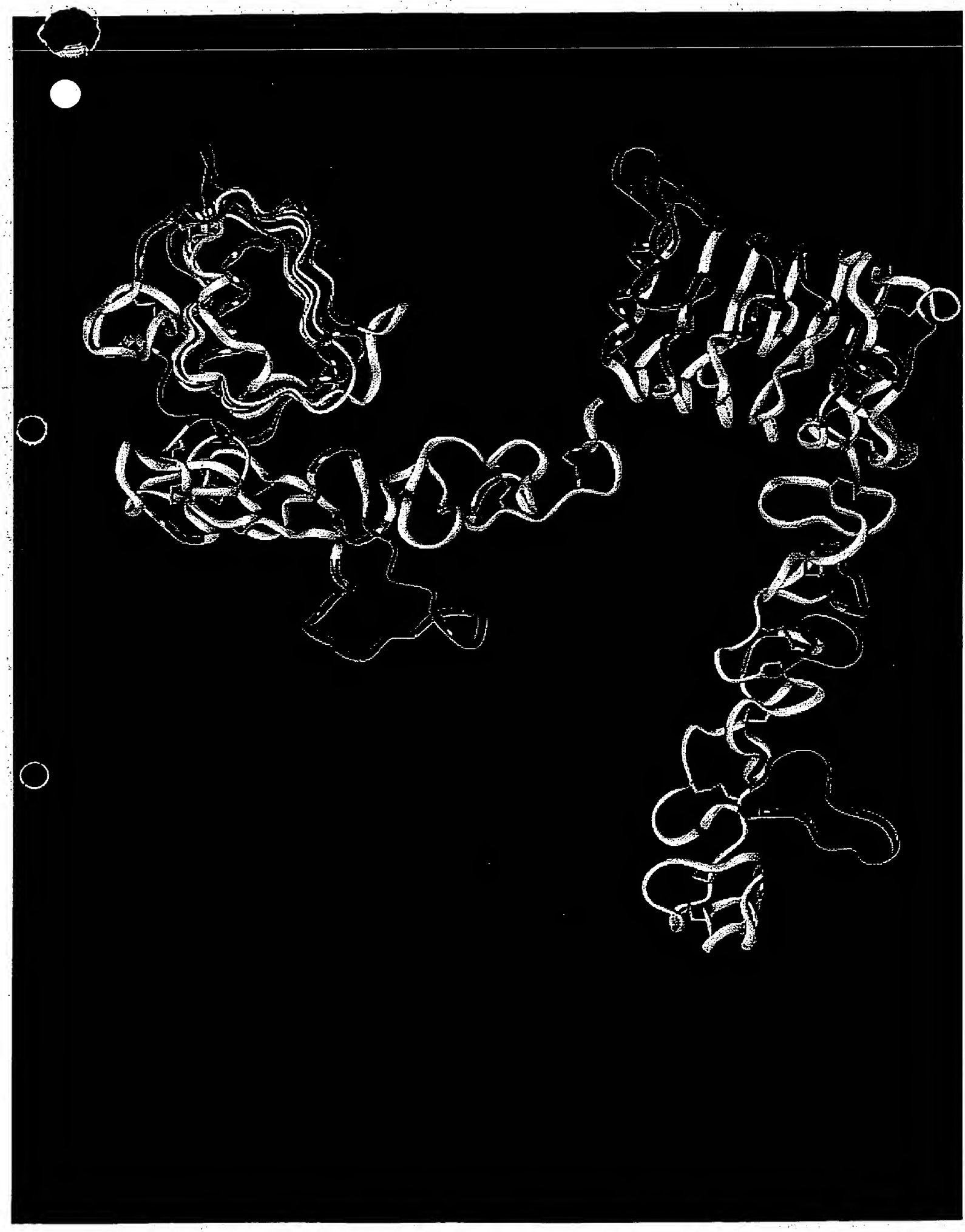

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Figure 6

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ATOM	96	CG2	THR	10	48.875	22.586	52.440	1.00	40.00
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ATOM	118	N	LYS	13	46.993	14.364	51.749	1.00	40.00
ATOM	120	CA	LYS	13	46.144	13.421	51.104	1.00	40.00
ATOM	121	CB	LYS	13	45.416	14.008	49.884	1.00	40.00
ATOM	122	CG	LYS	13	46.363	14.573	48.825	1.00	40.00
ATOM	123	CD	LYS	13	45.675	14.921	47.505	1.00	40.00
ATOM	124	CE	LYS	13	46.617	15.551	46.477	1.00	40.00
ATOM	125	NZ	LYS	13	45.877	15.863	45.233	1.00	40.00
ATOM	129	C	LYS	13	46.913	12.234	50.648	1.00	40.00
ATOM	130	O	LYS	13	47.735	12.310	49.737	1.00	40.00
ATOM	131	N	LEU	14	46.652	11.096	51.310	1.00	40.00
ATOM	133	CA	LEU	14	47.211	9.852	50.895	1.00	40.00
ATOM	134	CB	LEU	14	46.976	8.748	51.947	1.00	40.00
ATOM	135	CG	LEU	14	47.540	7.360	51.598	1.00	40.00
ATOM	136	CD1	LEU	14	46.871	6.739	50.371	1.00	40.00
ATOM	137	CD2	LEU	14	49.076	7.413	51.504	1.00	40.00
ATOM	138	C	LEU	14	46.341	9.560	49.715	1.00	40.00
ATOM	139	O	LEU	14	45.124	9.706	49.797	1.00	40.00
ATOM	140	N	THR	15	46.926	9.175	48.565	1.00	20.00
ATOM	142	CA	THR	15	46.046	8.932	47.460	1.00	20.00
ATOM	143	CB	THR	15	45.720	10.173	46.680	1.00	20.00
ATOM	144	OG1	THR	15	44.734	9.894	45.699	1.00	20.00
ATOM	146	CG2	THR	15	47.008	10.693	46.016	1.00	20.00
ATOM	147	C	THR	15	46.662	7.957	46.516	1.00	20.00
ATOM	148	O	THR	15	47.882	7.845	46.427	1.00	20.00
ATOM	149	N	GLN	16	45.812	7.213	45.784	1.00	20.00
ATOM	151	CA	GLN	16	46.308	6.267	44.830	1.00	20.00
ATOM	152	CB	GLN	16	45.194	5.417	44.193	1.00	20.00
ATOM	153	CG	GLN	16	45.677	4.384	43.166	1.00	20.00
ATOM	154	CD	GLN	16	45.903	5.076	41.826	1.00	20.00
ATOM	155	OE1	GLN	16	46.999	5.031	41.269	1.00	20.00
ATOM	156	NE2	GLN	16	44.838	5.737	41.296	1.00	20.00
ATOM	159	C	GLN	16	46.943	7.055	43.737	1.00	20.00
ATOM	160	O	GLN	16	48.054	6.749	43.312	1.00	20.00
ATOM	161	N	LEU	17	46.237	8.105	43.275	1.00	20.00
ATOM	163	CA	LEU	17	46.700	8.915	42.189	1.00	20.00
ATOM	164	CB	LEU	17	45.794	10.142	41.941	1.00	20.00
ATOM	165	CG	LEU	17	46.211	11.086	40.792	1.00	20.00

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ATOM    166  CD1 LEU    17      47.470  11.904  41.126  1.00 20.00
ATOM    167  CD2 LEU    17      46.324  10.326  39.462  1.00 20.00
ATOM    168  C   LEU    17      48.081   9.372  42.501  1.00 20.00
ATOM    169  O   LEU    17      48.436   9.591  43.657  1.00 20.00
ATOM    170  N   GLY    18      48.912   9.499  41.455  1.00 20.00
ATOM    172  CA  GLY    18      50.262   9.939  41.643  1.00 20.00
ATOM    173  C   GLY    18      51.057   9.374  40.516  1.00 20.00
ATOM    174  O   GLY    18      50.876   8.222  40.127  1.00 20.00
ATOM    175  N   THR    19      51.972  10.189  39.961  1.00 20.00
ATOM    177  CA  THR    19      52.782   9.709  38.886  1.00 20.00
ATOM    178  CB  THR    19      53.666  10.769  38.292  1.00 20.00
ATOM    179  OG1 THR    19      54.347  10.254  37.158  1.00 20.00
ATOM    181  CG2 THR    19      54.670  11.258  39.347  1.00 20.00
ATOM    182  C   THR    19      53.635   8.619  39.436  1.00 20.00
ATOM    183  O   THR    19      53.833   7.588  38.796  1.00 20.00
ATOM    184  N   PHE    20      54.148   8.817  40.664  1.00 20.00
ATOM    186  CA  PHE    20      54.987   7.834  41.278  1.00 20.00
ATOM    187  CB  PHE    20      55.635   8.347  42.579  1.00 20.00
ATOM    188  CG  PHE    20      56.659   7.367  43.040  1.00 20.00
ATOM    189  CD1 PHE    20      57.923   7.381  42.496  1.00 20.00
ATOM    190  CD2 PHE    20      56.398   6.515  44.089  1.00 20.00
ATOM    191  CE1 PHE    20      58.900   6.537  42.967  1.00 20.00
ATOM    192  CE2 PHE    20      57.373   5.673  44.569  1.00 20.00
ATOM    193  CZ  PHE    20      58.627   5.682  44.007  1.00 20.00
ATOM    194  C   PHE    20      54.090   6.693  41.619  1.00 20.00
ATOM    195  O   PHE    20      52.871   6.793  41.490  1.00 20.00
ATOM    196  N   GLU    21      54.671   5.558  42.047  1.00 20.00
ATOM    198  CA  GLU    21      53.833   4.450  42.396  1.00 20.00
ATOM    199  CB  GLU    21      54.593   3.121  42.541  1.00 20.00
ATOM    200  CG  GLU    21      55.122   2.564  41.219  1.00 20.00
ATOM    201  CD  GLU    21      55.844   1.259  41.522  1.00 20.00
ATOM    202  OE1 GLU    21      56.277   0.584  40.550  1.00 20.00
ATOM    203  OE2 GLU    21      55.970   0.918  42.729  1.00 20.00
ATOM    204  C   GLU    21      53.254   4.782  43.725  1.00 20.00
ATOM    205  O   GLU    21      53.828   4.458  44.764  1.00 20.00
ATOM    206  N   ASP    22      52.087   5.454  43.721  1.00 20.00
ATOM    208  CA  ASP    22      51.483   5.831  44.961  1.00 20.00
ATOM    209  CB  ASP    22      50.885   7.248  44.940  1.00 20.00
ATOM    210  CG  ASP    22      50.624   7.676  46.376  1.00 20.00
ATOM    211  OD1 ASP    22      50.950   8.847  46.707  1.00 20.00
ATOM    212  OD2 ASP    22      50.091   6.845  47.159  1.00 20.00
ATOM    213  C   ASP    22      50.379   4.864  45.231  1.00 20.00
ATOM    214  O   ASP    22      49.567   4.565  44.357  1.00 20.00
ATOM    215  N   HIS    23      50.341   4.335  46.467  1.00 40.00
ATOM    217  CA  HIS    23      49.347   3.384  46.853  1.00 40.00
ATOM    218  CB  HIS    23      49.761   1.915  46.649  1.00 40.00
ATOM    219  CG  HIS    23      49.838   1.473  45.220  1.00 40.00
ATOM    220  CD2 HIS    23      50.917   1.323  44.403  1.00 40.00
ATOM    221  ND1 HIS    23      48.750   1.052  44.486  1.00 40.00
ATOM    223  CE1 HIS    23      49.222   0.673  43.271  1.00 40.00
ATOM    224  NE2 HIS    23      50.530   0.820  43.174  1.00 40.00
ATOM    226  C   HIS    23      49.165   3.538  48.323  1.00 40.00
ATOM    227  O   HIS    23      49.412   4.596  48.899  1.00 40.00
ATOM    228  N   PHE    24      48.700   2.447  48.952  1.00 40.00
ATOM    230  CA  PHE    24      48.497   2.366  50.365  1.00 40.00
ATOM    231  CB  PHE    24      47.878   1.032  50.798  1.00 40.00
ATOM    232  CG  PHE    24      47.619   1.074  52.265  1.00 40.00
ATOM    233  CD1 PHE    24      46.418   1.545  52.742  1.00 40.00
ATOM    234  CD2 PHE    24      48.565   0.632  53.162  1.00 40.00
ATOM    235  CE1 PHE    24      46.157   1.564  54.092  1.00 40.00
ATOM    236  CE2 PHE    24      48.312   0.655  54.513  1.00 40.00
ATOM    237  CZ  PHE    24      47.105   1.118  54.981  1.00 40.00
ATOM    238  C   PHE    24      49.858   2.476  50.972  1.00 40.00
ATOM    239  O   PHE    24      50.016   2.876  52.124  1.00 40.00
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A[illegible]	554	C	LEU	55	48.807	3.909	63.695	1.00	40.00
ATOM	555	O	LEU	55	47.740	4.362	64.108	1.00	40.00
ATOM	556	N	LYS	56	49.696	3.297	64.498	1.00	40.00
[illegible]M	558	CA	LYS	56	49.497	3.101	65.901	1.00	40.00
ATOM	559	CB	LYS	56	50.576	2.185	66.506	1.00	40.00
ATOM	560	CG	LYS	56	50.417	1.939	68.008	1.00	40.00
ATOM	561	CD	LYS	56	51.365	0.867	68.554	1.00	40.00
ATOM	562	CE	LYS	56	52.806	1.355	68.725	1.00	40.00
ATOM	563	NZ	LYS	56	53.656	0.266	69.255	1.00	40.00
ATOM	567	C	LYS	56	49.574	4.403	66.636	1.00	40.00
ATOM	568	O	LYS	56	48.753	4.684	67.506	1.00	40.00
ATOM	569	N	THR	57	50.566	5.235	66.273	1.00	20.00
ATOM	571	CA	THR	57	50.892	6.456	66.958	1.00	20.00
ATOM	572	CB	THR	57	52.151	7.079	66.433	1.00	20.00
ATOM	573	OG1	THR	57	52.558	8.147	67.275	1.00	20.00
ATOM	575	CG2	THR	57	51.890	7.590	65.006	1.00	20.00
ATOM	576	C	THR	57	49.837	7.520	66.919	1.00	20.00
ATOM	577	O	THR	57	49.634	8.217	67.911	1.00	20.00
ATOM	578	N	ILE	58	49.134	7.669	65.781	1.00	20.00
ATOM	580	CA	ILE	58	48.202	8.749	65.585	1.00	20.00
ATOM	581	CB	ILE	58	47.381	8.578	64.339	1.00	20.00
ATOM	582	CG2	ILE	58	46.356	9.724	64.289	1.00	20.00
ATOM	583	CG1	ILE	58	48.286	8.508	63.097	1.00	20.00
ATOM	584	CD1	ILE	58	49.117	9.770	62.877	1.00	20.00
ATOM	585	C	ILE	58	47.233	8.931	66.716	1.00	20.00
ATOM	586	O	ILE	58	46.204	8.260	66.774	1.00	20.00
ATOM	587	N	GLN	59	47.579	9.822	67.672	1.00	20.00
ATOM	589	CA	GLN	59	46.734	10.199	68.773	1.00	20.00
ATOM	590	CB	GLN	59	47.517	10.863	69.915	1.00	20.00
ATOM	591	CG	GLN	59	48.143	12.195	69.501	1.00	20.00
ATOM	592	CD	GLN	59	48.757	12.832	70.736	1.00	20.00
ATOM	593	OE1	GLN	59	49.685	12.297	71.340	1.00	20.00
ATOM	594	NE2	GLN	59	48.215	14.014	71.129	1.00	20.00
ATOM	597	C	GLN	59	45.679	11.189	68.377	1.00	20.00
ATOM	598	O	GLN	59	44.530	11.095	68.808	1.00	20.00
ATOM	599	N	GLU	60	46.048	12.190	67.550	1.00	20.00
ATOM	601	CA	GLU	60	45.095	13.224	67.262	1.00	20.00
ATOM	602	CB	GLU	60	45.290	14.461	68.155	1.00	20.00
ATOM	603	CG	GLU	60	44.250	15.563	67.946	1.00	20.00
ATOM	604	CD	GLU	60	44.647	16.742	68.822	1.00	20.00
ATOM	605	OE1	GLU	60	43.756	17.283	69.530	1.00	20.00
ATOM	606	OE2	GLU	60	45.848	17.123	68.787	1.00	20.00
ATOM	607	C	GLU	60	45.206	13.695	65.848	1.00	20.00
ATOM	608	O	GLU	60	46.181	13.420	65.153	1.00	20.00
ATOM	609	N	VAL	61	44.145	14.383	65.381	1.00	20.00
ATOM	611	CA	VAL	61	44.109	15.031	64.104	1.00	20.00
ATOM	612	CB	VAL	61	43.283	14.315	63.069	1.00	20.00
ATOM	613	CG1	VAL	61	41.843	14.146	63.582	1.00	20.00
ATOM	614	CG2	VAL	61	43.376	15.105	61.752	1.00	20.00
ATOM	615	C	VAL	61	43.469	16.347	64.419	1.00	20.00
ATOM	616	O	VAL	61	42.399	16.407	65.018	1.00	20.00
ATOM	617	N	ALA	62	44.133	17.447	64.037	1.00	20.00
ATOM	619	CA	ALA	62	43.683	18.774	64.335	1.00	20.00
ATOM	620	CB	ALA	62	44.789	19.827	64.147	1.00	20.00
ATOM	621	C	ALA	62	42.528	19.201	63.488	1.00	20.00
ATOM	622	O	ALA	62	42.002	20.294	63.685	1.00	20.00
ATOM	623	N	GLY	63	42.161	18.409	62.461	1.00	20.00
ATOM	625	CA	GLY	63	41.087	18.809	61.595	1.00	20.00
ATOM	626	C	GLY	63	40.025	17.758	61.501	1.00	20.00
ATOM	627	O	GLY	63	39.332	17.458	62.470	1.00	20.00
ATOM	628	N	TYR	64	39.856	17.187	60.289	1.00	20.00
ATOM	630	CA	TYR	64	38.849	16.189	60.073	1.00	20.00
ATOM	631	CB	TYR	64	37.728	16.639	59.114	1.00	20.00
ATOM	632	CG	TYR	64	38.295	16.800	57.741	1.00	20.00

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ATOM    633  CD1 TYR    64      38.320  15.737  56.867  1.00 20.00
ATOM    634  CE1 TYR    64      38.835  15.874  55.599  1.00 20.00
ATOM    635  CD2 TYR    64      38.791  18.013  57.320  1.00 20.00
  ?M    636  CE2 TYR    64      39.310  18.157  56.054  1.00 20.00
...OM   637  CZ  TYR    64      39.335  17.086  55.193  1.00 20.00
ATOM    638  OH  TYR    64      39.880  17.228  53.899  1.00 20.00
ATOM    640  C   TYR    64      39.501  14.990  59.462  1.00 20.00
ATOM    641  O   TYR    64      40.654  15.050  59.040  1.00 20.00
ATOM    642  N   VAL    65      38.779  13.849  59.438  1.00 20.00
ATOM    644  CA  VAL    65      39.311  12.653  58.845  1.00 20.00
ATOM    645  CB  VAL    65      39.362  11.494  59.793  1.00 20.00
ATOM    646  CG1 VAL    65      39.871  10.259  59.032  1.00 20.00
ATOM    647  CG2 VAL    65      40.235  11.888  60.997  1.00 20.00
ATOM    648  C   VAL    65      38.415  12.249  57.708  1.00 20.00
ATOM    649  O   VAL    65      37.194  12.259  57.835  1.00 20.00
ATOM    650  N   LEU    66      39.004  11.884  56.549  1.00 20.00
ATOM    652  CA  LEU    66      38.207  11.501  55.412  1.00 20.00
ATOM    653  CB  LEU    66      38.272  12.530  54.268  1.00 20.00
ATOM    654  CG  LEU    66      37.431  12.161  53.034  1.00 20.00
ATOM    655  CD1 LEU    66      35.934  12.089  53.374  1.00 20.00
ATOM    656  CD2 LEU    66      37.726  13.110  51.858  1.00 20.00
ATOM    657  C   LEU    66      38.691  10.186  54.867  1.00 20.00
ATOM    658  O   LEU    66      39.892   9.925  54.848  1.00 20.00
ATOM    659  N   ILE    67      37.758   9.312  54.410  1.00 20.00
ATOM    661  CA  ILE    67      38.160   8.028  53.887  1.00 20.00
ATOM    662  CB  ILE    67      38.248   6.965  54.942  1.00 20.00
ATOM    663  CG2 ILE    67      39.328   7.382  55.955  1.00 20.00
ATOM    664  CG1 ILE    67      36.866   6.722  55.570  1.00 20.00
ATOM    665  CD1 ILE    67      36.803   5.463  56.434  1.00 20.00
ATOM    666  C   ILE    67      37.214   7.495  52.835  1.00 20.00
ATOM    667  O   ILE    67      36.047   7.879  52.768  1.00 20.00
ATOM    668  N   ALA    68      37.738   6.584  51.975  1.00 40.00
ATOM    670  CA  ALA    68      37.034   5.902  50.920  1.00 40.00
ATOM    671  CB  ALA    68      36.603   6.825  49.767  1.00 40.00
ATOM    672  C   ALA    68      38.026   4.927  50.364  1.00 40.00
ATOM    673  O   ALA    68      38.926   5.308  49.616  1.00 40.00
ATOM    674  N   LEU    69      37.895   3.634  50.721  1.00 40.00
ATOM    676  CA  LEU    69      38.868   2.675  50.282  1.00 40.00
ATOM    677  CB  LEU    69      39.908   2.322  51.360  1.00 40.00
ATOM    678  CG  LEU    69      40.796   3.485  51.840  1.00 40.00
ATOM    679  CD1 LEU    69      39.979   4.582  52.541  1.00 40.00
ATOM    680  CD2 LEU    69      41.929   2.963  52.738  1.00 40.00
ATOM    681  C   LEU    69      38.173   1.386  49.995  1.00 40.00
ATOM    682  O   LEU    69      36.949   1.285  50.065  1.00 40.00
ATOM    683  N   ASN    70      38.970   0.364  49.626  1.00 20.00
ATOM    685  CA  ASN    70      38.448  -0.949  49.395  1.00 20.00
ATOM    686  CB  ASN    70      38.493  -1.389  47.922  1.00 20.00
ATOM    687  CG  ASN    70      37.404  -0.633  47.175  1.00 20.00
ATOM    688  OD1 ASN    70      36.218  -0.806  47.450  1.00 20.00
ATOM    689  ND2 ASN    70      37.813   0.230  46.207  1.00 20.00
ATOM    692  C   ASN    70      39.314  -1.885  50.172  1.00 20.00
ATOM    693  O   ASN    70      40.387  -1.505  50.640  1.00 20.00
ATOM    694  N   THR    71      38.830  -3.132  50.348  1.00 20.00
ATOM    696  CA  THR    71      39.493  -4.195  51.056  1.00 20.00
ATOM    697  CB  THR    71      40.639  -4.813  50.298  1.00 20.00
ATOM    698  OG1 THR    71      41.089  -5.980  50.970  1.00 20.00
ATOM    700  CG2 THR    71      41.786  -3.803  50.147  1.00 20.00
ATOM    701  C   THR    71      39.925  -3.813  52.440  1.00 20.00
ATOM    702  O   THR    71      40.538  -4.614  53.145  1.00 20.00
ATOM    703  N   VAL    72      39.580  -2.590  52.888  1.00 20.00
ATOM    705  CA  VAL    72      39.932  -2.171  54.215  1.00 20.00
ATOM    706  CB  VAL    72      40.149  -0.691  54.328  1.00 20.00
ATOM    707  CG1 VAL    72      40.470  -0.349  55.792  1.00 20.00
ATOM    708  CG2 VAL    72      41.247  -0.280  53.333  1.00 20.00
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ATOM	709	C	VAL	72	38.758	-2.514	55.074	1.00	20.00
ATOM	710	O	VAL	72	37.671	-1.965	54.911	1.00	20.00
ATOM	711	N	GLU	73	38.955	-3.480	55.988	1.00	20.00
ATOM	713	CA	GLU	73	37.923	-3.967	56.856	1.00	20.00
ATOM	714	CB	GLU	73	38.349	-5.279	57.534	1.00	20.00
ATOM	715	CG	GLU	73	38.561	-6.403	56.516	1.00	20.00
ATOM	716	CD	GLU	73	39.076	-7.630	57.251	1.00	20.00
ATOM	717	OE1	GLU	73	39.263	-7.542	58.493	1.00	20.00
ATOM	718	OE2	GLU	73	39.289	-8.674	56.578	1.00	20.00
ATOM	719	C	GLU	73	37.499	-3.001	57.921	1.00	20.00
ATOM	720	O	GLU	73	36.306	-2.829	58.162	1.00	20.00
ATOM	721	N	ARG	74	38.454	-2.328	58.590	1.00	20.00
ATOM	723	CA	ARG	74	38.077	-1.471	59.680	1.00	20.00
ATOM	724	CB	ARG	74	38.258	-2.160	61.043	1.00	20.00
ATOM	725	CG	ARG	74	37.398	-3.418	61.198	1.00	20.00
ATOM	726	CD	ARG	74	37.779	-4.286	62.399	1.00	20.00
ATOM	727	NE	ARG	74	39.121	-4.874	62.119	1.00	20.00
ATOM	729	CZ	ARG	74	40.196	-4.529	62.887	1.00	20.00
ATOM	730	NH1	ARG	74	40.047	-3.644	63.915	1.00	20.00
ATOM	733	NH2	ARG	74	41.422	-5.075	62.631	1.00	20.00
ATOM	736	C	ARG	74	38.988	-0.290	59.663	1.00	20.00
ATOM	737	O	ARG	74	39.927	-0.235	58.875	1.00	20.00
ATOM	738	N	ILE	75	38.743	0.708	60.536	1.00	20.00
ATOM	740	CA	ILE	75	39.646	1.827	60.611	1.00	20.00
ATOM	741	CB	ILE	75	38.942	3.150	60.486	1.00	20.00
ATOM	742	CG2	ILE	75	39.993	4.273	60.555	1.00	20.00
ATOM	743	CG1	ILE	75	38.138	3.193	59.175	1.00	20.00
ATOM	744	CD1	ILE	75	39.003	3.053	57.923	1.00	20.00
ATOM	745	C	ILE	75	40.260	1.740	61.980	1.00	20.00
ATOM	746	O	ILE	75	40.265	2.684	62.765	1.00	20.00
ATOM	747	N	PRO	76	40.856	0.609	62.211	1.00	20.00
ATOM	748	CD	PRO	76	41.577	-0.084	61.161	1.00	20.00
ATOM	749	CA	PRO	76	41.328	0.159	63.486	1.00	20.00
ATOM	750	CB	PRO	76	41.810	-1.276	63.244	1.00	20.00
ATOM	751	CG	PRO	76	41.661	-1.506	61.724	1.00	20.00
ATOM	752	C	PRO	76	42.464	0.947	64.063	1.00	20.00
ATOM	753	O	PRO	76	43.009	0.430	65.036	1.00	20.00
ATOM	754	N	LEU	77	42.891	2.094	63.463	1.00	20.00
ATOM	756	CA	LEU	77	43.941	2.919	64.023	1.00	20.00
ATOM	757	CB	LEU	77	43.971	4.354	63.475	1.00	20.00
ATOM	758	CG	LEU	77	44.267	4.436	61.970	1.00	20.00
ATOM	759	CD1	LEU	77	43.148	3.768	61.153	1.00	20.00
ATOM	760	CD2	LEU	77	44.552	5.887	61.547	1.00	20.00
ATOM	761	C	LEU	77	43.653	3.019	65.485	1.00	20.00
ATOM	762	O	LEU	77	42.773	3.760	65.919	1.00	20.00
ATOM	763	N	GLU	78	44.422	2.245	66.273	1.00	20.00
ATOM	765	CA	GLU	78	44.154	2.030	67.661	1.00	20.00
ATOM	766	CB	GLU	78	45.215	1.126	68.313	1.00	20.00
ATOM	767	CG	GLU	78	45.162	-0.337	67.872	1.00	20.00
ATOM	768	CD	GLU	78	44.210	-1.063	68.810	1.00	20.00
ATOM	769	OE1	GLU	78	43.065	-0.569	68.991	1.00	20.00
ATOM	770	OE2	GLU	78	44.620	-2.117	69.367	1.00	20.00
ATOM	771	C	GLU	78	44.131	3.271	68.485	1.00	20.00
ATOM	772	O	GLU	78	43.173	3.510	69.214	1.00	20.00
ATOM	773	N	ASN	79	45.182	4.097	68.380	1.00	20.00
ATOM	775	CA	ASN	79	45.370	5.233	69.236	1.00	20.00
ATOM	776	CB	ASN	79	46.830	5.720	69.251	1.00	20.00
ATOM	777	CG	ASN	79	47.647	4.686	70.016	1.00	20.00
ATOM	778	OD1	ASN	79	48.858	4.827	70.181	1.00	20.00
ATOM	779	ND2	ASN	79	46.968	3.609	70.494	1.00	20.00
ATOM	782	C	ASN	79	44.505	6.442	69.057	1.00	20.00
ATOM	783	O	ASN	79	44.285	7.157	70.033	1.00	20.00
ATOM	784	N	LEU	80	44.011	6.718	67.831	1.00	20.00
ATOM	786	CA	LEU	80	43.334	7.957	67.532	1.00	20.00

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ATOM    787  CB  LEU    80      42.657   7.950  66.151  1.00 20.00
ATOM    788  CG  LEU    80      42.050   9.307  65.757  1.00 20.00
ATOM    789  CD1 LEU    80      43.147  10.376  65.627  1.00 20.00
ATOM    790  CD2 LEU    80      41.188   9.195  64.492  1.00 20.00
ATOM    791  C   LEU    80      42.315   8.342  68.565  1.00 20.00
ATOM    792  O   LEU    80      41.225   7.776  68.629  1.00 20.00
ATOM    793  N   GLN    81      42.728   9.271  69.461  1.00 20.00
ATOM    795  CA  GLN    81      41.964   9.831  70.544  1.00 20.00
ATOM    796  CB  GLN    81      42.877  10.381  71.654  1.00 20.00
ATOM    797  CG  GLN    81      43.812   9.339  72.267  1.00 20.00
ATOM    798  CD  GLN    81      42.971   8.360  73.071  1.00 20.00
ATOM    799  OE1 GLN    81      41.955   8.730  73.659  1.00 20.00
ATOM    800  NE2 GLN    81      43.406   7.072  73.096  1.00 20.00
ATOM    803  C   GLN    81      40.993  10.945  70.241  1.00 20.00
ATOM    804  O   GLN    81      39.869  10.940  70.741  1.00 20.00
ATOM    805  N   ILE    82      41.401  11.959  69.443  1.00 20.00
ATOM    807  CA  ILE    82      40.535  13.097  69.267  1.00 20.00
ATOM    808  CB  ILE    82      40.842  14.181  70.259  1.00 20.00
ATOM    809  CG2 ILE    82      39.994  15.403  69.898  1.00 20.00
ATOM    810  CG1 ILE    82      40.626  13.682  71.699  1.00 20.00
ATOM    811  CD1 ILE    82      39.183  13.280  72.002  1.00 20.00
ATOM    812  C   ILE    82      40.686  13.698  67.897  1.00 20.00
ATOM    813  O   ILE    82      41.764  13.658  67.307  1.00 20.00
ATOM    814  N   ILE    83      39.580  14.259  67.352  1.00 20.00
ATOM    816  CA  ILE    83      39.588  14.935  66.082  1.00 20.00
ATOM    817  CB  ILE    83      38.670  14.293  65.081  1.00 20.00
ATOM    818  CG2 ILE    83      38.638  15.171  63.821  1.00 20.00
ATOM    819  CG1 ILE    83      39.099  12.841  64.812  1.00 20.00
ATOM    820  CD1 ILE    83      38.048  12.026  64.060  1.00 20.00
ATOM    821  C   ILE    83      39.032  16.298  66.376  1.00 20.00
ATOM    822  O   ILE    83      37.822  16.488  66.434  1.00 20.00
ATOM    823  N   ARG    84      39.907  17.309  66.484  1.00 20.00
ATOM    825  CA  ARG    84      39.536  18.627  66.922  1.00 20.00
ATOM    826  CB  ARG    84      40.749  19.570  66.962  1.00 20.00
ATOM    827  CG  ARG    84      41.796  19.151  67.993  1.00 20.00
ATOM    828  CD  ARG    84      43.065  20.005  67.955  1.00 20.00
ATOM    829  NE  ARG    84      42.674  21.408  68.266  1.00 20.00
ATOM    831  CZ  ARG    84      42.606  21.830  69.563  1.00 20.00
ATOM    832  NH1 ARG    84      42.894  20.965  70.579  1.00 20.00
ATOM    835  NH2 ARG    84      42.252  23.118  69.842  1.00 20.00
ATOM    838  C   ARG    84      38.485  19.300  66.091  1.00 20.00
ATOM    839  O   ARG    84      37.694  20.079  66.618  1.00 20.00
ATOM    840  N   GLY    85      38.462  19.077  64.768  1.00 20.00
ATOM    842  CA  GLY    85      37.451  19.713  63.971  1.00 20.00
ATOM    843  C   GLY    85      37.729  21.178  63.827  1.00 20.00
ATOM    844  O   GLY    85      36.814  21.971  63.607  1.00 20.00
ATOM    845  N   ASN    86      39.009  21.579  63.922  1.00 20.00
ATOM    847  CA  ASN    86      39.344  22.971  63.806  1.00 20.00
ATOM    848  CB  ASN    86      40.860  23.225  63.837  1.00 20.00
ATOM    849  CG  ASN    86      41.372  22.841  65.216  1.00 20.00
ATOM    850  OD1 ASN    86      40.593  22.557  66.124  1.00 20.00
ATOM    851  ND2 ASN    86      42.722  22.838  65.381  1.00 20.00
ATOM    854  C   ASN    86      38.845  23.418  62.473  1.00 20.00
ATOM    855  O   ASN    86      38.279  24.503  62.339  1.00 20.00
ATOM    856  N   MET    87      39.054  22.584  61.441  1.00 20.00
ATOM    858  CA  MET    87      38.530  22.905  60.148  1.00 20.00
ATOM    859  CB  MET    87      39.596  23.081  59.054  1.00 20.00
ATOM    860  CG  MET    87      40.482  21.853  58.857  1.00 20.00
ATOM    861  SD  MET    87      41.713  21.605  60.170  1.00 20.00
ATOM    862  CE  MET    87      42.788  22.960  59.615  1.00 20.00
ATOM    863  C   MET    87      37.681  21.741  59.775  1.00 20.00
ATOM    864  O   MET    87      38.064  20.591  59.980  1.00 20.00
ATOM    865  N   TYR    88      36.497  22.022  59.204  1.00 20.00
ATOM    867  CA  TYR    88      35.560  20.985  58.901  1.00 20.00
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A[illegible]	868	CB	TYR	88	34.142	21.317	59.393	1.00	20.00
ATOM	869	CG	TYR	88	33.731	22.569	58.691	1.00	20.00
ATOM	870	CD1	TYR	88	34.124	23.798	59.169	1.00	20.00
[illegible]M	871	CE1	TYR	88	33.792	24.953	58.499	1.00	20.00
ATOM	872	CD2	TYR	88	32.989	22.515	57.532	1.00	20.00
ATOM	873	CE2	TYR	88	32.653	23.666	56.858	1.00	20.00
ATOM	874	CZ	TYR	88	33.059	24.887	57.339	1.00	20.00
ATOM	875	OH	TYR	88	32.726	26.069	56.643	1.00	20.00
ATOM	877	C	TYR	88	35.452	20.773	57.431	1.00	20.00
ATOM	878	O	TYR	88	35.783	21.643	56.625	1.00	20.00
ATOM	879	N	TYR	89	34.990	19.565	57.059	1.00	20.00
ATOM	881	CA	TYR	89	34.771	19.226	55.689	1.00	20.00
ATOM	882	CB	TYR	89	34.865	17.713	55.436	1.00	20.00
ATOM	883	CG	TYR	89	34.869	17.477	53.966	1.00	20.00
ATOM	884	CD1	TYR	89	36.035	17.628	53.253	1.00	20.00
ATOM	885	CE1	TYR	89	36.078	17.349	51.908	1.00	20.00
ATOM	886	CD2	TYR	89	33.745	17.019	53.320	1.00	20.00
ATOM	887	CE2	TYR	89	33.781	16.737	51.975	1.00	20.00
ATOM	888	CZ	TYR	89	34.949	16.901	51.269	1.00	20.00
ATOM	889	OH	TYR	89	34.989	16.606	49.890	1.00	20.00
ATOM	891	C	TYR	89	33.357	19.658	55.493	1.00	20.00
ATOM	892	O	TYR	89	32.594	19.687	56.458	1.00	20.00
ATOM	893	N	GLU	90	32.995	20.007	54.240	1.00	20.00
ATOM	895	CA	GLU	90	31.712	20.544	53.872	1.00	20.00
ATOM	896	CB	GLU	90	31.383	20.403	52.373	1.00	20.00
ATOM	897	CG	GLU	90	32.243	21.273	51.449	1.00	20.00
ATOM	898	CD	GLU	90	33.488	20.498	51.031	1.00	20.00
ATOM	899	OE1	GLU	90	33.999	19.684	51.845	1.00	20.00
ATOM	900	OE2	GLU	90	33.942	20.710	49.875	1.00	20.00
ATOM	901	C	GLU	90	30.596	19.920	54.637	1.00	20.00
ATOM	902	O	GLU	90	30.669	18.760	55.034	1.00	20.00
ATOM	903	N	ASN	91	29.540	20.711	54.890	1.00	20.00
ATOM	905	CA	ASN	91	28.425	20.266	55.671	1.00	20.00
ATOM	906	CB	ASN	91	27.743	19.004	55.118	1.00	20.00
ATOM	907	CG	ASN	91	26.376	18.884	55.782	1.00	20.00
ATOM	908	OD1	ASN	91	26.067	19.584	56.745	1.00	20.00
ATOM	909	ND2	ASN	91	25.526	17.968	55.247	1.00	20.00
ATOM	912	C	ASN	91	28.955	19.976	57.037	1.00	20.00
ATOM	913	O	ASN	91	28.340	19.265	57.830	1.00	20.00
ATOM	914	N	SER	92	30.120	20.575	57.343	1.00	20.00
ATOM	916	CA	SER	92	30.775	20.462	58.611	1.00	20.00
ATOM	917	CB	SER	92	30.121	21.328	59.705	1.00	20.00
ATOM	918	OG	SER	92	28.804	20.867	59.972	1.00	20.00
ATOM	920	C	SER	92	30.861	19.058	59.117	1.00	20.00
ATOM	921	O	SER	92	30.223	18.715	60.111	1.00	20.00
ATOM	922	N	TYR	93	31.668	18.203	58.453	1.00	20.00
ATOM	924	CA	TYR	93	31.828	16.876	58.966	1.00	20.00
ATOM	925	CB	TYR	93	31.560	15.753	57.946	1.00	20.00
ATOM	926	CG	TYR	93	30.103	15.728	57.618	1.00	20.00
ATOM	927	CD1	TYR	93	29.612	16.358	56.497	1.00	20.00
ATOM	928	CE1	TYR	93	28.270	16.311	56.196	1.00	20.00
ATOM	929	CD2	TYR	93	29.220	15.080	58.452	1.00	20.00
ATOM	930	CE2	TYR	93	27.876	15.039	58.163	1.00	20.00
ATOM	931	CZ	TYR	93	27.400	15.650	57.028	1.00	20.00
ATOM	932	OH	TYR	93	26.023	15.603	56.722	1.00	20.00
ATOM	934	C	TYR	93	33.237	16.716	59.448	1.00	20.00
ATOM	935	O	TYR	93	34.195	17.026	58.744	1.00	20.00
ATOM	936	N	ALA	94	33.384	16.307	60.722	1.00	20.00
ATOM	938	CA	ALA	94	34.651	16.026	61.332	1.00	20.00
ATOM	939	CB	ALA	94	34.568	15.964	62.866	1.00	20.00
ATOM	940	C	ALA	94	35.172	14.706	60.866	1.00	20.00
ATOM	941	O	ALA	94	36.378	14.536	60.696	1.00	20.00
ATOM	942	N	LEU	95	34.266	13.724	60.696	1.00	20.00
ATOM	944	CA	LEU	95	34.661	12.411	60.279	1.00	20.00

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ATOM    945  CB  LEU    95      34.488  11.374  61.403  1.00 20.00
ATOM    946  CG  LEU    95      34.889   9.936  61.030  1.00 20.00
ATOM    947  CD1 LEU    95      36.389   9.831  60.704  1.00 20.00
  OM    948  CD2 LEU    95      34.445   8.947  62.122  1.00 20.00
...OM    949  C   LEU    95      33.775  12.005  59.148  1.00 20.00
ATOM    950  O   LEU    95      32.580  11.774  59.326  1.00 20.00
ATOM    951  N   ALA    96      34.344  11.901  57.934  1.00 20.00
ATOM    953  CA  ALA    96      33.529  11.501  56.828  1.00 20.00
ATOM    954  CB  ALA    96      33.592  12.471  55.636  1.00 20.00
ATOM    955  C   ALA    96      34.041  10.183  56.352  1.00 20.00
ATOM    956  O   ALA    96      35.222  10.053  56.040  1.00 20.00
ATOM    957  N   VAL    97      33.165   9.160  56.327  1.00 20.00
ATOM    959  CA  VAL    97      33.548   7.887  55.793  1.00 20.00
ATOM    960  CB  VAL    97      33.554   6.778  56.812  1.00 20.00
ATOM    961  CG1 VAL    97      34.698   7.057  57.803  1.00 20.00
ATOM    962  CG2 VAL    97      32.183   6.709  57.507  1.00 20.00
ATOM    963  C   VAL    97      32.560   7.591  54.706  1.00 20.00
ATOM    964  O   VAL    97      31.395   7.287  54.955  1.00 20.00
ATOM    965  N   LEU    98      33.010   7.671  53.443  1.00 20.00
ATOM    967  CA  LEU    98      32.089   7.495  52.359  1.00 20.00
ATOM    968  CB  LEU    98      32.012   8.718  51.428  1.00 20.00
ATOM    969  CG  LEU    98      31.150   8.489  50.171  1.00 20.00
ATOM    970  CD1 LEU    98      29.683   8.208  50.525  1.00 20.00
ATOM    971  CD2 LEU    98      31.312   9.645  49.170  1.00 20.00
ATOM    972  C   LEU    98      32.469   6.338  51.501  1.00 20.00
ATOM    973  O   LEU    98      33.649   6.086  51.273  1.00 20.00
ATOM    974  N   SER    99      31.427   5.622  51.017  1.00 20.00
ATOM    976  CA  SER    99      31.533   4.513  50.113  1.00 20.00
ATOM    977  CB  SER    99      31.565   4.948  48.637  1.00 20.00
ATOM    978  OG  SER    99      31.664   3.812  47.792  1.00 20.00
ATOM    980  C   SER    99      32.738   3.676  50.385  1.00 20.00
ATOM    981  O   SER    99      33.741   3.777  49.679  1.00 20.00
ATOM    982  N   ASN   100      32.683   2.847  51.441  1.00 40.00
ATOM    984  CA  ASN   100      33.796   1.990  51.716  1.00 40.00
ATOM    985  CB  ASN   100      34.171   1.941  53.206  1.00 40.00
ATOM    986  CG  ASN   100      34.709   3.304  53.612  1.00 40.00
ATOM    987  OD1 ASN   100      34.075   4.033  54.371  1.00 40.00
ATOM    988  ND2 ASN   100      35.912   3.661  53.088  1.00 40.00
ATOM    991  C   ASN   100      33.361   0.605  51.348  1.00 40.00
ATOM    992  O   ASN   100      32.801  -0.113  52.172  1.00 40.00
ATOM    993  N   TYR   101      33.630   0.186  50.097  1.00 40.00
ATOM    995  CA  TYR   101      33.219  -1.112  49.639  1.00 40.00
ATOM    996  CB  TYR   101      32.957  -1.200  48.122  1.00 40.00
ATOM    997  CG  TYR   101      31.781  -0.366  47.741  1.00 40.00
ATOM    998  CD1 TYR   101      30.502  -0.820  47.972  1.00 40.00
ATOM    999  CE1 TYR   101      29.415  -0.125  47.495  1.00 40.00
ATOM   1000  CD2 TYR   101      31.958   0.775  46.992  1.00 40.00
ATOM   1001  CE2 TYR   101      30.875   1.470  46.507  1.00 40.00
ATOM   1002  CZ  TYR   101      29.601   1.021  46.761  1.00 40.00
ATOM   1003  OH  TYR   101      28.489   1.723  46.251  1.00 40.00
ATOM   1005  C   TYR   101      34.312  -2.096  49.893  1.00 40.00
ATOM   1006  O   TYR   101      35.170  -1.894  50.752  1.00 40.00
ATOM   1007  N   ASP   102      34.256  -3.225  49.153  1.00 60.00
ATOM   1009  CA  ASP   102      35.256  -4.250  49.221  1.00 60.00
ATOM   1010  CB  ASP   102      34.979  -5.334  50.276  1.00 60.00
ATOM   1011  CG  ASP   102      36.283  -6.075  50.550  1.00 60.00
ATOM   1012  OD1 ASP   102      37.327  -5.662  49.979  1.00 60.00
ATOM   1013  OD2 ASP   102      36.252  -7.065  51.329  1.00 60.00
ATOM   1014  C   ASP   102      35.215  -4.938  47.893  1.00 60.00
ATOM   1015  O   ASP   102      34.499  -4.515  46.986  1.00 60.00
ATOM   1016  N   ALA   103      36.007  -6.017  47.742  1.00 60.00
ATOM   1018  CA  ALA   103      36.008  -6.756  46.516  1.00 60.00
ATOM   1019  CB  ALA   103      37.015  -7.919  46.523  1.00 60.00
ATOM   1020  C   ALA   103      34.647  -7.347  46.359  1.00 60.00
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ATOM   1021  O   ALA   103      34.025  -7.233  45.304  1.00 60.00
ATOM   1022  N   ASN   104      34.138  -7.984  47.430  1.00 60.00
ATOM   1024  CA  ASN   104      32.835  -8.569  47.350  1.00 60.00
ATOM   1025  CB  ASN   104      32.720  -9.946  48.030  1.00 60.00
ATOM   1026  CG  ASN   104      32.998  -9.784  49.516  1.00 60.00
ATOM   1027  OD1 ASN   104      32.112  -9.433  50.294  1.00 60.00
ATOM   1028  ND2 ASN   104      34.266 -10.058  49.926  1.00 60.00
ATOM   1031  C   ASN   104      31.884  -7.637  48.020  1.00 60.00
ATOM   1032  O   ASN   104      32.185  -6.462  48.219  1.00 60.00
ATOM   1033  N   LYS   105      30.692  -8.148  48.379  1.00 60.00
ATOM   1035  CA  LYS   105      29.702  -7.312  48.989  1.00 60.00
ATOM   1036  CB  LYS   105      28.296  -7.937  48.947  1.00 60.00
ATOM   1037  CG  LYS   105      27.168  -6.984  49.345  1.00 60.00
ATOM   1038  CD  LYS   105      25.778  -7.506  48.968  1.00 60.00
ATOM   1039  CE  LYS   105      25.542  -7.581  47.458  1.00 60.00
ATOM   1040  NZ  LYS   105      24.184  -8.102  47.179  1.00 60.00
ATOM   1044  C   LYS   105      30.074  -7.109  50.420  1.00 60.00
ATOM   1045  O   LYS   105      29.596  -7.823  51.301  1.00 60.00
ATOM   1046  N   THR   106      30.953  -6.121  50.683  1.00 60.00
ATOM   1048  CA  THR   106      31.369  -5.845  52.027  1.00 60.00
ATOM   1049  CB  THR   106      31.793  -7.084  52.771  1.00 60.00
ATOM   1050  OG1 THR   106      31.980  -6.802  54.151  1.00 60.00
ATOM   1052  CG2 THR   106      33.086  -7.635  52.145  1.00 60.00
ATOM   1053  C   THR   106      32.528  -4.897  51.936  1.00 60.00
ATOM   1054  O   THR   106      32.620  -4.105  51.000  1.00 60.00
ATOM   1055  N   GLY   107      33.435  -4.946  52.930  1.00 40.00
ATOM   1057  CA  GLY   107      34.619  -4.142  52.938  1.00 40.00
ATOM   1058  C   GLY   107      34.820  -3.603  54.311  1.00 40.00
ATOM   1059  O   GLY   107      35.592  -4.153  55.094  1.00 40.00
ATOM   1060  N   LEU   108      34.103  -2.527  54.668  1.00 20.00
ATOM   1062  CA  LEU   108      34.303  -1.977  55.974  1.00 20.00
ATOM   1063  CB  LEU   108      34.097  -0.453  56.025  1.00 20.00
ATOM   1064  CG  LEU   108      34.309   0.161  57.420  1.00 20.00
ATOM   1065  CD1 LEU   108      35.765  -0.006  57.885  1.00 20.00
ATOM   1066  CD2 LEU   108      33.842   1.625  57.463  1.00 20.00
ATOM   1067  C   LEU   108      33.283  -2.598  56.868  1.00 20.00
ATOM   1068  O   LEU   108      32.105  -2.259  56.795  1.00 20.00
ATOM   1069  N   LYS   109      33.711  -3.570  57.691  1.00 20.00
ATOM   1071  CA  LYS   109      32.849  -4.236  58.625  1.00 20.00
ATOM   1072  CB  LYS   109      33.493  -5.499  59.220  1.00 20.00
ATOM   1073  CG  LYS   109      33.728  -6.599  58.181  1.00 20.00
ATOM   1074  CD  LYS   109      34.771  -6.233  57.124  1.00 20.00
ATOM   1075  CE  LYS   109      35.007  -7.330  56.084  1.00 20.00
ATOM   1076  NZ  LYS   109      35.648  -8.503  56.719  1.00 20.00
ATOM   1080  C   LYS   109      32.486  -3.335  59.761  1.00 20.00
ATOM   1081  O   LYS   109      31.356  -3.352  60.243  1.00 20.00
ATOM   1082  N   GLU   110      33.452  -2.532  60.241  1.00 20.00
ATOM   1084  CA  GLU   110      33.191  -1.699  61.375  1.00 20.00
ATOM   1085  CB  GLU   110      33.243  -2.506  62.686  1.00 20.00
ATOM   1086  CG  GLU   110      34.443  -3.458  62.753  1.00 20.00
ATOM   1087  CD  GLU   110      34.394  -4.215  64.072  1.00 20.00
ATOM   1088  OE1 GLU   110      33.311  -4.770  64.393  1.00 20.00
ATOM   1089  OE2 GLU   110      35.438  -4.249  64.776  1.00 20.00
ATOM   1090  C   GLU   110      34.192  -0.592  61.413  1.00 20.00
ATOM   1091  O   GLU   110      35.084  -0.516  60.570  1.00 20.00
ATOM   1092  N   LEU   111      33.987   0.344  62.363  1.00 20.00
ATOM   1094  CA  LEU   111      34.824   1.475  62.663  1.00 20.00
ATOM   1095  CB  LEU   111      34.012   2.581  63.358  1.00 20.00
ATOM   1096  CG  LEU   111      34.824   3.839  63.700  1.00 20.00
ATOM   1097  CD1 LEU   111      35.301   4.544  62.419  1.00 20.00
ATOM   1098  CD2 LEU   111      34.041   4.771  64.638  1.00 20.00
ATOM   1099  C   LEU   111      36.051   1.204  63.522  1.00 20.00
ATOM   1100  O   LEU   111      37.050   1.894  63.330  1.00 20.00
ATOM   1101  N   PRO   112      36.057   0.168  64.355  1.00 20.00
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ATOM   1102  CD  PRO   112      36.108  -1.117  63.673  1.00 20.00
ATOM   1103  CA  PRO   112      36.946   0.092  65.507  1.00 20.00
ATOM   1104  CB  PRO   112      37.607  -1.286  65.523  1.00 20.00
ATOM   1105  CG  PRO   112      37.399  -1.812  64.107  1.00 20.00
ATOM   1106  C   PRO   112      37.924   1.181  65.815  1.00 20.00
ATOM   1107  O   PRO   112      39.116   0.935  65.971  1.00 20.00
ATOM   1108  N   MET   113      37.371   2.381  66.007  1.00 20.00
ATOM   1110  CA  MET   113      37.969   3.619  66.401  1.00 20.00
ATOM   1111  CB  MET   113      37.208   4.872  65.938  1.00 20.00
ATOM   1112  CG  MET   113      37.357   5.147  64.443  1.00 20.00
ATOM   1113  SD  MET   113      39.035   5.590  63.905  1.00 20.00
ATOM   1114  CE  MET   113      38.968   7.272  64.579  1.00 20.00
ATOM   1115  C   MET   113      38.023   3.646  67.891  1.00 20.00
ATOM   1116  O   MET   113      38.035   4.725  68.468  1.00 20.00
ATOM   1117  N   ARG   114      37.983   2.481  68.565  1.00 20.00
ATOM   1119  CA  ARG   114      37.744   2.375  69.983  1.00 20.00
ATOM   1120  CB  ARG   114      38.199   1.019  70.550  1.00 20.00
ATOM   1121  CG  ARG   114      39.689   0.735  70.352  1.00 20.00
ATOM   1122  CD  ARG   114      39.990  -0.125  69.122  1.00 20.00
ATOM   1123  NE  ARG   114      39.362  -1.457  69.345  1.00 20.00
ATOM   1125  CZ  ARG   114      39.850  -2.557  68.703  1.00 20.00
ATOM   1126  NH1 ARG   114      39.275  -3.778  68.906  1.00 20.00
ATOM   1129  NH2 ARG   114      40.917  -2.437  67.859  1.00 20.00
ATOM   1132  C   ARG   114      38.335   3.440  70.870  1.00 20.00
ATOM   1133  O   ARG   114      37.721   3.778  71.879  1.00 20.00
ATOM   1134  N   ASN   115      39.533   3.969  70.584  1.00 20.00
ATOM   1136  CA  ASN   115      40.116   5.009  71.396  1.00 20.00
ATOM   1137  CB  ASN   115      41.633   5.149  71.193  1.00 20.00
ATOM   1138  CG  ASN   115      42.267   3.951  71.883  1.00 20.00
ATOM   1139  OD1 ASN   115      41.577   3.133  72.489  1.00 20.00
ATOM   1140  ND2 ASN   115      43.619   3.851  71.812  1.00 20.00
ATOM   1143  C   ASN   115      39.483   6.371  71.233  1.00 20.00
ATOM   1144  O   ASN   115      39.737   7.272  72.029  1.00 20.00
ATOM   1145  N   LEU   116      38.690   6.577  70.164  1.00 20.00
ATOM   1147  CA  LEU   116      38.092   7.838  69.813  1.00 20.00
ATOM   1148  CB  LEU   116      37.302   7.771  68.493  1.00 20.00
ATOM   1149  CG  LEU   116      36.636   9.094  68.073  1.00 20.00
ATOM   1150  CD1 LEU   116      37.689  10.176  67.784  1.00 20.00
ATOM   1151  CD2 LEU   116      35.666   8.886  66.901  1.00 20.00
ATOM   1152  C   LEU   116      37.155   8.329  70.876  1.00 20.00
ATOM   1153  O   LEU   116      36.014   7.880  70.973  1.00 20.00
ATOM   1154  N   GLN   117      37.673   9.215  71.750  1.00 20.00
ATOM   1156  CA  GLN   117      36.955   9.843  72.820  1.00 20.00
ATOM   1157  CB  GLN   117      37.897  10.308  73.944  1.00 20.00
ATOM   1158  CG  GLN   117      38.698   9.182  74.599  1.00 20.00
ATOM   1159  CD  GLN   117      37.734   8.298  75.375  1.00 20.00
ATOM   1160  OE1 GLN   117      36.848   7.672  74.795  1.00 20.00
ATOM   1161  NE2 GLN   117      37.907   8.244  76.724  1.00 20.00
ATOM   1164  C   GLN   117      36.146  11.051  72.455  1.00 20.00
ATOM   1165  O   GLN   117      35.059  11.239  72.993  1.00 20.00
ATOM   1166  N   GLU   118      36.662  11.951  71.587  1.00 20.00
ATOM   1168  CA  GLU   118      35.860  13.113  71.321  1.00 20.00
ATOM   1169  CB  GLU   118      35.913  14.183  72.424  1.00 20.00
ATOM   1170  CG  GLU   118      34.858  15.275  72.226  1.00 20.00
ATOM   1171  CD  GLU   118      34.975  16.291  73.350  1.00 20.00
ATOM   1172  OE1 GLU   118      33.956  16.974  73.630  1.00 20.00
ATOM   1173  OE2 GLU   118      36.084  16.402  73.940  1.00 20.00
ATOM   1174  C   GLU   118      36.217  13.797  70.043  1.00 20.00
ATOM   1175  O   GLU   118      37.375  13.829  69.629  1.00 20.00
ATOM   1176  N   ILE   119      35.185  14.358  69.380  1.00 20.00
ATOM   1178  CA  ILE   119      35.360  15.138  68.194  1.00 20.00
ATOM   1179  CB  ILE   119      34.474  14.698  67.059  1.00 20.00
ATOM   1180  CG2 ILE   119      34.603  15.722  65.922  1.00 20.00
ATOM   1181  CG1 ILE   119      34.829  13.264  66.628  1.00 20.00
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ATOM	1182	CD1	ILE	119	33.826	12.644	65.654	1.00	20.00
ATOM	1183	C	ILE	119	34.944	16.515	68.607	1.00	20.00
ATOM	1184	O	ILE	119	33.767	16.862	68.525	1.00	20.00
ATOM	1185	N	LEU	120	35.925	17.373	68.955	1.00	20.00
ATOM	1187	CA	LEU	120	35.647	18.662	69.531	1.00	20.00
ATOM	1188	CB	LEU	120	36.861	19.604	69.661	1.00	20.00
ATOM	1189	CG	LEU	120	37.871	19.235	70.761	1.00	20.00
ATOM	1190	CD1	LEU	120	38.609	17.938	70.424	1.00	20.00
ATOM	1191	CD2	LEU	120	38.825	20.404	71.057	1.00	20.00
ATOM	1192	C	LEU	120	34.660	19.438	68.726	1.00	20.00
ATOM	1193	O	LEU	120	33.852	20.172	69.292	1.00	20.00
ATOM	1194	N	HIS	121	34.699	19.344	67.387	1.00	20.00
ATOM	1196	CA	HIS	121	33.731	20.124	66.677	1.00	20.00
ATOM	1197	CB	HIS	121	34.231	21.527	66.296	1.00	20.00
ATOM	1198	CG	HIS	121	33.162	22.376	65.673	1.00	20.00
ATOM	1199	CD2	HIS	121	32.867	22.598	64.363	1.00	20.00
ATOM	1200	ND1	HIS	121	32.234	23.095	66.393	1.00	20.00
ATOM	1202	CE1	HIS	121	31.430	23.713	65.490	1.00	20.00
ATOM	1203	NE2	HIS	121	31.776	23.441	64.245	1.00	20.00
ATOM	1205	C	HIS	121	33.334	19.442	65.411	1.00	20.00
ATOM	1206	O	HIS	121	34.098	18.668	64.840	1.00	20.00
ATOM	1207	N	GLY	122	32.099	19.720	64.947	1.00	20.00
ATOM	1209	CA	GLY	122	31.633	19.168	63.714	1.00	20.00
ATOM	1210	C	GLY	122	30.940	17.873	63.991	1.00	20.00
ATOM	1211	O	GLY	122	31.039	17.322	65.086	1.00	20.00
ATOM	1212	N	ALA	123	30.204	17.370	62.978	1.00	20.00
ATOM	1214	CA	ALA	123	29.471	16.140	63.080	1.00	20.00
ATOM	1215	CB	ALA	123	28.040	16.233	62.527	1.00	20.00
ATOM	1216	C	ALA	123	30.174	15.063	62.315	1.00	20.00
ATOM	1217	O	ALA	123	31.321	15.229	61.909	1.00	20.00
ATOM	1218	N	VAL	124	29.500	13.906	62.126	1.00	20.00
ATOM	1220	CA	VAL	124	30.075	12.810	61.392	1.00	20.00
ATOM	1221	CB	VAL	124	30.249	11.569	62.219	1.00	20.00
ATOM	1222	CG1	VAL	124	28.855	11.048	62.614	1.00	20.00
ATOM	1223	CG2	VAL	124	31.094	10.562	61.420	1.00	20.00
ATOM	1224	C	VAL	124	29.175	12.455	60.246	1.00	20.00
ATOM	1225	O	VAL	124	28.001	12.822	60.226	1.00	20.00
ATOM	1226	N	ARG	125	29.718	11.762	59.223	1.00	20.00
ATOM	1228	CA	ARG	125	28.902	11.392	58.101	1.00	20.00
ATOM	1229	CB	ARG	125	29.175	12.269	56.870	1.00	20.00
ATOM	1230	CG	ARG	125	28.335	11.918	55.646	1.00	20.00
ATOM	1231	CD	ARG	125	28.619	12.837	54.459	1.00	20.00
ATOM	1232	NE	ARG	125	27.732	12.408	53.345	1.00	20.00
ATOM	1234	CZ	ARG	125	26.442	12.852	53.316	1.00	20.00
ATOM	1235	NH1	ARG	125	25.626	12.509	52.278	1.00	20.00
ATOM	1238	NH2	ARG	125	25.966	13.637	54.325	1.00	20.00
ATOM	1241	C	ARG	125	29.243	9.985	57.723	1.00	20.00
ATOM	1242	O	ARG	125	30.297	9.728	57.145	1.00	20.00
ATOM	1243	N	PHE	126	28.354	9.023	58.025	1.00	20.00
ATOM	1245	CA	PHE	126	28.636	7.664	57.661	1.00	20.00
ATOM	1246	CB	PHE	126	28.341	6.650	58.781	1.00	20.00
ATOM	1247	CG	PHE	126	29.317	6.817	59.893	1.00	20.00
ATOM	1248	CD1	PHE	126	30.518	6.145	59.875	1.00	20.00
ATOM	1249	CD2	PHE	126	28.994	7.566	61.000	1.00	20.00
ATOM	1250	CE1	PHE	126	31.389	6.236	60.934	1.00	20.00
ATOM	1251	CE2	PHE	126	29.861	7.662	62.062	1.00	20.00
ATOM	1252	CZ	PHE	126	31.060	6.993	62.033	1.00	20.00
ATOM	1253	C	PHE	126	27.707	7.295	56.548	1.00	20.00
ATOM	1254	O	PHE	126	26.558	6.923	56.781	1.00	20.00
ATOM	1255	N	SER	127	28.193	7.340	55.295	1.00	20.00
ATOM	1257	CA	SER	127	27.298	7.056	54.219	1.00	20.00
ATOM	1258	CB	SER	127	26.962	8.291	53.365	1.00	20.00
ATOM	1259	OG	SER	127	28.137	8.806	52.760	1.00	20.00
ATOM	1261	C	SER	127	27.798	5.986	53.302	1.00	20.00

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ATOM   1262  O   SER   127      28.995   5.712  53.212  1.00 20.00
ATOM   1263  N   ASN   128      26.840   5.341  52.604  1.00 20.00
ATOM   1265  CA  ASN   128      27.126   4.347  51.610  1.00 20.00
ATOM   1266  CB  ASN   128      27.619   4.946  50.280  1.00 20.00
ATOM   1267  CG  ASN   128      26.461   5.697  49.637  1.00 20.00
ATOM   1268  OD1 ASN   128      25.444   5.108  49.275  1.00 20.00
ATOM   1269  ND2 ASN   128      26.617   7.041  49.494  1.00 20.00
ATOM   1272  C   ASN   128      28.134   3.339  52.055  1.00 20.00
ATOM   1273  O   ASN   128      29.252   3.306  51.542  1.00 20.00
ATOM   1274  N   ASN   129      27.778   2.502  53.050  1.00 20.00
ATOM   1276  CA  ASN   129      28.702   1.470  53.428  1.00 20.00
ATOM   1277  CB  ASN   129      29.436   1.800  54.735  1.00 20.00
ATOM   1278  CG  ASN   129      30.295   3.030  54.482  1.00 20.00
ATOM   1279  OD1 ASN   129      31.229   2.993  53.682  1.00 20.00
ATOM   1280  ND2 ASN   129      29.965   4.156  55.170  1.00 20.00
ATOM   1283  C   ASN   129      27.923   0.211  53.673  1.00 20.00
ATOM   1284  O   ASN   129      27.696  -0.162  54.821  1.00 20.00
ATOM   1285  N   PRO   130      27.598  -0.495  52.620  1.00 20.00
ATOM   1286  CD  PRO   130      28.347  -0.415  51.380  1.00 20.00
ATOM   1287  CA  PRO   130      26.725  -1.646  52.666  1.00 20.00
ATOM   1288  CB  PRO   130      26.874  -2.340  51.311  1.00 20.00
ATOM   1289  CG  PRO   130      27.546  -1.292  50.404  1.00 20.00
ATOM   1290  C   PRO   130      27.007  -2.592  53.801  1.00 20.00
ATOM   1291  O   PRO   130      26.073  -2.963  54.510  1.00 20.00
ATOM   1292  N   ALA   131      28.280  -2.993  53.967  1.00 20.00
ATOM   1294  CA  ALA   131      28.763  -3.910  54.962  1.00 20.00
ATOM   1295  CB  ALA   131      30.131  -4.505  54.587  1.00 20.00
ATOM   1296  C   ALA   131      28.907  -3.352  56.350  1.00 20.00
ATOM   1297  O   ALA   131      28.971  -4.114  57.312  1.00 20.00
ATOM   1298  N   LEU   132      29.031  -2.020  56.492  1.00 20.00
ATOM   1300  CA  LEU   132      29.337  -1.428  57.767  1.00 20.00
ATOM   1301  CB  LEU   132      29.400   0.108  57.704  1.00 20.00
ATOM   1302  CG  LEU   132      29.742   0.793  59.038  1.00 20.00
ATOM   1303  CD1 LEU   132      31.129   0.382  59.549  1.00 20.00
ATOM   1304  CD2 LEU   132      29.586   2.318  58.928  1.00 20.00
ATOM   1305  C   LEU   132      28.388  -1.818  58.852  1.00 20.00
ATOM   1306  O   LEU   132      27.174  -1.653  58.743  1.00 20.00
ATOM   1307  N   CYS   133      28.965  -2.335  59.955  1.00 20.00
ATOM   1309  CA  CYS   133      28.236  -2.785  61.096  1.00 20.00
ATOM   1310  CB  CYS   133      28.392  -4.290  61.352  1.00 20.00
ATOM   1311  SG  CYS   133      27.437  -5.281  60.176  1.00 20.00
ATOM   1312  C   CYS   133      28.804  -2.090  62.292  1.00 20.00
ATOM   1313  O   CYS   133      29.656  -1.214  62.167  1.00 20.00
ATOM   1314  N   ASN   134      28.310  -2.460  63.488  1.00 20.00
ATOM   1316  CA  ASN   134      28.773  -1.887  64.715  1.00 20.00
ATOM   1317  CB  ASN   134      30.193  -2.332  65.107  1.00 20.00
ATOM   1318  CG  ASN   134      30.101  -3.784  65.561  1.00 20.00
ATOM   1319  OD1 ASN   134      30.893  -4.632  65.156  1.00 20.00
ATOM   1320  ND2 ASN   134      29.102  -4.078  66.436  1.00 20.00
ATOM   1323  C   ASN   134      28.729  -0.397  64.609  1.00 20.00
ATOM   1324  O   ASN   134      29.653   0.292  65.040  1.00 20.00
ATOM   1325  N   VAL   135      27.731   0.107  63.854  1.00 20.00
ATOM   1327  CA  VAL   135      27.391   1.500  63.755  1.00 20.00
ATOM   1328  CB  VAL   135      26.828   1.846  62.408  1.00 20.00
ATOM   1329  CG1 VAL   135      27.912   1.585  61.349  1.00 20.00
ATOM   1330  CG2 VAL   135      25.538   1.036  62.190  1.00 20.00
ATOM   1331  C   VAL   135      26.393   1.959  64.782  1.00 20.00
ATOM   1332  O   VAL   135      26.512   3.040  65.353  1.00 20.00
ATOM   1333  N   GLU   136      25.349   1.136  65.009  1.00 20.00
ATOM   1335  CA  GLU   136      24.252   1.436  65.892  1.00 20.00
ATOM   1336  CB  GLU   136      23.078   0.452  65.745  1.00 20.00
ATOM   1337  CG  GLU   136      21.911   0.768  66.680  1.00 20.00
ATOM   1338  CD  GLU   136      21.210   2.009  66.147  1.00 20.00
ATOM   1339  OE1 GLU   136      20.551   1.899  65.079  1.00 20.00
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ATOM   1340  OE2 GLU   136      21.327   3.082  66.798  1.00 20.00
ATOM   1341  C   GLU   136      24.708   1.359  67.305  1.00 20.00
ATOM   1342  O   GLU   136      24.139   1.986  68.196  1.00 20.00
ATOM   1343  N   SER   137      25.749   0.542  67.513  1.00 20.00
ATOM   1345  CA  SER   137      26.349   0.181  68.762  1.00 20.00
ATOM   1346  CB  SER   137      27.419  -0.903  68.574  1.00 20.00
ATOM   1347  OG  SER   137      26.854  -2.020  67.907  1.00 20.00
ATOM   1349  C   SER   137      27.023   1.314  69.462  1.00 20.00
ATOM   1350  O   SER   137      27.244   1.223  70.667  1.00 20.00
ATOM   1351  N   ILE   138      27.452   2.377  68.753  1.00 20.00
ATOM   1353  CA  ILE   138      28.131   3.385  69.515  1.00 20.00
ATOM   1354  CB  ILE   138      29.429   3.894  68.940  1.00 20.00
ATOM   1355  CG2 ILE   138      30.414   2.715  68.934  1.00 20.00
ATOM   1356  CG1 ILE   138      29.257   4.560  67.568  1.00 20.00
ATOM   1357  CD1 ILE   138      28.957   3.567  66.454  1.00 20.00
ATOM   1358  C   ILE   138      27.294   4.575  69.845  1.00 20.00
ATOM   1359  O   ILE   138      26.422   4.989  69.082  1.00 20.00
ATOM   1360  N   GLN   139      27.544   5.144  71.044  1.00 20.00
ATOM   1362  CA  GLN   139      26.824   6.306  71.473  1.00 20.00
ATOM   1363  CB  GLN   139      26.612   6.369  72.996  1.00 20.00
ATOM   1364  CG  GLN   139      25.723   5.254  73.550  1.00 20.00
ATOM   1365  CD  GLN   139      25.608   5.455  75.055  1.00 20.00
ATOM   1366  OE1 GLN   139      26.228   6.352  75.625  1.00 20.00
ATOM   1367  NE2 GLN   139      24.789   4.599  75.721  1.00 20.00
ATOM   1370  C   GLN   139      27.653   7.494  71.108  1.00 20.00
ATOM   1371  O   GLN   139      28.533   7.915  71.854  1.00 20.00
ATOM   1372  N   TRP   140      27.351   8.092  69.948  1.00 20.00
ATOM   1374  CA  TRP   140      28.071   9.224  69.450  1.00 20.00
ATOM   1375  CB  TRP   140      27.692   9.605  68.010  1.00 20.00
ATOM   1376  CG  TRP   140      28.076   8.535  67.013  1.00 20.00
ATOM   1377  CD2 TRP   140      29.428   8.220  66.635  1.00 20.00
ATOM   1378  CE2 TRP   140      29.372   7.119  65.780  1.00 20.00
ATOM   1379  CE3 TRP   140      30.620   8.790  66.980  1.00 20.00
ATOM   1380  CD1 TRP   140      27.281   7.613  66.398  1.00 20.00
ATOM   1381  NE1 TRP   140      28.048   6.762  65.638  1.00 20.00
ATOM   1383  CZ2 TRP   140      30.508   6.574  65.251  1.00 20.00
ATOM   1384  CZ3 TRP   140      31.763   8.237  66.445  1.00 20.00
ATOM   1385  CH2 TRP   140      31.709   7.152  65.595  1.00 20.00
ATOM   1386  C   TRP   140      27.801  10.373  70.359  1.00 20.00
ATOM   1387  O   TRP   140      28.476  11.394  70.301  1.00 20.00
ATOM   1388  N   ARG   141      26.754  10.253  71.190  1.00 20.00
ATOM   1390  CA  ARG   141      26.397  11.300  72.099  1.00 20.00
ATOM   1391  CB  ARG   141      25.226  10.879  73.005  1.00 20.00
ATOM   1392  CG  ARG   141      24.596  12.002  73.831  1.00 20.00
ATOM   1393  CD  ARG   141      23.535  11.481  74.804  1.00 20.00
ATOM   1394  NE  ARG   141      22.804  12.651  75.364  1.00 20.00
ATOM   1396  CZ  ARG   141      21.689  13.118  74.730  1.00 20.00
ATOM   1397  NH1 ARG   141      21.013  14.190  75.237  1.00 20.00
ATOM   1400  NH2 ARG   141      21.246  12.509  73.591  1.00 20.00
ATOM   1403  C   ARG   141      27.568  11.603  72.983  1.00 20.00
ATOM   1404  O   ARG   141      27.850  12.769  73.253  1.00 20.00
ATOM   1405  N   ASP   142      28.270  10.571  73.493  1.00 20.00
ATOM   1407  CA  ASP   142      29.398  10.884  74.323  1.00 20.00
ATOM   1408  CB  ASP   142      29.869   9.726  75.243  1.00 20.00
ATOM   1409  CG  ASP   142      30.337   8.470  74.513  1.00 20.00
ATOM   1410  OD1 ASP   142      30.547   8.500  73.274  1.00 20.00
ATOM   1411  OD2 ASP   142      30.493   7.437  75.218  1.00 20.00
ATOM   1412  C   ASP   142      30.543  11.452  73.533  1.00 20.00
ATOM   1413  O   ASP   142      31.222  12.373  73.987  1.00 20.00
ATOM   1414  N   ILE   143      30.787  10.913  72.324  1.00 20.00
ATOM   1416  CA  ILE   143      31.880  11.333  71.493  1.00 20.00
ATOM   1417  CB  ILE   143      32.102  10.348  70.369  1.00 20.00
ATOM   1418  CG2 ILE   143      30.926  10.462  69.391  1.00 20.00
ATOM   1419  CG1 ILE   143      33.460  10.541  69.684  1.00 20.00
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ATOM   1420  CD1 ILE   143      33.543  11.814  68.850  1.00 20.00
ATOM   1421  C   ILE   143      31.688  12.725  70.950  1.00 20.00
ATOM   1422  O   ILE   143      32.602  13.546  70.998  1.00 20.00
  OM   1423  N   VAL   144      30.480  13.041  70.442  1.00 20.00
ATOM   1425  CA  VAL   144      30.207  14.324  69.854  1.00 20.00
ATOM   1426  CB  VAL   144      29.753  14.239  68.426  1.00 20.00
ATOM   1427  CG1 VAL   144      30.892  13.642  67.582  1.00 20.00
ATOM   1428  CG2 VAL   144      28.449  13.425  68.377  1.00 20.00
ATOM   1429  C   VAL   144      29.090  14.942  70.630  1.00 20.00
ATOM   1430  O   VAL   144      28.288  14.241  71.240  1.00 20.00
ATOM   1431  N   SER   145      29.004  16.285  70.626  1.00 20.00
ATOM   1433  CA  SER   145      27.993  16.945  71.401  1.00 20.00
ATOM   1434  CB  SER   145      27.967  18.470  71.217  1.00 20.00
ATOM   1435  OG  SER   145      29.188  19.039  71.669  1.00 20.00
ATOM   1437  C   SER   145      26.640  16.424  71.040  1.00 20.00
ATOM   1438  O   SER   145      26.434  15.869  69.963  1.00 20.00
ATOM   1439  N   SER   146      25.678  16.577  71.968  1.00 40.00
ATOM   1441  CA  SER   146      24.344  16.120  71.722  1.00 40.00
ATOM   1442  CB  SER   146      23.417  16.297  72.935  1.00 40.00
ATOM   1443  OG  SER   146      23.868  15.487  74.011  1.00 40.00
ATOM   1445  C   SER   146      23.801  16.949  70.609  1.00 40.00
ATOM   1446  O   SER   146      23.167  16.436  69.688  1.00 40.00
ATOM   1447  N   ASP   147      24.059  18.268  70.664  1.00 40.00
ATOM   1449  CA  ASP   147      23.578  19.139  69.638  1.00 40.00
ATOM   1450  CB  ASP   147      24.004  20.603  69.840  1.00 40.00
ATOM   1451  CG  ASP   147      23.299  21.444  68.785  1.00 40.00
ATOM   1452  OD1 ASP   147      22.361  20.911  68.135  1.00 40.00
ATOM   1453  OD2 ASP   147      23.693  22.629  68.613  1.00 40.00
ATOM   1454  C   ASP   147      24.208  18.667  68.373  1.00 40.00
ATOM   1455  O   ASP   147      23.561  18.599  67.329  1.00 40.00
ATOM   1456  N   PHE   148      25.502  18.307  68.448  1.00 40.00
ATOM   1458  CA  PHE   148      26.182  17.857  67.280  1.00 40.00
ATOM   1459  CB  PHE   148      27.692  17.655  67.485  1.00 40.00
ATOM   1460  CG  PHE   148      28.305  19.013  67.455  1.00 40.00
ATOM   1461  CD1 PHE   148      28.659  19.580  66.253  1.00 40.00
ATOM   1462  CD2 PHE   148      28.480  19.742  68.608  1.00 40.00
ATOM   1463  CE1 PHE   148      29.191  20.846  66.203  1.00 40.00
ATOM   1464  CE2 PHE   148      29.014  21.009  68.565  1.00 40.00
ATOM   1465  CZ  PHE   148      29.373  21.564  67.361  1.00 40.00
ATOM   1466  C   PHE   148      25.596  16.582  66.770  1.00 40.00
ATOM   1467  O   PHE   148      25.551  16.361  65.562  1.00 40.00
ATOM   1468  N   LEU   149      25.100  15.717  67.672  1.00 40.00
ATOM   1470  CA  LEU   149      24.608  14.440  67.240  1.00 40.00
ATOM   1471  CB  LEU   149      24.069  13.569  68.387  1.00 40.00
ATOM   1472  CG  LEU   149      23.546  12.205  67.900  1.00 40.00
ATOM   1473  CD1 LEU   149      24.670  11.377  67.254  1.00 40.00
ATOM   1474  CD2 LEU   149      22.825  11.446  69.023  1.00 40.00
ATOM   1475  C   LEU   149      23.505  14.619  66.249  1.00 40.00
ATOM   1476  O   LEU   149      23.379  13.843  65.303  1.00 40.00
ATOM   1477  N   SER   150      22.675  15.664  66.425  1.00 40.00
ATOM   1479  CA  SER   150      21.578  15.868  65.523  1.00 40.00
ATOM   1480  CB  SER   150      20.763  17.128  65.857  1.00 40.00
ATOM   1481  OG  SER   150      21.564  18.288  65.698  1.00 40.00
ATOM   1483  C   SER   150      22.114  16.030  64.135  1.00 40.00
ATOM   1484  O   SER   150      21.501  15.583  63.167  1.00 40.00
ATOM   1485  N   ASN   151      23.286  16.678  64.015  1.00 40.00
ATOM   1487  CA  ASN   151      23.919  16.977  62.762  1.00 40.00
ATOM   1488  CB  ASN   151      25.177  17.844  62.937  1.00 40.00
ATOM   1489  CG  ASN   151      24.741  19.195  63.487  1.00 40.00
ATOM   1490  OD1 ASN   151      23.656  19.688  63.180  1.00 40.00
ATOM   1491  ND2 ASN   151      25.612  19.813  64.329  1.00 40.00
ATOM   1494  C   ASN   151      24.341  15.743  62.019  1.00 40.00
ATOM   1495  O   ASN   151      24.380  15.740  60.790  1.00 40.00
ATOM   1496  N   MET   152      24.686  14.664  62.747  1.00 40.00
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ATOM	1498	CA	MET	152	25.193	13.461	62.147	1.00	40.00
ATOM	1499	CB	MET	152	25.308	12.309	63.162	1.00	40.00
ATOM	1500	CG	MET	152	25.897	11.013	62.602	1.00	40.00
ATOM	1501	SD	MET	152	26.051	9.686	63.835	1.00	40.00
ATOM	1502	CE	MET	152	26.754	8.460	62.697	1.00	40.00
ATOM	1503	C	MET	152	24.326	13.011	61.016	1.00	40.00
ATOM	1504	O	MET	152	23.101	13.009	61.115	1.00	40.00
ATOM	1505	N	SER	153	24.967	12.636	59.887	1.00	40.00
ATOM	1507	CA	SER	153	24.220	12.200	58.745	1.00	40.00
ATOM	1508	CB	SER	153	24.502	13.023	57.473	1.00	40.00
ATOM	1509	OG	SER	153	23.728	12.530	56.390	1.00	40.00
ATOM	1511	C	SER	153	24.586	10.788	58.441	1.00	40.00
ATOM	1512	O	SER	153	25.725	10.484	58.086	1.00	40.00
ATOM	1513	N	MET	154	23.612	9.872	58.577	1.00	40.00
ATOM	1515	CA	MET	154	23.874	8.509	58.242	1.00	40.00
ATOM	1516	CB	MET	154	23.599	7.514	59.384	1.00	40.00
ATOM	1517	CG	MET	154	23.890	6.064	58.993	1.00	40.00
ATOM	1518	SD	MET	154	23.588	4.841	60.306	1.00	40.00
ATOM	1519	CE	MET	154	25.146	5.148	61.184	1.00	40.00
ATOM	1520	C	MET	154	22.942	8.173	57.137	1.00	40.00
ATOM	1521	O	MET	154	21.741	8.426	57.230	1.00	40.00
ATOM	1522	N	ASP	155	23.463	7.600	56.040	1.00	40.00
ATOM	1524	CA	ASP	155	22.536	7.273	55.010	1.00	40.00
ATOM	1525	CB	ASP	155	22.995	7.565	53.563	1.00	40.00
ATOM	1526	CG	ASP	155	24.145	6.657	53.156	1.00	40.00
ATOM	1527	OD1	ASP	155	24.405	6.563	51.927	1.00	40.00
ATOM	1528	OD2	ASP	155	24.773	6.038	54.051	1.00	40.00
ATOM	1529	C	ASP	155	22.264	5.822	55.133	1.00	40.00
ATOM	1530	O	ASP	155	23.085	5.059	55.646	1.00	40.00
ATOM	1531	N	PHE	156	21.080	5.440	54.628	1.00	40.00
ATOM	1533	CA	PHE	156	20.544	4.117	54.646	1.00	40.00
ATOM	1534	CB	PHE	156	19.243	4.042	53.826	1.00	40.00
ATOM	1535	CG	PHE	156	18.768	2.632	53.757	1.00	40.00
ATOM	1536	CD1	PHE	156	18.067	2.069	54.797	1.00	40.00
ATOM	1537	CD2	PHE	156	18.934	1.913	52.596	1.00	40.00
ATOM	1538	CE1	PHE	156	17.563	0.794	54.688	1.00	40.00
ATOM	1539	CE2	PHE	156	18.435	0.637	52.482	1.00	40.00
ATOM	1540	CZ	PHE	156	17.747	0.076	53.531	1.00	40.00
ATOM	1541	C	PHE	156	21.540	3.207	54.022	1.00	40.00
ATOM	1542	O	PHE	156	21.535	2.002	54.267	1.00	40.00
ATOM	1543	N	GLN	157	22.447	3.768	53.207	1.00	40.00
ATOM	1545	CA	GLN	157	23.349	2.907	52.518	1.00	40.00
ATOM	1546	CB	GLN	157	24.276	3.608	51.518	1.00	40.00
ATOM	1547	CG	GLN	157	24.984	2.599	50.609	1.00	40.00
ATOM	1548	CD	GLN	157	23.914	1.839	49.835	1.00	40.00
ATOM	1549	OE1	GLN	157	22.728	2.158	49.910	1.00	40.00
ATOM	1550	NE2	GLN	157	24.342	0.797	49.072	1.00	40.00
ATOM	1553	C	GLN	157	24.172	2.079	53.456	1.00	40.00
ATOM	1554	O	GLN	157	24.886	1.187	53.008	1.00	40.00
ATOM	1555	N	ASN	158	24.126	2.350	54.776	1.00	40.00
ATOM	1557	CA	ASN	158	24.867	1.507	55.675	1.00	40.00
ATOM	1558	CB	ASN	158	25.044	2.095	57.084	1.00	40.00
ATOM	1559	CG	ASN	158	26.028	3.251	56.984	1.00	40.00
ATOM	1560	OD1	ASN	158	26.920	3.251	56.136	1.00	40.00
ATOM	1561	ND2	ASN	158	25.869	4.264	57.877	1.00	40.00
ATOM	1564	C	ASN	158	24.131	0.208	55.803	1.00	40.00
ATOM	1565	O	ASN	158	23.093	0.012	55.175	1.00	40.00
ATOM	1566	N	HIS	159	24.671	-0.732	56.607	1.00	40.00
ATOM	1568	CA	HIS	159	24.049	-2.020	56.748	1.00	40.00
ATOM	1569	CB	HIS	159	25.033	-3.127	57.165	1.00	40.00
ATOM	1570	CG	HIS	159	24.457	-4.507	57.054	1.00	40.00
ATOM	1571	CD2	HIS	159	24.069	-5.379	58.023	1.00	40.00
ATOM	1572	ND1	HIS	159	24.246	-5.157	55.858	1.00	40.00
ATOM	1574	CE1	HIS	159	23.740	-6.379	56.160	1.00	40.00

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ATOM   1575  NE2 HIS   159      23.614  -6.560  57.463  1.00 40.00
ATOM   1577  C   HIS   159      22.963  -1.954  57.779  1.00 40.00
ATOM   1578  O   HIS   159      22.940  -1.052  58.614  1.00 40.00
  OM   1579  N   LEU   160      22.020  -2.922  57.735  1.00 40.00
...OM  1581  CA  LEU   160      20.933  -2.939  58.671  1.00 40.00
ATOM   1582  CB  LEU   160      19.700  -3.721  58.183  1.00 40.00
ATOM   1583  CG  LEU   160      19.036  -3.116  56.933  1.00 40.00
ATOM   1584  CD1 LEU   160      19.969  -3.190  55.714  1.00 40.00
ATOM   1585  CD2 LEU   160      17.660  -3.751  56.672  1.00 40.00
ATOM   1586  C   LEU   160      21.396  -3.580  59.941  1.00 40.00
ATOM   1587  O   LEU   160      22.356  -4.345  59.956  1.00 40.00
ATOM   1588  N   GLY   161      20.671  -3.307  61.042  1.00 40.00
ATOM   1590  CA  GLY   161      20.984  -3.755  62.372  1.00 40.00
ATOM   1591  C   GLY   161      21.076  -5.247  62.474  1.00 40.00
ATOM   1592  O   GLY   161      21.366  -5.783  63.542  1.00 40.00
ATOM   1593  N   SER   162      20.837  -5.955  61.359  1.00 40.00
ATOM   1595  CA  SER   162      20.887  -7.388  61.308  1.00 40.00
ATOM   1596  CB  SER   162      20.644  -7.945  59.896  1.00 40.00
ATOM   1597  OG  SER   162      20.708  -9.364  59.915  1.00 40.00
ATOM   1599  C   SER   162      22.260  -7.815  61.734  1.00 40.00
ATOM   1600  O   SER   162      22.481  -8.959  62.127  1.00 40.00
ATOM   1601  N   CYS   163      23.229  -6.888  61.661  1.00 40.00
ATOM   1603  CA  CYS   163      24.610  -7.156  61.943  1.00 40.00
ATOM   1604  CB  CYS   163      25.371  -5.859  62.222  1.00 40.00
ATOM   1605  SG  CYS   163      25.554  -4.822  60.750  1.00 40.00
ATOM   1606  C   CYS   163      24.886  -8.059  63.119  1.00 40.00
ATOM   1607  O   CYS   163      25.394  -9.158  62.913  1.00 40.00
ATOM   1608  N   GLN   164      24.587  -7.659  64.380  1.00 40.00
ATOM   1610  CA  GLN   164      24.973  -8.554  65.450  1.00 40.00
ATOM   1611  CB  GLN   164      26.484  -8.826  65.471  1.00 40.00
ATOM   1612  CG  GLN   164      27.309  -7.566  65.753  1.00 40.00
ATOM   1613  CD  GLN   164      28.783  -7.943  65.755  1.00 40.00
ATOM   1614  OE1 GLN   164      29.153  -9.070  65.434  1.00 40.00
ATOM   1615  NE2 GLN   164      29.654  -6.968  66.131  1.00 40.00
ATOM   1618  C   GLN   164      24.637  -8.001  66.809  1.00 40.00
ATOM   1619  O   GLN   164      23.602  -7.363  66.996  1.00 40.00
ATOM   1620  N   LYS   165      25.511  -8.286  67.811  1.00 40.00
ATOM   1622  CA  LYS   165      25.328  -7.828  69.167  1.00 40.00
ATOM   1623  CB  LYS   165      24.424  -8.751  70.000  1.00 40.00
ATOM   1624  CG  LYS   165      22.993  -8.779  69.455  1.00 40.00
ATOM   1625  CD  LYS   165      22.111  -9.891  70.021  1.00 40.00
ATOM   1626  CE  LYS   165      20.752  -9.994  69.322  1.00 40.00
ATOM   1627  NZ  LYS   165      20.004  -8.724  69.468  1.00 40.00
ATOM   1631  C   LYS   165      26.668  -7.709  69.849  1.00 40.00
ATOM   1632  O   LYS   165      27.674  -8.220  69.358  1.00 40.00
ATOM   1633  N   CYS   166      26.712  -7.013  71.011  1.00 20.00
ATOM   1635  CA  CYS   166      27.947  -6.772  71.718  1.00 20.00
ATOM   1636  CB  CYS   166      28.006  -5.409  72.445  1.00 20.00
ATOM   1637  SG  CYS   166      27.870  -3.949  71.364  1.00 20.00
ATOM   1638  C   CYS   166      28.175  -7.810  72.772  1.00 20.00
ATOM   1639  O   CYS   166      27.458  -8.806  72.858  1.00 20.00
ATOM   1640  N   ASP   167      29.221  -7.588  73.598  1.00 20.00
ATOM   1642  CA  ASP   167      29.568  -8.493  74.655  1.00 20.00
ATOM   1643  CB  ASP   167      31.034  -8.383  75.105  1.00 20.00
ATOM   1644  CG  ASP   167      31.911  -8.872  73.962  1.00 20.00
ATOM   1645  OD1 ASP   167      31.345  -9.325  72.932  1.00 20.00
ATOM   1646  OD2 ASP   167      33.160  -8.804  74.107  1.00 20.00
ATOM   1647  C   ASP   167      28.717  -8.188  75.845  1.00 20.00
ATOM   1648  O   ASP   167      28.188  -7.087  75.987  1.00 20.00
ATOM   1649  N   PRO   168      28.553  -9.167  76.691  1.00 20.00
ATOM   1650  CD  PRO   168      28.483 -10.545  76.233  1.00 20.00
ATOM   1651  CA  PRO   168      27.792  -8.962  77.891  1.00 20.00
ATOM   1652  CB  PRO   168      27.541 -10.352  78.468  1.00 20.00
ATOM   1653  CG  PRO   168      27.548 -11.259  77.224  1.00 20.00
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A[illegible]	1654	C	PRO	168	28.529	-8.037	78.800	1.00	20.00
ATOM	1655	O	PRO	168	27.901	-7.408	79.651	1.00	20.00
ATOM	1656	N	SER	169	29.863	-7.961	78.653	1.00	20.00
[illegible]M	1658	CA	SER	169	30.671	-7.115	79.481	1.00	20.00
A[illegible]OM	1659	CB	SER	169	32.175	-7.337	79.251	1.00	20.00
ATOM	1660	OG	SER	169	32.929	-6.474	80.089	1.00	20.00
ATOM	1662	C	SER	169	30.385	-5.681	79.188	1.00	20.00
ATOM	1663	O	SER	169	30.266	-4.860	80.096	1.00	20.00
ATOM	1664	N	CYS	170	30.245	-5.338	77.893	1.00	20.00
ATOM	1666	CA	CYS	170	30.047	-3.970	77.527	1.00	20.00
ATOM	1667	CB	CYS	170	29.930	-3.734	76.011	1.00	20.00
ATOM	1668	SG	CYS	170	31.315	-4.412	75.053	1.00	20.00
ATOM	1669	C	CYS	170	28.745	-3.530	78.102	1.00	20.00
ATOM	1670	O	CYS	170	27.974	-4.316	78.647	1.00	20.00
ATOM	1671	N	PRO	171	28.514	-2.253	78.002	1.00	20.00
ATOM	1672	CD	PRO	171	29.596	-1.292	78.150	1.00	20.00
ATOM	1673	CA	PRO	171	27.261	-1.721	78.446	1.00	20.00
ATOM	1674	CB	PRO	171	27.450	-0.210	78.515	1.00	20.00
ATOM	1675	CG	PRO	171	28.955	-0.053	78.798	1.00	20.00
ATOM	1676	C	PRO	171	26.247	-2.180	77.457	1.00	20.00
ATOM	1677	O	PRO	171	26.624	-2.504	76.332	1.00	20.00
ATOM	1678	N	ASN	172	24.962	-2.223	77.846	1.00	20.00
ATOM	1680	CA	ASN	172	23.973	-2.748	76.955	1.00	20.00
ATOM	1681	CB	ASN	172	22.540	-2.700	77.517	1.00	20.00
ATOM	1682	CG	ASN	172	22.449	-3.681	78.675	1.00	20.00
ATOM	1683	OD1	ASN	172	23.461	-4.092	79.240	1.00	20.00
ATOM	1684	ND2	ASN	172	21.198	-4.074	79.036	1.00	20.00
ATOM	1687	C	ASN	172	23.961	-2.023	75.651	1.00	20.00
ATOM	1688	O	ASN	172	23.484	-0.894	75.552	1.00	20.00
ATOM	1689	N	GLY	173	24.513	-2.674	74.609	1.00	20.00
ATOM	1691	CA	GLY	173	24.434	-2.157	73.276	1.00	20.00
ATOM	1692	C	GLY	173	25.496	-1.168	72.921	1.00	20.00
ATOM	1693	O	GLY	173	25.466	-0.616	71.822	1.00	20.00
ATOM	1694	N	SER	174	26.471	-0.895	73.807	1.00	20.00
ATOM	1696	CA	SER	174	27.427	0.082	73.367	1.00	20.00
ATOM	1697	CB	SER	174	27.613	1.251	74.348	1.00	20.00
ATOM	1698	OG	SER	174	26.414	2.007	74.427	1.00	20.00
ATOM	1700	C	SER	174	28.770	-0.540	73.156	1.00	20.00
ATOM	1701	O	SER	174	29.426	-0.961	74.108	1.00	20.00
ATOM	1702	N	CYS	175	29.213	-0.629	71.883	1.00	20.00
ATOM	1704	CA	CYS	175	30.524	-1.156	71.631	1.00	20.00
ATOM	1705	CB	CYS	175	30.629	-2.687	71.827	1.00	20.00
ATOM	1706	SG	CYS	175	29.735	-3.685	70.593	1.00	20.00
ATOM	1707	C	CYS	175	30.933	-0.843	70.226	1.00	20.00
ATOM	1708	O	CYS	175	30.096	-0.687	69.339	1.00	20.00
ATOM	1709	N	TRP	176	32.254	-0.693	70.011	1.00	20.00
ATOM	1711	CA	TRP	176	32.809	-0.427	68.715	1.00	20.00
ATOM	1712	CB	TRP	176	34.264	0.062	68.806	1.00	20.00
ATOM	1713	CG	TRP	176	34.394	1.381	69.536	1.00	20.00
ATOM	1714	CD2	TRP	176	34.070	2.660	68.967	1.00	20.00
ATOM	1715	CE2	TRP	176	34.267	3.619	69.961	1.00	20.00
ATOM	1716	CE3	TRP	176	33.638	3.006	67.718	1.00	20.00
ATOM	1717	CD1	TRP	176	34.748	1.618	70.833	1.00	20.00
ATOM	1718	NE1	TRP	176	34.689	2.966	71.100	1.00	20.00
ATOM	1720	CZ2	TRP	176	34.039	4.945	69.718	1.00	20.00
ATOM	1721	CZ3	TRP	176	33.404	4.341	67.480	1.00	20.00
ATOM	1722	CH2	TRP	176	33.601	5.292	68.458	1.00	20.00
ATOM	1723	C	TRP	176	32.767	-1.662	67.868	1.00	20.00
ATOM	1724	O	TRP	176	32.515	-1.602	66.665	1.00	20.00
ATOM	1725	N	GLY	177	33.028	-2.826	68.493	1.00	20.00
ATOM	1727	CA	GLY	177	33.027	-4.074	67.786	1.00	20.00
ATOM	1728	C	GLY	177	32.794	-5.125	68.820	1.00	20.00
ATOM	1729	O	GLY	177	32.595	-4.818	69.994	1.00	20.00
ATOM	1730	N	ALA	178	32.791	-6.406	68.410	1.00	20.00

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ATOM   1732  CA  ALA   178      32.582  -7.432  69.385  1.00 20.00
ATOM   1733  CB  ALA   178      32.153  -8.780  68.782  1.00 20.00
ATOM   1734  C   ALA   178      33.875  -7.645  70.100  1.00 20.00
   OM  1735  O   ALA   178      34.887  -7.982  69.487  1.00 20.00
ATOM   1736  N   GLY   179      33.868  -7.445  71.431  1.00 20.00
ATOM   1738  CA  GLY   179      35.059  -7.639  72.203  1.00 20.00
ATOM   1739  C   GLY   179      34.927  -6.812  73.439  1.00 20.00
ATOM   1740  O   GLY   179      34.295  -5.757  73.429  1.00 20.00
ATOM   1741  N   GLU   180      35.529  -7.282  74.546  1.00 20.00
ATOM   1743  CA  GLU   180      35.459  -6.562  75.782  1.00 20.00
ATOM   1744  CB  GLU   180      36.109  -7.332  76.946  1.00 20.00
ATOM   1745  CG  GLU   180      35.881  -6.693  78.317  1.00 20.00
ATOM   1746  CD  GLU   180      36.375  -7.672  79.373  1.00 20.00
ATOM   1747  OE1 GLU   180      36.831  -8.780  78.984  1.00 20.00
ATOM   1748  OE2 GLU   180      36.297  -7.327  80.582  1.00 20.00
ATOM   1749  C   GLU   180      36.192  -5.273  75.597  1.00 20.00
ATOM   1750  O   GLU   180      35.742  -4.217  76.036  1.00 20.00
ATOM   1751  N   GLU   181      37.353  -5.343  74.924  1.00 20.00
ATOM   1753  CA  GLU   181      38.158  -4.188  74.662  1.00 20.00
ATOM   1754  CB  GLU   181      39.505  -4.543  74.007  1.00 20.00
ATOM   1755  CG  GLU   181      40.467  -3.359  73.892  1.00 20.00
ATOM   1756  CD  GLU   181      41.744  -3.859  73.231  1.00 20.00
ATOM   1757  OE1 GLU   181      42.734  -3.080  73.194  1.00 20.00
ATOM   1758  OE2 GLU   181      41.750  -5.028  72.761  1.00 20.00
ATOM   1759  C   GLU   181      37.399  -3.309  73.724  1.00 20.00
ATOM   1760  O   GLU   181      37.473  -2.083  73.798  1.00 20.00
ATOM   1761  N   ASN   182      36.632  -3.946  72.821  1.00 20.00
ATOM   1763  CA  ASN   182      35.877  -3.278  71.806  1.00 20.00
ATOM   1764  CB  ASN   182      35.133  -4.250  70.876  1.00 20.00
ATOM   1765  CG  ASN   182      36.159  -4.895  69.958  1.00 20.00
ATOM   1766  OD1 ASN   182      36.626  -6.006  70.202  1.00 20.00
ATOM   1767  ND2 ASN   182      36.519  -4.174  68.863  1.00 20.00
ATOM   1770  C   ASN   182      34.862  -2.373  72.420  1.00 20.00
ATOM   1771  O   ASN   182      34.486  -1.378  71.802  1.00 20.00
ATOM   1772  N   CYS   183      34.385  -2.721  73.636  1.00 20.00
ATOM   1774  CA  CYS   183      33.391  -1.959  74.344  1.00 20.00
ATOM   1775  CB  CYS   183      33.302  -2.281  75.846  1.00 20.00
ATOM   1776  SG  CYS   183      32.927  -4.017  76.211  1.00 20.00
ATOM   1777  C   CYS   183      33.734  -0.519  74.270  1.00 20.00
ATOM   1778  O   CYS   183      34.905  -0.150  74.228  1.00 20.00
ATOM   1779  N   GLN   184      32.705   0.341  74.212  1.00 60.00
ATOM   1781  CA  GLN   184      33.052   1.720  74.177  1.00 60.00
ATOM   1782  CB  GLN   184      31.868   2.667  73.922  1.00 60.00
ATOM   1783  CG  GLN   184      32.280   4.138  73.840  1.00 60.00
ATOM   1784  CD  GLN   184      31.040   4.956  73.509  1.00 60.00
ATOM   1785  OE1 GLN   184      30.966   5.609  72.468  1.00 60.00
ATOM   1786  NE2 GLN   184      30.032   4.919  74.420  1.00 60.00
ATOM   1789  C   GLN   184      33.564   1.942  75.554  1.00 60.00
ATOM   1790  O   GLN   184      32.819   1.836  76.528  1.00 60.00
ATOM   1791  N   LYS   185      34.872   2.229  75.669  1.00 60.00
ATOM   1793  CA  LYS   185      35.432   2.376  76.975  1.00 60.00
ATOM   1794  CB  LYS   185      36.970   2.443  77.002  1.00 60.00
ATOM   1795  CG  LYS   185      37.567   3.707  76.384  1.00 60.00
ATOM   1796  CD  LYS   185      39.064   3.845  76.667  1.00 60.00
ATOM   1797  CE  LYS   185      39.403   3.882  78.159  1.00 60.00
ATOM   1798  NZ  LYS   185      40.861   3.722  78.351  1.00 60.00
ATOM   1802  C   LYS   185      34.883   3.614  77.587  1.00 60.00
ATOM   1803  O   LYS   185      33.880   4.162  77.131  1.00 60.00
ATOM   1804  N   LEU   186      35.533   4.091  78.659  1.00 60.00
ATOM   1806  CA  LEU   186      34.995   5.238  79.314  1.00 60.00
ATOM   1807  CB  LEU   186      35.506   5.439  80.750  1.00 60.00
ATOM   1808  CG  LEU   186      35.069   4.350  81.745  1.00 60.00
ATOM   1809  CD1 LEU   186      35.653   2.978  81.374  1.00 60.00
ATOM   1810  CD2 LEU   186      35.392   4.768  83.189  1.00 60.00
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A	1811	C	LEU	186	35.332	6.483	78.571	1.00	60.00
ATOM	1812	O	LEU	186	36.484	6.913	78.546	1.00	60.00
ATOM	1813	N	THR	187	34.321	7.095	77.925	1.00	60.00
)M	1815	CA	THR	187	34.573	8.363	77.316	1.00	60.00
ATOM	1816	CB	THR	187	33.595	8.756	76.246	1.00	60.00
ATOM	1817	OG1	THR	187	34.062	9.910	75.563	1.00	60.00
ATOM	1819	CG2	THR	187	32.231	9.048	76.894	1.00	60.00
ATOM	1820	C	THR	187	34.396	9.281	78.474	1.00	60.00
ATOM	1821	O	THR	187	33.991	8.833	79.544	1.00	60.00
ATOM	1822	N	LYS	188	34.687	10.584	78.305	1.00	60.00
ATOM	1824	CA	LYS	188	34.575	11.445	79.444	1.00	60.00
ATOM	1825	CB	LYS	188	34.925	12.915	79.163	1.00	60.00
ATOM	1826	CG	LYS	188	33.900	13.660	78.310	1.00	60.00
ATOM	1827	CD	LYS	188	34.040	15.179	78.415	1.00	60.00
ATOM	1828	CE	LYS	188	33.643	15.726	79.789	1.00	60.00
ATOM	1829	NZ	LYS	188	33.913	17.179	79.862	1.00	60.00
ATOM	1833	C	LYS	188	33.160	11.416	79.909	1.00	60.00
ATOM	1834	O	LYS	188	32.887	11.311	81.104	1.00	60.00
ATOM	1835	N	ILE	189	32.213	11.488	78.959	1.00	60.00
ATOM	1837	CA	ILE	189	30.839	11.477	79.346	1.00	60.00
ATOM	1838	CB	ILE	189	29.899	11.547	78.180	1.00	60.00
ATOM	1839	CG2	ILE	189	28.472	11.349	78.715	1.00	60.00
ATOM	1840	CG1	ILE	189	30.091	12.869	77.420	1.00	60.00
ATOM	1841	CD1	ILE	189	29.811	14.102	78.279	1.00	60.00
ATOM	1842	C	ILE	189	30.579	10.189	80.048	1.00	60.00
ATOM	1843	O	ILE	189	30.049	10.175	81.158	1.00	60.00
ATOM	1844	N	ILE	190	30.968	9.063	79.422	1.00	60.00
ATOM	1846	CA	ILE	190	30.707	7.809	80.057	1.00	60.00
ATOM	1847	CB	ILE	190	30.069	6.798	79.136	1.00	60.00
ATOM	1848	CG2	ILE	190	30.963	6.582	77.901	1.00	60.00
ATOM	1849	CG1	ILE	190	29.724	5.515	79.908	1.00	60.00
ATOM	1850	CD1	ILE	190	28.793	4.578	79.140	1.00	60.00
ATOM	1851	C	ILE	190	31.955	7.237	80.652	1.00	60.00
ATOM	1852	O	ILE	190	32.644	6.419	80.050	1.00	60.00
ATOM	1853	N	CYS	191	32.266	7.679	81.882	1.00	20.00
ATOM	1855	CA	CYS	191	33.355	7.192	82.682	1.00	20.00
ATOM	1856	CB	CYS	191	34.411	8.248	83.072	1.00	20.00
ATOM	1857	SG	CYS	191	35.657	8.621	81.806	1.00	20.00
ATOM	1858	C	CYS	191	32.642	6.902	83.953	1.00	20.00
ATOM	1859	O	CYS	191	31.452	6.592	83.949	1.00	20.00
ATOM	1860	N	ALA	192	33.354	6.979	85.089	1.00	20.00
ATOM	1862	CA	ALA	192	32.632	6.815	86.308	1.00	20.00
ATOM	1863	CB	ALA	192	33.504	6.907	87.572	1.00	20.00
ATOM	1864	C	ALA	192	31.709	7.988	86.298	1.00	20.00
ATOM	1865	O	ALA	192	31.983	8.996	85.650	1.00	20.00
ATOM	1866	N	GLN	193	30.575	7.883	87.007	1.00	20.00
ATOM	1868	CA	GLN	193	29.623	8.951	86.991	1.00	20.00
ATOM	1869	CB	GLN	193	28.408	8.660	87.885	1.00	20.00
ATOM	1870	CG	GLN	193	27.614	7.421	87.466	1.00	20.00
ATOM	1871	CD	GLN	193	26.463	7.264	88.448	1.00	20.00
ATOM	1872	OE1	GLN	193	26.124	8.194	89.178	1.00	20.00
ATOM	1873	NE2	GLN	193	25.849	6.051	88.477	1.00	20.00
ATOM	1876	C	GLN	193	30.284	10.164	87.555	1.00	20.00
ATOM	1877	O	GLN	193	30.100	11.276	87.061	1.00	20.00
ATOM	1878	N	GLN	194	31.080	9.962	88.619	1.00	20.00
ATOM	1880	CA	GLN	194	31.727	11.025	89.328	1.00	20.00
ATOM	1881	CB	GLN	194	32.421	10.520	90.602	1.00	20.00
ATOM	1882	CG	GLN	194	31.452	9.916	91.618	1.00	20.00
ATOM	1883	CD	GLN	194	32.266	9.456	92.816	1.00	20.00
ATOM	1884	OE1	GLN	194	31.735	8.876	93.761	1.00	20.00
ATOM	1885	NE2	GLN	194	33.600	9.717	92.775	1.00	20.00
ATOM	1888	C	GLN	194	32.762	11.748	88.527	1.00	20.00
ATOM	1889	O	GLN	194	32.822	12.976	88.557	1.00	20.00
ATOM	1890	N	CYS	195	33.601	11.012	87.775	1.00	20.00

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ATOM   1892  CA  CYS   195      34.677  11.669  87.090  1.00 20.00
ATOM   1893  CB  CYS   195      35.560  10.744  86.234  1.00 20.00
ATOM   1894  SG  CYS   195      36.498   9.530  87.203  1.00 20.00
ATOM   1895  C   CYS   195      34.166  12.729  86.178  1.00 20.00
ATOM   1896  O   CYS   195      33.102  12.601  85.575  1.00 20.00
ATOM   1897  N   SER   196      34.923  13.837  86.088  1.00 20.00
ATOM   1899  CA  SER   196      34.550  14.887  85.197  1.00 20.00
ATOM   1900  CB  SER   196      34.101  16.172  85.910  1.00 20.00
ATOM   1901  OG  SER   196      32.911  15.924  86.644  1.00 20.00
ATOM   1903  C   SER   196      35.763  15.221  84.395  1.00 20.00
ATOM   1904  O   SER   196      36.859  15.369  84.932  1.00 20.00
ATOM   1905  N   GLY   197      35.597  15.299  83.064  1.00 20.00
ATOM   1907  CA  GLY   197      36.671  15.699  82.207  1.00 20.00
ATOM   1908  C   GLY   197      37.113  14.530  81.389  1.00 20.00
ATOM   1909  O   GLY   197      36.915  14.511  80.176  1.00 20.00
ATOM   1910  N   ARG   198      37.712  13.515  82.048  1.00 20.00
ATOM   1912  CA  ARG   198      38.178  12.340  81.363  1.00 20.00
ATOM   1913  CB  ARG   198      39.450  12.556  80.522  1.00 20.00
ATOM   1914  CG  ARG   198      39.207  13.349  79.238  1.00 20.00
ATOM   1915  CD  ARG   198      38.159  12.693  78.335  1.00 20.00
ATOM   1916  NE  ARG   198      37.917  13.606  77.184  1.00 20.00
ATOM   1918  CZ  ARG   198      36.929  13.329  76.284  1.00 20.00
ATOM   1919  NH1 ARG   198      36.724  14.156  75.219  1.00 20.00
ATOM   1922  NH2 ARG   198      36.145  12.222  76.452  1.00 20.00
ATOM   1925  C   ARG   198      38.529  11.321  82.396  1.00 20.00
ATOM   1926  O   ARG   198      38.423  11.580  83.594  1.00 20.00
ATOM   1927  N   CYS   199      38.930  10.109  81.955  1.00 20.00
ATOM   1929  CA  CYS   199      39.312   9.139  82.937  1.00 20.00
ATOM   1930  CB  CYS   199      38.123   8.371  83.541  1.00 20.00
ATOM   1931  SG  CYS   199      37.204   7.408  82.306  1.00 20.00
ATOM   1932  C   CYS   199      40.245   8.116  82.374  1.00 20.00
ATOM   1933  O   CYS   199      40.231   7.815  81.181  1.00 20.00
ATOM   1934  N   ARG   200      41.117   7.581  83.252  1.00 20.00
ATOM   1936  CA  ARG   200      42.032   6.538  82.900  1.00 20.00
ATOM   1937  CB  ARG   200      43.077   6.284  84.002  1.00 20.00
ATOM   1938  CG  ARG   200      44.151   5.262  83.625  1.00 20.00
ATOM   1939  CD  ARG   200      43.815   3.826  84.030  1.00 20.00
ATOM   1940  NE  ARG   200      44.952   2.965  83.598  1.00 20.00
ATOM   1942  CZ  ARG   200      44.960   2.419  82.346  1.00 20.00
ATOM   1943  NH1 ARG   200      43.921   2.651  81.491  1.00 20.00
ATOM   1946  NH2 ARG   200      46.010   1.641  81.951  1.00 20.00
ATOM   1949  C   ARG   200      41.239   5.282  82.719  1.00 20.00
ATOM   1950  O   ARG   200      41.464   4.523  81.778  1.00 20.00
ATOM   1951  N   GLY   201      40.266   5.045  83.622  1.00 20.00
ATOM   1953  CA  GLY   201      39.478   3.849  83.551  1.00 20.00
ATOM   1954  C   GLY   201      38.275   4.028  84.422  1.00 20.00
ATOM   1955  O   GLY   201      37.966   5.138  84.852  1.00 20.00
ATOM   1956  N   LYS   202      37.561   2.918  84.701  1.00 20.00
ATOM   1958  CA  LYS   202      36.372   2.971  85.502  1.00 20.00
ATOM   1959  CB  LYS   202      35.473   1.729  85.344  1.00 20.00
ATOM   1960  CG  LYS   202      34.536   1.759  84.136  1.00 20.00
ATOM   1961  CD  LYS   202      33.447   2.827  84.254  1.00 20.00
ATOM   1962  CE  LYS   202      32.464   2.569  85.398  1.00 20.00
ATOM   1963  NZ  LYS   202      31.492   3.680  85.500  1.00 20.00
ATOM   1967  C   LYS   202      36.702   3.052  86.956  1.00 20.00
ATOM   1968  O   LYS   202      36.693   2.042  87.657  1.00 20.00
ATOM   1969  N   SER   203      37.015   4.264  87.450  1.00 20.00
ATOM   1971  CA  SER   203      37.229   4.428  88.857  1.00 20.00
ATOM   1972  CB  SER   203      38.515   3.773  89.388  1.00 20.00
ATOM   1973  OG  SER   203      39.656   4.451  88.885  1.00 20.00
ATOM   1975  C   SER   203      37.339   5.895  89.101  1.00 20.00
ATOM   1976  O   SER   203      37.694   6.662  88.207  1.00 20.00
ATOM   1977  N   PRO   204      37.009   6.306  90.290  1.00 20.00
ATOM   1978  CD  PRO   204      35.914   5.677  91.012  1.00 20.00
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ATOM	1979	CA	PRO	204	37.136	7.697	90.613	1.00	20.00
ATOM	1980	CB	PRO	204	36.361	7.894	91.912	1.00	20.00
ATOM	1981	CG	PRO	204	35.277	6.800	91.847	1.00	20.00
ATOM	1982	C	PRO	204	38.584	8.051	90.685	1.00	20.00
ATOM	1983	O	PRO	204	38.925	9.227	90.563	1.00	20.00
ATOM	1984	N	SER	205	39.445	7.045	90.920	1.00	20.00
ATOM	1986	CA	SER	205	40.861	7.250	90.973	1.00	20.00
ATOM	1987	CB	SER	205	41.623	5.985	91.400	1.00	20.00
ATOM	1988	OG	SER	205	41.259	5.621	92.723	1.00	20.00
ATOM	1990	C	SER	205	41.298	7.589	89.587	1.00	20.00
ATOM	1991	O	SER	205	42.189	8.412	89.379	1.00	20.00
ATOM	1992	N	ASP	206	40.643	6.948	88.604	1.00	20.00
ATOM	1994	CA	ASP	206	40.948	7.079	87.212	1.00	20.00
ATOM	1995	CB	ASP	206	40.180	6.094	86.316	1.00	20.00
ATOM	1996	CG	ASP	206	40.887	4.749	86.409	1.00	20.00
ATOM	1997	OD1	ASP	206	40.184	3.704	86.368	1.00	20.00
ATOM	1998	OD2	ASP	206	42.142	4.751	86.518	1.00	20.00
ATOM	1999	C	ASP	206	40.703	8.452	86.687	1.00	20.00
ATOM	2000	O	ASP	206	41.286	8.800	85.661	1.00	20.00
ATOM	2001	N	CYS	207	39.811	9.229	87.348	1.00	20.00
ATOM	2003	CA	CYS	207	39.456	10.559	86.921	1.00	20.00
ATOM	2004	CB	CYS	207	38.758	11.404	88.000	1.00	20.00
ATOM	2005	SG	CYS	207	37.287	10.620	88.721	1.00	20.00
ATOM	2006	C	CYS	207	40.702	11.297	86.535	1.00	20.00
ATOM	2007	O	CYS	207	41.765	11.068	87.110	1.00	20.00
ATOM	2008	N	CYS	208	40.612	12.192	85.530	1.00	20.00
ATOM	2010	CA	CYS	208	41.814	12.830	85.073	1.00	20.00
ATOM	2011	CB	CYS	208	42.132	12.584	83.584	1.00	20.00
ATOM	2012	SG	CYS	208	43.890	12.887	83.236	1.00	20.00
ATOM	2013	C	CYS	208	41.703	14.311	85.255	1.00	20.00
ATOM	2014	O	CYS	208	40.680	14.824	85.707	1.00	20.00
ATOM	2015	N	HIS	209	42.788	15.037	84.915	1.00	20.00
ATOM	2017	CA	HIS	209	42.827	16.460	85.083	1.00	20.00
ATOM	2018	CB	HIS	209	44.187	17.074	84.698	1.00	20.00
ATOM	2019	CG	HIS	209	44.306	18.531	85.033	1.00	20.00
ATOM	2020	CD2	HIS	209	44.765	19.137	86.163	1.00	20.00
ATOM	2021	ND1	HIS	209	43.946	19.550	84.181	1.00	20.00
ATOM	2023	CE1	HIS	209	44.203	20.713	84.830	1.00	20.00
ATOM	2024	NE2	HIS	209	44.701	20.513	86.037	1.00	20.00
ATOM	2026	C	HIS	209	41.760	17.080	84.239	1.00	20.00
ATOM	2027	O	HIS	209	41.311	16.503	83.251	1.00	20.00
ATOM	2028	N	ASN	210	41.317	18.289	84.632	1.00	20.00
ATOM	2030	CA	ASN	210	40.255	18.971	83.952	1.00	20.00
ATOM	2031	CB	ASN	210	39.810	20.259	84.670	1.00	20.00
ATOM	2032	CG	ASN	210	40.987	21.221	84.745	1.00	20.00
ATOM	2033	OD1	ASN	210	41.375	21.838	83.754	1.00	20.00
ATOM	2034	ND2	ASN	210	41.562	21.368	85.969	1.00	20.00
ATOM	2037	C	ASN	210	40.644	19.322	82.547	1.00	20.00
ATOM	2038	O	ASN	210	39.809	19.293	81.644	1.00	20.00
ATOM	2039	N	GLN	211	41.920	19.698	82.340	1.00	20.00
ATOM	2041	CA	GLN	211	42.433	20.094	81.056	1.00	20.00
ATOM	2042	CB	GLN	211	43.817	20.754	81.156	1.00	20.00
ATOM	2043	CG	GLN	211	43.804	22.051	81.966	1.00	20.00
ATOM	2044	CD	GLN	211	42.967	23.077	81.212	1.00	20.00
ATOM	2045	OE1	GLN	211	42.714	22.936	80.016	1.00	20.00
ATOM	2046	NE2	GLN	211	42.528	24.144	81.931	1.00	20.00
ATOM	2049	C	GLN	211	42.545	18.956	80.093	1.00	20.00
ATOM	2050	O	GLN	211	42.326	19.106	78.892	1.00	20.00
ATOM	2051	N	CYS	212	42.911	17.779	80.608	1.00	20.00
ATOM	2053	CA	CYS	212	43.108	16.604	79.822	1.00	20.00
ATOM	2054	CB	CYS	212	43.214	15.421	80.762	1.00	20.00
ATOM	2055	SG	CYS	212	44.657	15.757	81.777	1.00	20.00
ATOM	2056	C	CYS	212	41.941	16.393	78.929	1.00	20.00
ATOM	2057	O	CYS	212	40.802	16.652	79.309	1.00	20.00

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ATOM   2058  N   ALA  213      42.212  15.952  77.688  1.00 20.00
ATOM   2060  CA  ALA  213      41.143  15.660  76.792  1.00 20.00
ATOM   2061  CB  ALA  213      41.084  16.582  75.562  1.00 20.00
   OM  2062  C   ALA  213      41.425  14.273  76.320  1.00 20.00
ATOM   2063  O   ALA  213      42.577  13.844  76.300  1.00 20.00
ATOM   2064  N   ALA  214      40.368  13.525  75.957  1.00 20.00
ATOM   2066  CA  ALA  214      40.528  12.175  75.504  1.00 20.00
ATOM   2067  CB  ALA  214      41.699  11.962  74.525  1.00 20.00
ATOM   2068  C   ALA  214      40.711  11.263  76.677  1.00 20.00
ATOM   2069  O   ALA  214      39.751  10.646  77.138  1.00 20.00
ATOM   2070  N   GLY  215      41.955  11.149  77.192  1.00 20.00
ATOM   2072  CA  GLY  215      42.196  10.264  78.303  1.00 20.00
ATOM   2073  C   GLY  215      43.502  10.625  78.944  1.00 20.00
ATOM   2074  O   GLY  215      43.975  11.754  78.818  1.00 20.00
ATOM   2075  N   CYS  216      44.101   9.684  79.707  1.00 20.00
ATOM   2077  CA  CYS  216      45.376   9.987  80.283  1.00 20.00
ATOM   2078  CB  CYS  216      45.343  11.252  81.161  1.00 20.00
ATOM   2079  SG  CYS  216      44.623  11.038  82.816  1.00 20.00
ATOM   2080  C   CYS  216      45.875   8.808  81.064  1.00 20.00
ATOM   2081  O   CYS  216      45.119   7.884  81.362  1.00 20.00
ATOM   2082  N   THR  217      47.189   8.779  81.372  1.00 20.00
ATOM   2084  CA  THR  217      47.714   7.670  82.119  1.00 20.00
ATOM   2085  CB  THR  217      49.218   7.605  82.163  1.00 20.00
ATOM   2086  OG1 THR  217      49.627   6.333  82.641  1.00 20.00
ATOM   2088  CG2 THR  217      49.764   8.698  83.093  1.00 20.00
ATOM   2089  C   THR  217      47.201   7.681  83.529  1.00 20.00
ATOM   2090  O   THR  217      46.827   6.639  84.065  1.00 20.00
ATOM   2091  N   GLY  218      47.162   8.869  84.167  1.00 20.00
ATOM   2093  CA  GLY  218      46.700   8.971  85.525  1.00 20.00
ATOM   2094  C   GLY  218      46.499  10.427  85.785  1.00 20.00
ATOM   2095  O   GLY  218      47.164  11.256  85.168  1.00 20.00
ATOM   2096  N   PRO  219      45.620  10.765  86.692  1.00 40.00
ATOM   2097  CD  PRO  219      45.358   9.917  87.844  1.00 40.00
ATOM   2098  CA  PRO  219      45.286  12.142  86.948  1.00 40.00
ATOM   2099  CB  PRO  219      44.421  12.125  88.206  1.00 40.00
ATOM   2100  CG  PRO  219      44.931  10.884  88.961  1.00 40.00
ATOM   2101  C   PRO  219      46.484  13.028  87.106  1.00 40.00
ATOM   2102  O   PRO  219      47.146  12.971  88.140  1.00 40.00
ATOM   2103  N   ARG  220      46.763  13.856  86.079  1.00 40.00
ATOM   2105  CA  ARG  220      47.847  14.791  86.092  1.00 40.00
ATOM   2106  CB  ARG  220      49.241  14.143  86.156  1.00 40.00
ATOM   2107  CG  ARG  220      50.377  15.168  86.169  1.00 40.00
ATOM   2108  CD  ARG  220      51.759  14.562  86.416  1.00 40.00
ATOM   2109  NE  ARG  220      51.806  14.132  87.842  1.00 40.00
ATOM   2111  CZ  ARG  220      51.345  12.899  88.204  1.00 40.00
ATOM   2112  NH1 ARG  220      51.379  12.520  89.515  1.00 40.00
ATOM   2115  NH2 ARG  220      50.852  12.044  87.262  1.00 40.00
ATOM   2118  C   ARG  220      47.752  15.546  84.804  1.00 40.00
ATOM   2119  O   ARG  220      47.161  15.067  83.839  1.00 40.00
ATOM   2120  N   GLU  221      48.316  16.765  84.767  1.00 20.00
ATOM   2122  CA  GLU  221      48.290  17.606  83.602  1.00 20.00
ATOM   2123  CB  GLU  221      48.797  19.024  83.910  1.00 20.00
ATOM   2124  CG  GLU  221      47.920  19.795  84.898  1.00 20.00
ATOM   2125  CD  GLU  221      48.628  21.101  85.230  1.00 20.00
ATOM   2126  OE1 GLU  221      48.993  21.839  84.276  1.00 20.00
ATOM   2127  OE2 GLU  221      48.817  21.375  86.446  1.00 20.00
ATOM   2128  C   GLU  221      49.156  17.082  82.491  1.00 20.00
ATOM   2129  O   GLU  221      48.814  17.193  81.316  1.00 20.00
ATOM   2130  N   SER  222      50.334  16.539  82.848  1.00 20.00
ATOM   2132  CA  SER  222      51.324  16.099  81.902  1.00 20.00
ATOM   2133  CB  SER  222      52.691  15.855  82.565  1.00 20.00
ATOM   2134  OG  SER  222      52.603  14.778  83.487  1.00 20.00
ATOM   2136  C   SER  222      50.999  14.860  81.120  1.00 20.00
ATOM   2137  O   SER  222      51.361  14.741  79.952  1.00 20.00
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ATOM	2138	N	ASP	223	50.342	13.881	81.759	1.00	20.00
ATOM	2140	CA	ASP	223	50.110	12.593	81.165	1.00	20.00
ATOM	2141	CB	ASP	223	49.830	11.500	82.195	1.00	20.00
ATOM	2142	CG	ASP	223	48.518	11.829	82.857	1.00	20.00
ATOM	2143	OD1	ASP	223	47.585	11.000	82.697	1.00	20.00
ATOM	2144	OD2	ASP	223	48.422	12.888	83.529	1.00	20.00
ATOM	2145	C	ASP	223	49.059	12.514	80.099	1.00	20.00
ATOM	2146	O	ASP	223	48.972	11.524	79.377	1.00	20.00
ATOM	2147	N	CYS	224	48.181	13.518	80.001	1.00	20.00
ATOM	2149	CA	CYS	224	47.069	13.416	79.106	1.00	20.00
ATOM	2150	CB	CYS	224	46.143	14.588	79.372	1.00	20.00
ATOM	2151	SG	CYS	224	45.836	14.280	81.137	1.00	20.00
ATOM	2152	C	CYS	224	47.403	13.115	77.677	1.00	20.00
ATOM	2153	O	CYS	224	48.507	13.379	77.209	1.00	20.00
ATOM	2154	N	LEU	225	46.474	12.399	77.001	1.00	20.00
ATOM	2156	CA	LEU	225	46.601	12.001	75.627	1.00	20.00
ATOM	2157	CB	LEU	225	45.630	10.880	75.219	1.00	20.00
ATOM	2158	CG	LEU	225	45.984	9.523	75.857	1.00	20.00
ATOM	2159	CD1	LEU	225	45.831	9.559	77.387	1.00	20.00
ATOM	2160	CD2	LEU	225	45.207	8.373	75.198	1.00	20.00
ATOM	2161	C	LEU	225	46.402	13.160	74.708	1.00	20.00
ATOM	2162	O	LEU	225	46.995	13.214	73.631	1.00	20.00
ATOM	2163	N	VAL	226	45.504	14.090	75.082	1.00	20.00
ATOM	2165	CA	VAL	226	45.314	15.266	74.290	1.00	20.00
ATOM	2166	CB	VAL	226	44.276	15.130	73.206	1.00	20.00
ATOM	2167	CG1	VAL	226	42.883	14.999	73.839	1.00	20.00
ATOM	2168	CG2	VAL	226	44.408	16.330	72.253	1.00	20.00
ATOM	2169	C	VAL	226	44.898	16.356	75.224	1.00	20.00
ATOM	2170	O	VAL	226	44.618	16.100	76.395	1.00	20.00
ATOM	2171	N	CYS	227	44.864	17.613	74.730	1.00	20.00
ATOM	2173	CA	CYS	227	44.543	18.697	75.608	1.00	20.00
ATOM	2174	CB	CYS	227	45.567	19.841	75.570	1.00	20.00
ATOM	2175	SG	CYS	227	47.232	19.319	76.080	1.00	20.00
ATOM	2176	C	CYS	227	43.223	19.274	75.223	1.00	20.00
ATOM	2177	O	CYS	227	42.833	19.255	74.056	1.00	20.00
ATOM	2178	N	ARG	228	42.474	19.758	76.233	1.00	20.00
ATOM	2180	CA	ARG	228	41.201	20.357	75.988	1.00	20.00
ATOM	2181	CB	ARG	228	40.368	20.572	77.259	1.00	20.00
ATOM	2182	CG	ARG	228	38.907	20.875	76.928	1.00	20.00
ATOM	2183	CD	ARG	228	37.939	20.635	78.084	1.00	20.00
ATOM	2184	NE	ARG	228	36.571	20.659	77.498	1.00	20.00
ATOM	2186	CZ	ARG	228	36.083	19.543	76.880	1.00	20.00
ATOM	2187	NH1	ARG	228	36.848	18.415	76.804	1.00	20.00
ATOM	2190	NH2	ARG	228	34.836	19.558	76.326	1.00	20.00
ATOM	2193	C	ARG	228	41.409	21.673	75.318	1.00	20.00
ATOM	2194	O	ARG	228	40.688	22.039	74.391	1.00	20.00
ATOM	2195	N	LYS	229	42.443	22.406	75.766	1.00	20.00
ATOM	2197	CA	LYS	229	42.692	23.714	75.244	1.00	20.00
ATOM	2198	CB	LYS	229	42.841	24.767	76.353	1.00	20.00
ATOM	2199	CG	LYS	229	41.624	24.772	77.280	1.00	20.00
ATOM	2200	CD	LYS	229	40.295	24.908	76.533	1.00	20.00
ATOM	2201	CE	LYS	229	39.074	24.570	77.392	1.00	20.00
ATOM	2202	NZ	LYS	229	37.854	24.553	76.554	1.00	20.00
ATOM	2206	C	LYS	229	43.956	23.664	74.448	1.00	20.00
ATOM	2207	O	LYS	229	44.019	23.016	73.403	1.00	20.00
ATOM	2208	N	PHE	230	45.000	24.379	74.908	1.00	20.00
ATOM	2210	CA	PHE	230	46.218	24.397	74.149	1.00	20.00
ATOM	2211	CB	PHE	230	46.761	25.815	73.900	1.00	20.00
ATOM	2212	CG	PHE	230	45.779	26.531	73.039	1.00	20.00
ATOM	2213	CD1	PHE	230	44.688	27.156	73.599	1.00	20.00
ATOM	2214	CD2	PHE	230	45.955	26.592	71.677	1.00	20.00
ATOM	2215	CE1	PHE	230	43.786	27.829	72.809	1.00	20.00
ATOM	2216	CE2	PHE	230	45.058	27.265	70.882	1.00	20.00
ATOM	2217	CZ	PHE	230	43.970	27.884	71.448	1.00	20.00

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ATOM   2218  C   PHE   230      47.283  23.651  74.882  1.00 20.00
ATOM   2219  O   PHE   230      47.373  23.717  76.105  1.00 20.00
ATOM   2220  N   ARG   231      48.130  22.916  74.135  1.00 20.00
ATOM   2222  CA  ARG   231      49.172  22.161  74.761  1.00 20.00
ATOM   2223  CB  ARG   231      49.466  20.819  74.071  1.00 20.00
ATOM   2224  CG  ARG   231      50.426  19.926  74.861  1.00 20.00
ATOM   2225  CD  ARG   231      51.000  18.772  74.036  1.00 20.00
ATOM   2226  NE  ARG   231      49.855  18.058  73.407  1.00 20.00
ATOM   2228  CZ  ARG   231      50.080  17.186  72.382  1.00 20.00
ATOM   2229  NH1 ARG   231      51.359  16.908  71.991  1.00 20.00
ATOM   2232  NH2 ARG   231      49.025  16.602  71.746  1.00 20.00
ATOM   2235  C   ARG   231      50.423  22.969  74.676  1.00 20.00
ATOM   2236  O   ARG   231      50.752  23.510  73.621  1.00 20.00
ATOM   2237  N   ASP   232      51.144  23.103  75.804  1.00 20.00
ATOM   2239  CA  ASP   232      52.359  23.853  75.739  1.00 20.00
ATOM   2240  CB  ASP   232      52.188  25.331  76.136  1.00 20.00
ATOM   2241  CG  ASP   232      53.432  26.092  75.694  1.00 20.00
ATOM   2242  OD1 ASP   232      53.480  27.330  75.921  1.00 20.00
ATOM   2243  OD2 ASP   232      54.346  25.446  75.114  1.00 20.00
ATOM   2244  C   ASP   232      53.358  23.243  76.667  1.00 20.00
ATOM   2245  O   ASP   232      53.050  22.936  77.816  1.00 20.00
ATOM   2246  N   GLU   233      54.597  23.062  76.174  1.00 20.00
ATOM   2248  CA  GLU   233      55.662  22.517  76.963  1.00 20.00
ATOM   2249  CB  GLU   233      56.221  23.517  77.989  1.00 20.00
ATOM   2250  CG  GLU   233      56.969  24.685  77.346  1.00 20.00
ATOM   2251  CD  GLU   233      58.294  24.153  76.822  1.00 20.00
ATOM   2252  OE1 GLU   233      59.095  23.647  77.652  1.00 20.00
ATOM   2253  OE2 GLU   233      58.524  24.243  75.586  1.00 20.00
ATOM   2254  C   GLU   233      55.237  21.291  77.701  1.00 20.00
ATOM   2255  O   GLU   233      55.325  21.232  78.926  1.00 20.00
ATOM   2256  N   ALA   234      54.756  20.278  76.961  1.00 20.00
ATOM   2258  CA  ALA   234      54.388  19.025  77.554  1.00 20.00
ATOM   2259  CB  ALA   234      55.569  18.320  78.244  1.00 20.00
ATOM   2260  C   ALA   234      53.298  19.181  78.564  1.00 20.00
ATOM   2261  O   ALA   234      52.972  18.229  79.270  1.00 20.00
ATOM   2262  N   THR   235      52.681  20.374  78.663  1.00 20.00
ATOM   2264  CA  THR   235      51.626  20.486  79.626  1.00 20.00
ATOM   2265  CB  THR   235      51.897  21.482  80.717  1.00 20.00
ATOM   2266  OG1 THR   235      52.016  22.789  80.175  1.00 20.00
ATOM   2268  CG2 THR   235      53.198  21.086  81.434  1.00 20.00
ATOM   2269  C   THR   235      50.387  20.928  78.924  1.00 20.00
ATOM   2270  O   THR   235      50.447  21.651  77.930  1.00 20.00
ATOM   2271  N   CYS   236      49.216  20.483  79.421  1.00 20.00
ATOM   2273  CA  CYS   236      47.989  20.894  78.810  1.00 20.00
ATOM   2274  CB  CYS   236      46.819  19.910  78.989  1.00 20.00
ATOM   2275  SG  CYS   236      46.939  18.467  77.899  1.00 20.00
ATOM   2276  C   CYS   236      47.599  22.168  79.473  1.00 20.00
ATOM   2277  O   CYS   236      47.313  22.189  80.669  1.00 20.00
ATOM   2278  N   LYS   237      47.579  23.269  78.694  1.00 20.00
ATOM   2280  CA  LYS   237      47.273  24.556  79.241  1.00 20.00
ATOM   2281  CB  LYS   237      48.296  25.640  78.862  1.00 20.00
ATOM   2282  CG  LYS   237      49.668  25.442  79.509  1.00 20.00
ATOM   2283  CD  LYS   237      50.763  26.323  78.905  1.00 20.00
ATOM   2284  CE  LYS   237      52.133  26.124  79.556  1.00 20.00
ATOM   2285  NZ  LYS   237      53.141  26.973  78.882  1.00 20.00
ATOM   2289  C   LYS   237      45.937  25.018  78.754  1.00 20.00
ATOM   2290  O   LYS   237      45.538  24.748  77.623  1.00 20.00
ATOM   2291  N   ASP   238      45.193  25.697  79.650  1.00 20.00
ATOM   2293  CA  ASP   238      43.904  26.249  79.350  1.00 20.00
ATOM   2294  CB  ASP   238      43.207  26.805  80.606  1.00 20.00
ATOM   2295  CG  ASP   238      41.761  27.127  80.258  1.00 20.00
ATOM   2296  OD1 ASP   238      41.399  27.014  79.057  1.00 20.00
ATOM   2297  OD2 ASP   238      40.999  27.492  81.194  1.00 20.00
ATOM   2298  C   ASP   238      44.080  27.378  78.383  1.00 20.00
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A     2299  O    ASP  238      43.294  27.553  77.452  1.00 20.00
ATOM  2300  N    THR  239      45.124  28.195  78.604  1.00 20.00
ATOM  2302  CA   THR  239      45.395  29.288  77.721  1.00 20.00
  OM  2303  CB   THR  239      44.901  30.613  78.222  1.00 20.00
 ..OM  2304  OG1  THR  239      45.004  31.594  77.201  1.00 20.00
ATOM  2306  CG2  THR  239      45.744  31.022  79.442  1.00 20.00
ATOM  2307  C    THR  239      46.879  29.365  77.641  1.00 20.00
ATOM  2308  O    THR  239      47.581  28.773  78.459  1.00 20.00
ATOM  2309  N    CYS  240      47.410  30.087  76.640  1.00 20.00
ATOM  2311  CA   CYS  240      48.835  30.120  76.543  1.00 20.00
ATOM  2312  CB   CYS  240      49.340  30.107  75.100  1.00 20.00
ATOM  2313  SG   CYS  240      49.026  28.455  74.421  1.00 20.00
ATOM  2314  C    CYS  240      49.397  31.268  77.303  1.00 20.00
ATOM  2315  O    CYS  240      48.974  32.417  77.198  1.00 20.00
ATOM  2316  N    PRO  241      50.343  30.894  78.119  1.00 40.00
ATOM  2317  CD   PRO  241      50.319  29.560  78.691  1.00 40.00
ATOM  2318  CA   PRO  241      51.014  31.831  78.973  1.00 40.00
ATOM  2319  CB   PRO  241      51.531  31.028  80.169  1.00 40.00
ATOM  2320  CG   PRO  241      51.463  29.562  79.714  1.00 40.00
ATOM  2321  C    PRO  241      52.097  32.561  78.253  1.00 40.00
ATOM  2322  O    PRO  241      52.520  32.130  77.181  1.00 40.00
ATOM  2323  N    PRO  242      52.520  33.654  78.820  1.00 60.00
ATOM  2324  CD   PRO  242      51.564  34.527  79.485  1.00 60.00
ATOM  2325  CA   PRO  242      53.598  34.393  78.227  1.00 60.00
ATOM  2326  CB   PRO  242      53.501  35.808  78.793  1.00 60.00
ATOM  2327  CG   PRO  242      52.014  35.959  79.154  1.00 60.00
ATOM  2328  C    PRO  242      54.875  33.709  78.587  1.00 60.00
ATOM  2329  O    PRO  242      54.870  32.896  79.510  1.00 60.00
ATOM  2330  N    LEU  243      55.978  34.015  77.877  1.00 60.00
ATOM  2332  CA   LEU  243      57.227  33.396  78.202  1.00 60.00
ATOM  2333  CB   LEU  243      58.383  33.812  77.277  1.00 60.00
ATOM  2334  CG   LEU  243      59.726  33.148  77.636  1.00 60.00
ATOM  2335  CD1  LEU  243      59.643  31.616  77.513  1.00 60.00
ATOM  2336  CD2  LEU  243      60.879  33.743  76.813  1.00 60.00
ATOM  2337  C    LEU  243      57.575  33.816  79.591  1.00 60.00
ATOM  2338  O    LEU  243      57.890  34.978  79.848  1.00 60.00
ATOM  2339  N    MET  244      57.507  32.862  80.533  1.00 60.00
ATOM  2341  CA   MET  244      57.791  33.161  81.903  1.00 60.00
ATOM  2342  CB   MET  244      57.482  31.989  82.850  1.00 60.00
ATOM  2343  CG   MET  244      55.997  31.625  82.878  1.00 60.00
ATOM  2344  SD   MET  244      54.903  32.969  83.429  1.00 60.00
ATOM  2345  CE   MET  244      55.431  32.907  85.165  1.00 60.00
ATOM  2346  C    MET  244      59.235  33.503  82.057  1.00 60.00
ATOM  2347  O    MET  244      59.576  34.511  82.673  1.00 60.00
ATOM  2348  N    LEU  245      60.134  32.684  81.481  1.00 60.00
ATOM  2350  CA   LEU  245      61.525  32.981  81.643  1.00 60.00
ATOM  2351  CB   LEU  245      62.469  31.955  80.994  1.00 60.00
ATOM  2352  CG   LEU  245      62.377  30.548  81.616  1.00 60.00
ATOM  2353  CD1  LEU  245      63.367  29.579  80.947  1.00 60.00
ATOM  2354  CD2  LEU  245      62.526  30.598  83.146  1.00 60.00
ATOM  2355  C    LEU  245      61.771  34.296  80.992  1.00 60.00
ATOM  2356  O    LEU  245      61.191  34.605  79.952  1.00 60.00
ATOM  2357  N    TYR  246      62.630  35.127  81.612  1.00 60.00
ATOM  2359  CA   TYR  246      62.896  36.400  81.021  1.00 60.00
ATOM  2360  CB   TYR  246      62.429  37.596  81.868  1.00 60.00
ATOM  2361  CG   TYR  246      60.948  37.506  81.992  1.00 60.00
ATOM  2362  CD1  TYR  246      60.132  37.819  80.930  1.00 60.00
ATOM  2363  CE1  TYR  246      58.765  37.758  81.055  1.00 60.00
ATOM  2364  CD2  TYR  246      60.374  37.171  83.196  1.00 60.00
ATOM  2365  CE2  TYR  246      59.008  37.115  83.331  1.00 60.00
ATOM  2366  CZ   TYR  246      58.200  37.401  82.257  1.00 60.00
ATOM  2367  OH   TYR  246      56.798  37.332  82.389  1.00 60.00
ATOM  2369  C    TYR  246      64.369  36.547  80.860  1.00 60.00
ATOM  2370  O    TYR  246      65.152  36.112  81.704  1.00 60.00
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ATOM   2371  N   ASN  247      64.781  37.156  79.735  1.00 60.00
ATOM   2373  CA  ASN  247      66.166  37.413  79.494  1.00 60.00
ATOM   2374  CB  ASN  247      66.751  36.629  78.307  1.00 60.00
   )M  2375  CG  ASN  247      66.747  35.150  78.654  1.00 60.00
A.OM   2376  OD1 ASN  247      66.946  34.764  79.804  1.00 60.00
ATOM   2377  ND2 ASN  247      66.512  34.291  77.626  1.00 60.00
ATOM   2380  C   ASN  247      66.194  38.845  79.091  1.00 60.00
ATOM   2381  O   ASN  247      65.156  39.427  78.784  1.00 60.00
ATOM   2382  N   PRO  248      67.343  39.452  79.108  1.00 60.00
ATOM   2383  CD  PRO  248      68.307  39.227  80.172  1.00 60.00
ATOM   2384  CA  PRO  248      67.376  40.798  78.633  1.00 60.00
ATOM   2385  CB  PRO  248      68.694  41.391  79.120  1.00 60.00
ATOM   2386  CG  PRO  248      68.980  40.592  80.407  1.00 60.00
ATOM   2387  C   PRO  248      67.231  40.707  77.156  1.00 60.00
ATOM   2388  O   PRO  248      67.940  39.912  76.542  1.00 60.00
ATOM   2389  N   THR  249      66.324  41.498  76.561  1.00 60.00
ATOM   2391  CA  THR  249      66.157  41.376  75.148  1.00 60.00
ATOM   2392  CB  THR  249      64.766  40.988  74.743  1.00 60.00
ATOM   2393  OG1 THR  249      63.842  41.988  75.145  1.00 60.00
ATOM   2395  CG2 THR  249      64.419  39.645  75.406  1.00 60.00
ATOM   2396  C   THR  249      66.445  42.695  74.528  1.00 60.00
ATOM   2397  O   THR  249      65.998  43.736  75.007  1.00 60.00
ATOM   2398  N   THR  250      67.235  42.676  73.442  1.00 60.00
ATOM   2400  CA  THR  250      67.522  43.894  72.758  1.00 60.00
ATOM   2401  CB  THR  250      68.975  44.063  72.421  1.00 60.00
ATOM   2402  OG1 THR  250      69.407  43.023  71.556  1.00 60.00
ATOM   2404  CG2 THR  250      69.784  44.032  73.728  1.00 60.00
ATOM   2405  C   THR  250      66.755  43.825  71.483  1.00 60.00
ATOM   2406  O   THR  250      66.991  42.953  70.648  1.00 60.00
ATOM   2407  N   TYR  251      65.783  44.738  71.313  1.00 60.00
ATOM   2409  CA  TYR  251      65.019  44.726  70.106  1.00 60.00
ATOM   2410  CB  TYR  251      63.510  44.525  70.343  1.00 60.00
ATOM   2411  CG  TYR  251      62.876  44.130  69.052  1.00 60.00
ATOM   2412  CD1 TYR  251      62.473  45.067  68.128  1.00 60.00
ATOM   2413  CE1 TYR  251      61.893  44.675  66.943  1.00 60.00
ATOM   2414  CD2 TYR  251      62.678  42.796  68.774  1.00 60.00
ATOM   2415  CE2 TYR  251      62.096  42.398  67.594  1.00 60.00
ATOM   2416  CZ  TYR  251      61.705  43.340  66.674  1.00 60.00
ATOM   2417  OH  TYR  251      61.127  42.937  65.452  1.00 60.00
ATOM   2419  C   TYR  251      65.225  46.096  69.557  1.00 60.00
ATOM   2420  O   TYR  251      65.588  47.013  70.292  1.00 60.00
ATOM   2421  N   GLN  252      65.022  46.278  68.241  1.00 60.00
ATOM   2423  CA  GLN  252      65.242  47.587  67.707  1.00 60.00
ATOM   2424  CB  GLN  252      65.041  47.680  66.183  1.00 60.00
ATOM   2425  CG  GLN  252      63.628  47.363  65.693  1.00 60.00
ATOM   2426  CD  GLN  252      63.638  47.511  64.177  1.00 60.00
ATOM   2427  OE1 GLN  252      62.715  47.085  63.482  1.00 60.00
ATOM   2428  NE2 GLN  252      64.724  48.132  63.642  1.00 60.00
ATOM   2431  C   GLN  252      64.296  48.522  68.381  1.00 60.00
ATOM   2432  O   GLN  252      64.693  49.599  68.823  1.00 60.00
ATOM   2433  N   MET  253      63.015  48.127  68.504  1.00 60.00
ATOM   2435  CA  MET  253      62.094  49.001  69.160  1.00 60.00
ATOM   2436  CB  MET  253      60.612  48.669  68.906  1.00 60.00
ATOM   2437  CG  MET  253      60.179  48.955  67.466  1.00 60.00
ATOM   2438  SD  MET  253      58.436  48.593  67.098  1.00 60.00
ATOM   2439  CE  MET  253      58.658  46.796  66.971  1.00 60.00
ATOM   2440  C   MET  253      62.362  48.933  70.627  1.00 60.00
ATOM   2441  O   MET  253      63.037  48.023  71.106  1.00 60.00
ATOM   2442  N   ASP  254      61.848  49.926  71.374  1.00 60.00
ATOM   2444  CA  ASP  254      62.085  50.003  72.785  1.00 60.00
ATOM   2445  CB  ASP  254      61.483  51.270  73.416  1.00 60.00
ATOM   2446  CG  ASP  254      62.283  52.468  72.924  1.00 60.00
ATOM   2447  OD1 ASP  254      61.662  53.540  72.691  1.00 60.00
ATOM   2448  OD2 ASP  254      63.526  52.327  72.780  1.00 60.00
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A	2449	C	ASP	254	61.474	48.832	73.480	1.00	60.00
ATOM	2450	O	ASP	254	62.122	48.178	74.295	1.00	60.00
ATOM	2451	N	VAL	255	60.204	48.520	73.162	1.00	60.00
M	2453	CA	VAL	255	59.561	47.442	73.852	1.00	60.00
ATOM	2454	CB	VAL	255	58.158	47.754	74.280	1.00	60.00
ATOM	2455	CG1	VAL	255	57.299	47.953	73.020	1.00	60.00
ATOM	2456	CG2	VAL	255	57.663	46.622	75.196	1.00	60.00
ATOM	2457	C	VAL	255	59.483	46.261	72.950	1.00	60.00
ATOM	2458	O	VAL	255	59.474	46.394	71.727	1.00	60.00
ATOM	2459	N	ASN	256	59.448	45.058	73.554	1.00	60.00
ATOM	2461	CA	ASN	256	59.348	43.852	72.791	1.00	60.00
ATOM	2462	CB	ASN	256	60.299	42.740	73.269	1.00	60.00
ATOM	2463	CG	ASN	256	60.098	41.520	72.379	1.00	60.00
ATOM	2464	OD1	ASN	256	59.716	40.451	72.854	1.00	60.00
ATOM	2465	ND2	ASN	256	60.362	41.679	71.055	1.00	60.00
ATOM	2468	C	ASN	256	57.957	43.344	72.963	1.00	60.00
ATOM	2469	O	ASN	256	57.392	43.371	74.055	1.00	60.00
ATOM	2470	N	PRO	257	57.384	42.907	71.879	1.00	60.00
ATOM	2471	CD	PRO	257	57.656	43.530	70.595	1.00	60.00
ATOM	2472	CA	PRO	257	56.058	42.359	71.940	1.00	60.00
ATOM	2473	CB	PRO	257	55.447	42.551	70.550	1.00	60.00
ATOM	2474	CG	PRO	257	56.643	42.882	69.640	1.00	60.00
ATOM	2475	C	PRO	257	56.163	40.932	72.357	1.00	60.00
ATOM	2476	O	PRO	257	57.229	40.343	72.188	1.00	60.00
ATOM	2477	N	GLU	258	55.084	40.355	72.921	1.00	60.00
ATOM	2479	CA	GLU	258	55.158	38.980	73.312	1.00	60.00
ATOM	2480	CB	GLU	258	56.103	38.741	74.504	1.00	60.00
ATOM	2481	CG	GLU	258	56.443	37.267	74.738	1.00	60.00
ATOM	2482	CD	GLU	258	57.436	36.838	73.666	1.00	60.00
ATOM	2483	OE1	GLU	258	57.797	35.632	73.640	1.00	60.00
ATOM	2484	OE2	GLU	258	57.850	37.712	72.857	1.00	60.00
ATOM	2485	C	GLU	258	53.785	38.555	73.725	1.00	60.00
ATOM	2486	O	GLU	258	52.822	39.305	73.579	1.00	60.00
ATOM	2487	N	GLY	259	53.662	37.318	74.242	1.00	60.00
ATOM	2489	CA	GLY	259	52.390	36.839	74.696	1.00	60.00
ATOM	2490	C	GLY	259	51.626	36.312	73.529	1.00	60.00
ATOM	2491	O	GLY	259	50.441	36.003	73.639	1.00	60.00
ATOM	2492	N	LYS	260	52.295	36.197	72.369	1.00	60.00
ATOM	2494	CA	LYS	260	51.630	35.712	71.199	1.00	60.00
ATOM	2495	CB	LYS	260	52.164	36.371	69.917	1.00	60.00
ATOM	2496	CG	LYS	260	53.689	36.306	69.792	1.00	60.00
ATOM	2497	CD	LYS	260	54.221	36.659	68.401	1.00	60.00
ATOM	2498	CE	LYS	260	54.298	35.459	67.454	1.00	60.00
ATOM	2499	NZ	LYS	260	52.941	35.089	66.995	1.00	60.00
ATOM	2503	C	LYS	260	51.855	34.239	71.090	1.00	60.00
ATOM	2504	O	LYS	260	52.807	33.792	70.452	1.00	60.00
ATOM	2505	N	TYR	261	50.981	33.433	71.727	1.00	40.00
ATOM	2507	CA	TYR	261	51.160	32.018	71.623	1.00	40.00
ATOM	2508	CB	TYR	261	51.545	31.368	72.964	1.00	40.00
ATOM	2509	CG	TYR	261	52.847	31.929	73.425	1.00	40.00
ATOM	2510	CD1	TYR	261	54.032	31.338	73.054	1.00	40.00
ATOM	2511	CE1	TYR	261	55.236	31.845	73.479	1.00	40.00
ATOM	2512	CD2	TYR	261	52.884	33.038	74.239	1.00	40.00
ATOM	2513	CE2	TYR	261	54.086	33.545	74.676	1.00	40.00
ATOM	2514	CZ	TYR	261	55.263	32.950	74.294	1.00	40.00
ATOM	2515	OH	TYR	261	56.497	33.472	74.737	1.00	40.00
ATOM	2517	C	TYR	261	49.844	31.408	71.265	1.00	40.00
ATOM	2518	O	TYR	261	48.937	31.398	72.092	1.00	40.00
ATOM	2519	N	SER	262	49.703	30.888	70.027	1.00	20.00
ATOM	2521	CA	SER	262	48.521	30.173	69.622	1.00	20.00
ATOM	2522	CB	SER	262	47.244	31.027	69.481	1.00	20.00
ATOM	2523	OG	SER	262	46.751	31.449	70.744	1.00	20.00
ATOM	2525	C	SER	262	48.809	29.661	68.248	1.00	20.00
ATOM	2526	O	SER	262	48.879	30.438	67.297	1.00	20.00

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ATOM   2527  N   PHE   263      49.007  28.337  68.103  1.00 20.00
ATOM   2529  CA  PHE   263      49.269  27.813  66.796  1.00 20.00
ATOM   2530  CB  PHE   263      50.756  27.487  66.589  1.00 20.00
ATOM   2531  CG  PHE   263      51.541  28.737  66.794  1.00 20.00
ATOM   2532  CD1 PHE   263      51.722  29.238  68.063  1.00 20.00
ATOM   2533  CD2 PHE   263      52.221  29.322  65.751  1.00 20.00
ATOM   2534  CE1 PHE   263      52.514  30.340  68.283  1.00 20.00
ATOM   2535  CE2 PHE   263      53.032  30.412  65.967  1.00 20.00
ATOM   2536  CZ  PHE   263      53.171  30.932  67.232  1.00 20.00
ATOM   2537  C   PHE   263      48.550  26.503  66.726  1.00 20.00
ATOM   2538  O   PHE   263      48.960  25.536  67.364  1.00 20.00
ATOM   2539  N   GLY   264      47.473  26.411  65.928  1.00 20.00
ATOM   2541  CA  GLY   264      46.785  25.154  65.871  1.00 20.00
ATOM   2542  C   GLY   264      46.317  24.803  67.261  1.00 20.00
ATOM   2543  O   GLY   264      45.573  25.563  67.871  1.00 20.00
ATOM   2544  N   ALA   265      46.670  23.590  67.748  1.00 40.00
ATOM   2546  CA  ALA   265      46.384  23.068  69.064  1.00 40.00
ATOM   2547  CB  ALA   265      46.496  21.535  69.117  1.00 40.00
ATOM   2548  C   ALA   265      47.277  23.601  70.145  1.00 40.00
ATOM   2549  O   ALA   265      46.844  23.768  71.284  1.00 40.00
ATOM   2550  N   THR   266      48.561  23.860  69.823  1.00 20.00
ATOM   2552  CA  THR   266      49.516  24.233  70.830  1.00 20.00
ATOM   2553  CB  THR   266      50.712  23.327  70.865  1.00 20.00
ATOM   2554  OG1 THR   266      51.422  23.408  69.638  1.00 20.00
ATOM   2556  CG2 THR   266      50.227  21.887  71.101  1.00 20.00
ATOM   2557  C   THR   266      50.034  25.609  70.581  1.00 20.00
ATOM   2558  O   THR   266      49.552  26.321  69.703  1.00 20.00
ATOM   2559  N   CYS   267      51.024  26.035  71.393  1.00 20.00
ATOM   2561  CA  CYS   267      51.536  27.360  71.222  1.00 20.00
ATOM   2562  CB  CYS   267      51.243  28.267  72.417  1.00 20.00
ATOM   2563  SG  CYS   267      49.476  28.652  72.467  1.00 20.00
ATOM   2564  C   CYS   267      53.003  27.395  70.932  1.00 20.00
ATOM   2565  O   CYS   267      53.762  26.529  71.362  1.00 20.00
ATOM   2566  N   VAL   268      53.425  28.426  70.165  1.00 20.00
ATOM   2568  CA  VAL   268      54.797  28.586  69.772  1.00 20.00
ATOM   2569  CB  VAL   268      54.998  28.615  68.284  1.00 20.00
ATOM   2570  CG1 VAL   268      56.489  28.857  67.997  1.00 20.00
ATOM   2571  CG2 VAL   268      54.457  27.305  67.684  1.00 20.00
ATOM   2572  C   VAL   268      55.307  29.884  70.309  1.00 20.00
ATOM   2573  O   VAL   268      54.571  30.863  70.413  1.00 20.00
ATOM   2574  N   LYS   269      56.608  29.908  70.657  1.00 20.00
ATOM   2576  CA  LYS   269      57.239  31.058  71.241  1.00 20.00
ATOM   2577  CB  LYS   269      58.729  30.813  71.532  1.00 20.00
ATOM   2578  CG  LYS   269      59.426  31.973  72.242  1.00 20.00
ATOM   2579  CD  LYS   269      60.879  31.668  72.615  1.00 20.00
ATOM   2580  CE  LYS   269      61.061  30.346  73.364  1.00 20.00
ATOM   2581  NZ  LYS   269      62.503  30.064  73.551  1.00 20.00
ATOM   2585  C   LYS   269      57.176  32.209  70.297  1.00 20.00
ATOM   2586  O   LYS   269      56.810  33.318  70.685  1.00 20.00
ATOM   2587  N   LYS   270      57.522  31.969  69.019  1.00 20.00
ATOM   2589  CA  LYS   270      57.534  33.036  68.064  1.00 20.00
ATOM   2590  CB  LYS   270      58.948  33.382  67.571  1.00 20.00
ATOM   2591  CG  LYS   270      59.831  34.001  68.657  1.00 20.00
ATOM   2592  CD  LYS   270      61.323  33.973  68.323  1.00 20.00
ATOM   2593  CE  LYS   270      61.984  32.627  68.625  1.00 20.00
ATOM   2594  NZ  LYS   270      63.403  32.653  68.209  1.00 20.00
ATOM   2598  C   LYS   270      56.741  32.590  66.885  1.00 20.00
ATOM   2599  O   LYS   270      56.481  31.401  66.702  1.00 20.00
ATOM   2600  N   CYS   271      56.320  33.559  66.057  1.00 20.00
ATOM   2602  CA  CYS   271      55.524  33.261  64.908  1.00 20.00
ATOM   2603  CB  CYS   271      54.812  34.532  64.403  1.00 20.00
ATOM   2604  SG  CYS   271      53.495  34.290  63.178  1.00 20.00
ATOM   2605  C   CYS   271      56.458  32.726  63.869  1.00 20.00
ATOM   2606  O   CYS   271      57.559  33.242  63.686  1.00 20.00
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ATOM	2607	N	PRO	272	56.054	31.683	63.193	1.00	20.00
ATOM	2608	CD	PRO	272	55.163	30.698	63.778	1.00	20.00
ATOM	2609	CA	PRO	272	56.883	31.103	62.177	1.00	20.00
ATOM	2610	CB	PRO	272	56.289	29.725	61.870	1.00	20.00
ATOM	2611	CG	PRO	272	54.955	29.688	62.639	1.00	20.00
ATOM	2612	C	PRO	272	56.936	32.042	61.023	1.00	20.00
ATOM	2613	O	PRO	272	56.040	32.873	60.891	1.00	20.00
ATOM	2614	N	ARG	273	57.979	31.943	60.181	1.00	20.00
ATOM	2616	CA	ARG	273	58.097	32.887	59.115	1.00	20.00
ATOM	2617	CB	ARG	273	59.407	32.762	58.313	1.00	20.00
ATOM	2618	CG	ARG	273	60.640	33.020	59.185	1.00	20.00
ATOM	2619	CD	ARG	273	61.938	33.257	58.409	1.00	20.00
ATOM	2620	NE	ARG	273	62.116	34.733	58.287	1.00	20.00
ATOM	2622	CZ	ARG	273	63.314	35.307	58.603	1.00	20.00
ATOM	2623	NH1	ARG	273	64.351	34.532	59.035	1.00	20.00
ATOM	2626	NH2	ARG	273	63.471	36.660	58.499	1.00	20.00
ATOM	2629	C	ARG	273	56.932	32.755	58.192	1.00	20.00
ATOM	2630	O	ARG	273	56.339	31.685	58.064	1.00	20.00
ATOM	2631	N	ASN	274	56.580	33.873	57.527	1.00	20.00
ATOM	2633	CA	ASN	274	55.465	33.937	56.628	1.00	20.00
ATOM	2634	CB	ASN	274	55.474	32.817	55.574	1.00	20.00
ATOM	2635	CG	ASN	274	56.592	33.129	54.587	1.00	20.00
ATOM	2636	OD1	ASN	274	56.601	34.187	53.960	1.00	20.00
ATOM	2637	ND2	ASN	274	57.566	32.189	54.450	1.00	20.00
ATOM	2640	C	ASN	274	54.178	33.873	57.388	1.00	20.00
ATOM	2641	O	ASN	274	53.123	33.612	56.812	1.00	20.00
ATOM	2642	N	TYR	275	54.234	34.130	58.709	1.00	20.00
ATOM	2644	CA	TYR	275	53.047	34.163	59.516	1.00	20.00
ATOM	2645	CB	TYR	275	52.918	32.988	60.503	1.00	20.00
ATOM	2646	CG	TYR	275	52.806	31.721	59.728	1.00	20.00
ATOM	2647	CD1	TYR	275	53.939	31.105	59.253	1.00	20.00
ATOM	2648	CE1	TYR	275	53.860	29.914	58.570	1.00	20.00
ATOM	2649	CD2	TYR	275	51.588	31.112	59.535	1.00	20.00
ATOM	2650	CE2	TYR	275	51.502	29.919	58.855	1.00	20.00
ATOM	2651	CZ	TYR	275	52.639	29.321	58.367	1.00	20.00
ATOM	2652	OH	TYR	275	52.555	28.099	57.668	1.00	20.00
ATOM	2654	C	TYR	275	53.176	35.407	60.339	1.00	20.00
ATOM	2655	O	TYR	275	54.285	35.859	60.621	1.00	20.00
ATOM	2656	N	VAL	276	52.038	36.005	60.741	1.00	20.00
ATOM	2658	CA	VAL	276	52.083	37.215	61.510	1.00	20.00
ATOM	2659	CB	VAL	276	51.371	38.363	60.858	1.00	20.00
ATOM	2660	CG1	VAL	276	52.076	38.692	59.532	1.00	20.00
ATOM	2661	CG2	VAL	276	49.884	37.996	60.703	1.00	20.00
ATOM	2662	C	VAL	276	51.393	36.980	62.815	1.00	20.00
ATOM	2663	O	VAL	276	50.633	36.025	62.967	1.00	20.00
ATOM	2664	N	VAL	277	51.665	37.850	63.808	1.00	20.00
ATOM	2666	CA	VAL	277	51.031	37.704	65.084	1.00	20.00
ATOM	2667	CB	VAL	277	51.935	38.005	66.244	1.00	20.00
ATOM	2668	CG1	VAL	277	52.485	39.435	66.102	1.00	20.00
ATOM	2669	CG2	VAL	277	51.138	37.780	67.538	1.00	20.00
ATOM	2670	C	VAL	277	49.878	38.649	65.131	1.00	20.00
ATOM	2671	O	VAL	277	50.037	39.853	64.942	1.00	20.00
ATOM	2672	N	THR	278	48.669	38.111	65.380	1.00	20.00
ATOM	2674	CA	THR	278	47.500	38.934	65.383	1.00	20.00
ATOM	2675	CB	THR	278	46.485	38.508	64.363	1.00	20.00
ATOM	2676	OG1	THR	278	45.427	39.452	64.293	1.00	20.00
ATOM	2678	CG2	THR	278	45.941	37.126	64.761	1.00	20.00
ATOM	2679	C	THR	278	46.832	38.866	66.713	1.00	20.00
ATOM	2680	O	THR	278	46.770	37.811	67.342	1.00	20.00
ATOM	2681	N	ASP	279	46.315	40.023	67.166	1.00	20.00
ATOM	2683	CA	ASP	279	45.606	40.114	68.405	1.00	20.00
ATOM	2684	CB	ASP	279	44.241	39.407	68.379	1.00	20.00
ATOM	2685	CG	ASP	279	43.322	40.199	67.462	1.00	20.00
ATOM	2686	OD1	ASP	279	42.154	39.763	67.277	1.00	20.00

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ATOM   2687  OD2 ASP   279      43.775  41.249  66.933  1.00 20.00
ATOM   2688  C   ASP   279      46.411  39.511  69.499  1.00 20.00
ATOM   2689  O   ASP   279      45.855  38.829  70.358  1.00 20.00
 OM    2690  N   HIS   280      47.734  39.785  69.489  1.00 20.00
 OM    2692  CA  HIS   280      48.681  39.334  70.470  1.00 20.00
ATOM   2693  CB  HIS   280      48.754  40.258  71.699  1.00 20.00
ATOM   2694  CG  HIS   280      49.135  41.666  71.348  1.00 20.00
ATOM   2695  CD2 HIS   280      48.349  42.719  70.991  1.00 20.00
ATOM   2696  ND1 HIS   280      50.429  42.135  71.310  1.00 20.00
ATOM   2698  CE1 HIS   280      50.362  43.439  70.939  1.00 20.00
ATOM   2699  NE2 HIS   280      49.120  43.838  70.734  1.00 20.00
ATOM   2701  C   HIS   280      48.366  37.953  70.952  1.00 20.00
ATOM   2702  O   HIS   280      47.580  37.776  71.881  1.00 20.00
ATOM   2703  N   GLY   281      48.995  36.923  70.355  1.00 20.00
ATOM   2705  CA  GLY   281      48.682  35.604  70.816  1.00 20.00
ATOM   2706  C   GLY   281      48.423  34.647  69.699  1.00 20.00
ATOM   2707  O   GLY   281      48.690  33.456  69.844  1.00 20.00
ATOM   2708  N   SER   282      47.885  35.107  68.558  1.00 20.00
ATOM   2710  CA  SER   282      47.678  34.134  67.527  1.00 20.00
ATOM   2711  CB  SER   282      46.238  34.105  66.986  1.00 20.00
ATOM   2712  OG  SER   282      45.340  33.698  68.009  1.00 20.00
ATOM   2714  C   SER   282      48.580  34.438  66.380  1.00 20.00
ATOM   2715  O   SER   282      48.556  35.531  65.817  1.00 20.00
ATOM   2716  N   CYS   283      49.418  33.454  66.015  1.00 20.00
ATOM   2718  CA  CYS   283      50.301  33.582  64.897  1.00 20.00
ATOM   2719  CB  CYS   283      51.643  32.884  65.166  1.00 20.00
ATOM   2720  SG  CYS   283      52.649  32.524  63.700  1.00 20.00
ATOM   2721  C   CYS   283      49.600  32.877  63.794  1.00 20.00
ATOM   2722  O   CYS   283      49.413  31.660  63.829  1.00 20.00
ATOM   2723  N   VAL   284      49.168  33.651  62.786  1.00 20.00
ATOM   2725  CA  VAL   284      48.455  33.081  61.690  1.00 20.00
ATOM   2726  CB  VAL   284      47.049  33.602  61.572  1.00 20.00
ATOM   2727  CG1 VAL   284      46.360  32.936  60.368  1.00 20.00
ATOM   2728  CG2 VAL   284      46.329  33.358  62.910  1.00 20.00
ATOM   2729  C   VAL   284      49.198  33.470  60.457  1.00 20.00
ATOM   2730  O   VAL   284      49.960  34.435  60.453  1.00 20.00
ATOM   2731  N   ARG   285      48.992  32.705  59.373  1.00 20.00
ATOM   2733  CA  ARG   285      49.660  32.950  58.131  1.00 20.00
ATOM   2734  CB  ARG   285      49.252  31.937  57.047  1.00 20.00
ATOM   2735  CG  ARG   285      49.876  32.202  55.676  1.00 20.00
ATOM   2736  CD  ARG   285      49.454  31.184  54.614  1.00 20.00
ATOM   2737  NE  ARG   285      49.985  31.653  53.304  1.00 20.00
ATOM   2739  CZ  ARG   285      50.013  30.806  52.234  1.00 20.00
ATOM   2740  NH1 ARG   285      49.586  29.517  52.373  1.00 20.00
ATOM   2743  NH2 ARG   285      50.465  31.249  51.025  1.00 20.00
ATOM   2746  C   ARG   285      49.296  34.308  57.634  1.00 20.00
ATOM   2747  O   ARG   285      50.145  35.029  57.112  1.00 20.00
ATOM   2748  N   ALA   286      48.017  34.702  57.781  1.00 20.00
ATOM   2750  CA  ALA   286      47.642  35.980  57.256  1.00 20.00
ATOM   2751  CB  ALA   286      46.727  35.885  56.023  1.00 20.00
ATOM   2752  C   ALA   286      46.913  36.796  58.272  1.00 20.00
ATOM   2753  O   ALA   286      46.410  36.290  59.274  1.00 20.00
ATOM   2754  N   CYS   287      46.855  38.113  58.006  1.00 20.00
ATOM   2756  CA  CYS   287      46.200  39.081  58.834  1.00 20.00
ATOM   2757  CB  CYS   287      46.299  40.502  58.269  1.00 20.00
ATOM   2758  SG  CYS   287      47.899  41.323  58.457  1.00 20.00
ATOM   2759  C   CYS   287      44.735  38.810  58.806  1.00 20.00
ATOM   2760  O   CYS   287      44.243  38.046  57.978  1.00 20.00
ATOM   2761  N   GLY   288      43.999  39.446  59.736  1.00 20.00
ATOM   2763  CA  GLY   288      42.575  39.329  59.719  1.00 20.00
ATOM   2764  C   GLY   288      42.177  40.174  58.549  1.00 20.00
ATOM   2765  O   GLY   288      42.978  40.948  58.028  1.00 20.00
ATOM   2766  N   ALA   289      40.906  40.066  58.126  1.00 20.00
ATOM   2768  CA  ALA   289      40.434  40.735  56.947  1.00 20.00
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ATOM	2769	CB	ALA	289	38.904	40.669	56.805	1.00	20.00
ATOM	2770	C	ALA	289	40.821	42.180	56.864	1.00	20.00
ATOM	2771	O	ALA	289	41.713	42.542	56.102	1.00	20.00
ATOM	2772	N	ASP	290	40.173	43.038	57.672	1.00	20.00
ATOM	2774	CA	ASP	290	40.355	44.462	57.620	1.00	20.00
ATOM	2775	CB	ASP	290	39.461	45.210	58.627	1.00	20.00
ATOM	2776	CG	ASP	290	38.016	45.075	58.168	1.00	20.00
ATOM	2777	OD1	ASP	290	37.104	45.361	58.989	1.00	20.00
ATOM	2778	OD2	ASP	290	37.805	44.683	56.989	1.00	20.00
ATOM	2779	C	ASP	290	41.768	44.843	57.925	1.00	20.00
ATOM	2780	O	ASP	290	42.165	45.983	57.690	1.00	20.00
ATOM	2781	N	SER	291	42.566	43.912	58.480	1.00	20.00
ATOM	2783	CA	SER	291	43.899	44.283	58.856	1.00	20.00
ATOM	2784	CB	SER	291	44.405	43.492	60.073	1.00	20.00
ATOM	2785	OG	SER	291	43.597	43.771	61.208	1.00	20.00
ATOM	2787	C	SER	291	44.881	44.081	57.740	1.00	20.00
ATOM	2788	O	SER	291	44.771	43.144	56.950	1.00	20.00
ATOM	2789	N	TYR	292	45.879	44.989	57.659	1.00	20.00
ATOM	2791	CA	TYR	292	46.897	44.937	56.647	1.00	20.00
ATOM	2792	CB	TYR	292	46.871	46.172	55.725	1.00	20.00
ATOM	2793	CG	TYR	292	47.867	45.995	54.629	1.00	20.00
ATOM	2794	CD1	TYR	292	47.565	45.202	53.546	1.00	20.00
ATOM	2795	CE1	TYR	292	48.422	45.115	52.473	1.00	20.00
ATOM	2796	CD2	TYR	292	49.031	46.728	54.606	1.00	20.00
ATOM	2797	CE2	TYR	292	49.894	46.647	53.537	1.00	20.00
ATOM	2798	CZ	TYR	292	49.588	45.840	52.468	1.00	20.00
ATOM	2799	OH	TYR	292	50.460	45.771	51.361	1.00	20.00
ATOM	2801	C	TYR	292	48.208	44.923	57.372	1.00	20.00
ATOM	2802	O	TYR	292	48.360	45.564	58.410	1.00	20.00
ATOM	2803	N	GLU	293	49.196	44.173	56.847	1.00	20.00
ATOM	2805	CA	GLU	293	50.458	44.087	57.520	1.00	20.00
ATOM	2806	CB	GLU	293	51.435	43.108	56.848	1.00	20.00
ATOM	2807	CG	GLU	293	50.980	41.649	56.936	1.00	20.00
ATOM	2808	CD	GLU	293	51.942	40.809	56.112	1.00	20.00
ATOM	2809	OE1	GLU	293	52.657	41.402	55.261	1.00	20.00
ATOM	2810	OE2	GLU	293	51.973	39.565	56.314	1.00	20.00
ATOM	2811	C	GLU	293	51.059	45.450	57.503	1.00	20.00
ATOM	2812	O	GLU	293	50.902	46.201	56.544	1.00	20.00
ATOM	2813	N	MET	294	51.769	45.811	58.585	1.00	20.00
ATOM	2815	CA	MET	294	52.333	47.123	58.656	1.00	20.00
ATOM	2816	CB	MET	294	53.112	47.352	59.960	1.00	20.00
ATOM	2817	CG	MET	294	53.536	48.804	60.183	1.00	20.00
ATOM	2818	SD	MET	294	54.296	49.118	61.805	1.00	20.00
ATOM	2819	CE	MET	294	52.763	48.901	62.755	1.00	20.00
ATOM	2820	C	MET	294	53.277	47.263	57.509	1.00	20.00
ATOM	2821	O	MET	294	53.288	48.282	56.821	1.00	20.00
ATOM	2822	N	GLU	295	54.092	46.223	57.261	1.00	20.00
ATOM	2824	CA	GLU	295	55.006	46.271	56.159	1.00	20.00
ATOM	2825	CB	GLU	295	56.483	46.382	56.567	1.00	20.00
ATOM	2826	CG	GLU	295	57.405	46.649	55.377	1.00	20.00
ATOM	2827	CD	GLU	295	57.090	48.047	54.861	1.00	20.00
ATOM	2828	OE1	GLU	295	56.385	48.150	53.821	1.00	20.00
ATOM	2829	OE2	GLU	295	57.540	49.030	55.507	1.00	20.00
ATOM	2830	C	GLU	295	54.838	44.988	55.415	1.00	20.00
ATOM	2831	O	GLU	295	54.121	44.094	55.859	1.00	20.00
ATOM	2832	N	GLU	296	55.490	44.866	54.244	1.00	20.00
ATOM	2834	CA	GLU	296	55.329	43.665	53.482	1.00	20.00
ATOM	2835	CB	GLU	296	56.167	43.632	52.194	1.00	20.00
ATOM	2836	CG	GLU	296	55.849	42.419	51.316	1.00	20.00
ATOM	2837	CD	GLU	296	56.724	42.489	50.075	1.00	20.00
ATOM	2838	OE1	GLU	296	57.977	42.466	50.233	1.00	20.00
ATOM	2839	OE2	GLU	296	56.157	42.569	48.956	1.00	20.00
ATOM	2840	C	GLU	296	55.774	42.521	54.331	1.00	20.00
ATOM	2841	O	GLU	296	55.066	41.525	54.468	1.00	20.00

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ATOM   2842  N   ASP  297      56.970  42.635  54.934  1.00 40.00
ATOM   2844  CA  ASP  297      57.418  41.570  55.776  1.00 40.00
ATOM   2845  CB  ASP  297      58.374  40.583  55.082  1.00 40.00
   OM  2846  CG  ASP  297      59.628  41.336  54.661  1.00 40.00
ATOM   2847  OD1 ASP  297      59.573  42.593  54.589  1.00 40.00
ATOM   2848  OD2 ASP  297      60.659  40.661  54.401  1.00 40.00
ATOM   2849  C   ASP  297      58.159  42.195  56.906  1.00 40.00
ATOM   2850  O   ASP  297      58.306  43.413  56.973  1.00 40.00
ATOM   2851  N   GLY  298      58.621  41.360  57.852  1.00 40.00
ATOM   2853  CA  GLY  298      59.365  41.874  58.959  1.00 40.00
ATOM   2854  C   GLY  298      58.382  42.422  59.933  1.00 40.00
ATOM   2855  O   GLY  298      58.728  42.737  61.071  1.00 40.00
ATOM   2856  N   VAL  299      57.114  42.556  59.503  1.00 40.00
ATOM   2858  CA  VAL  299      56.137  43.068  60.407  1.00 40.00
ATOM   2859  CB  VAL  299      55.345  44.214  59.844  1.00 40.00
ATOM   2860  CG1 VAL  299      56.292  45.415  59.674  1.00 40.00
ATOM   2861  CG2 VAL  299      54.702  43.772  58.520  1.00 40.00
ATOM   2862  C   VAL  299      55.203  41.967  60.792  1.00 40.00
ATOM   2863  O   VAL  299      54.374  41.506  60.010  1.00 40.00
ATOM   2864  N   ARG  300      55.364  41.477  62.030  1.00 20.00
ATOM   2866  CA  ARG  300      54.469  40.486  62.537  1.00 20.00
ATOM   2867  CB  ARG  300      54.946  39.864  63.859  1.00 20.00
ATOM   2868  CG  ARG  300      56.093  38.870  63.662  1.00 20.00
ATOM   2869  CD  ARG  300      57.381  39.499  63.127  1.00 20.00
ATOM   2870  NE  ARG  300      58.323  38.383  62.831  1.00 20.00
ATOM   2872  CZ  ARG  300      59.632  38.640  62.541  1.00 20.00
ATOM   2873  NH1 ARG  300      60.101  39.922  62.564  1.00 20.00
ATOM   2876  NH2 ARG  300      60.473  37.612  62.228  1.00 20.00
ATOM   2879  C   ARG  300      53.169  41.175  62.776  1.00 20.00
ATOM   2880  O   ARG  300      52.100  40.597  62.589  1.00 20.00
ATOM   2881  N   LYS  301      53.247  42.451  63.196  1.00 20.00
ATOM   2883  CA  LYS  301      52.083  43.220  63.518  1.00 20.00
ATOM   2884  CB  LYS  301      52.403  44.615  64.088  1.00 20.00
ATOM   2885  CG  LYS  301      52.891  44.624  65.538  1.00 20.00
ATOM   2886  CD  LYS  301      51.836  44.146  66.537  1.00 20.00
ATOM   2887  CE  LYS  301      52.219  44.386  68.000  1.00 20.00
ATOM   2888  NZ  LYS  301      51.988  45.804  68.357  1.00 20.00
ATOM   2892  C   LYS  301      51.244  43.447  62.312  1.00 20.00
ATOM   2893  O   LYS  301      51.740  43.586  61.194  1.00 20.00
ATOM   2894  N   CYS  302      49.917  43.473  62.525  1.00 20.00
ATOM   2896  CA  CYS  302      49.042  43.769  61.443  1.00 20.00
ATOM   2897  CB  CYS  302      48.002  42.684  61.152  1.00 20.00
ATOM   2898  SG  CYS  302      47.330  42.959  59.499  1.00 20.00
ATOM   2899  C   CYS  302      48.314  44.990  61.905  1.00 20.00
ATOM   2900  O   CYS  302      48.036  45.132  63.095  1.00 20.00
ATOM   2901  N   LYS  303      48.003  45.922  60.983  1.00 20.00
ATOM   2903  CA  LYS  303      47.356  47.128  61.407  1.00 20.00
ATOM   2904  CB  LYS  303      48.242  48.374  61.231  1.00 20.00
ATOM   2905  CG  LYS  303      48.792  48.550  59.816  1.00 20.00
ATOM   2906  CD  LYS  303      49.481  49.898  59.594  1.00 20.00
ATOM   2907  CE  LYS  303      50.235  49.985  58.265  1.00 20.00
ATOM   2908  NZ  LYS  303      50.850  51.323  58.116  1.00 20.00
ATOM   2912  C   LYS  303      46.078  47.329  60.654  1.00 20.00
ATOM   2913  O   LYS  303      45.879  46.778  59.574  1.00 20.00
ATOM   2914  N   LYS  304      45.169  48.129  61.247  1.00 20.00
ATOM   2916  CA  LYS  304      43.869  48.421  60.711  1.00 20.00
ATOM   2917  CB  LYS  304      43.032  49.283  61.672  1.00 20.00
ATOM   2918  CG  LYS  304      41.630  49.631  61.174  1.00 20.00
ATOM   2919  CD  LYS  304      40.782  50.330  62.240  1.00 20.00
ATOM   2920  CE  LYS  304      39.436  50.849  61.726  1.00 20.00
ATOM   2921  NZ  LYS  304      38.423  49.771  61.774  1.00 20.00
ATOM   2925  C   LYS  304      43.997  49.190  59.438  1.00 20.00
ATOM   2926  O   LYS  304      44.899  50.012  59.285  1.00 20.00
ATOM   2927  N   CYS  305      43.095  48.927  58.472  1.00 20.00
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ATOM   2929  CA  CYS   305      43.164  49.684  57.260  1.00 20.00
ATOM   2930  CB  CYS   305      43.302  48.823  55.985  1.00 20.00
ATOM   2931  SG  CYS   305      41.828  47.850  55.573  1.00 20.00
ATOM   2932  C   CYS   305      41.923  50.512  57.184  1.00 20.00
ATOM   2933  O   CYS   305      40.806  49.999  57.237  1.00 20.00
ATOM   2934  N   GLU   306      42.086  51.844  57.077  1.00 20.00
ATOM   2936  CA  GLU   306      40.918  52.669  57.024  1.00 20.00
ATOM   2937  CB  GLU   306      41.217  54.178  57.005  1.00 20.00
ATOM   2938  CG  GLU   306      41.776  54.707  58.328  1.00 20.00
ATOM   2939  CD  GLU   306      40.654  54.677  59.357  1.00 20.00
ATOM   2940  OE1 GLU   306      39.574  54.114  59.035  1.00 20.00
ATOM   2941  OE2 GLU   306      40.861  55.214  60.478  1.00 20.00
ATOM   2942  C   GLU   306      40.199  52.336  55.763  1.00 20.00
ATOM   2943  O   GLU   306      40.732  52.501  54.667  1.00 20.00
ATOM   2944  N   GLY   307      38.949  51.857  55.896  1.00 20.00
ATOM   2946  CA  GLY   307      38.172  51.522  54.741  1.00 20.00
ATOM   2947  C   GLY   307      38.614  50.195  54.230  1.00 20.00
ATOM   2948  O   GLY   307      39.196  49.387  54.951  1.00 20.00
ATOM   2949  N   PRO   308      38.336  49.955  52.980  1.00 20.00
ATOM   2950  CD  PRO   308      37.118  50.454  52.364  1.00 20.00
ATOM   2951  CA  PRO   308      38.754  48.713  52.409  1.00 20.00
ATOM   2952  CB  PRO   308      38.045  48.614  51.062  1.00 20.00
ATOM   2953  CG  PRO   308      36.747  49.414  51.290  1.00 20.00
ATOM   2954  C   PRO   308      40.240  48.737  52.352  1.00 20.00
ATOM   2955  O   PRO   308      40.805  49.802  52.108  1.00 20.00
ATOM   2956  N   CYS   309      40.901  47.588  52.578  1.00 20.00
ATOM   2958  CA  CYS   309      42.329  47.631  52.587  1.00 20.00
ATOM   2959  CB  CYS   309      43.015  46.386  53.168  1.00 20.00
ATOM   2960  SG  CYS   309      42.556  46.072  54.897  1.00 20.00
ATOM   2961  C   CYS   309      42.789  47.801  51.182  1.00 20.00
ATOM   2962  O   CYS   309      42.104  47.406  50.240  1.00 20.00
ATOM   2963  N   ARG   310      43.972  48.421  51.015  1.00 20.00
ATOM   2965  CA  ARG   310      44.498  48.664  49.709  1.00 20.00
ATOM   2966  CB  ARG   310      45.726  49.594  49.699  1.00 20.00
ATOM   2967  CG  ARG   310      45.450  51.064  50.032  1.00 20.00
ATOM   2968  CD  ARG   310      44.884  51.307  51.433  1.00 20.00
ATOM   2969  NE  ARG   310      43.403  51.169  51.346  1.00 20.00
ATOM   2971  CZ  ARG   310      42.641  52.281  51.125  1.00 20.00
ATOM   2972  NH1 ARG   310      43.236  53.506  51.036  1.00 20.00
ATOM   2975  NH2 ARG   310      41.286  52.172  50.995  1.00 20.00
ATOM   2978  C   ARG   310      44.942  47.373  49.114  1.00 20.00
ATOM   2979  O   ARG   310      45.419  46.479  49.811  1.00 20.00
ATOM   2980  N   LYS   311      44.756  47.247  47.787  1.00 20.00
ATOM   2982  CA  LYS   311      45.195  46.091  47.069  1.00 20.00
ATOM   2983  CB  LYS   311      44.107  45.021  46.887  1.00 20.00
ATOM   2984  CG  LYS   311      44.629  43.707  46.300  1.00 20.00
ATOM   2985  CD  LYS   311      45.570  42.946  47.238  1.00 20.00
ATOM   2986  CE  LYS   311      45.948  41.554  46.727  1.00 20.00
ATOM   2987  NZ  LYS   311      46.769  41.667  45.501  1.00 20.00
ATOM   2991  C   LYS   311      45.555  46.607  45.717  1.00 20.00
ATOM   2992  O   LYS   311      45.116  47.685  45.323  1.00 20.00
ATOM   2993  N   VAL   312      46.387  45.862  44.968  1.00 20.00
ATOM   2995  CA  VAL   312      46.732  46.345  43.667  1.00 20.00
ATOM   2996  CB  VAL   312      47.842  45.578  43.012  1.00 20.00
ATOM   2997  CG1 VAL   312      48.059  46.152  41.602  1.00 20.00
ATOM   2998  CG2 VAL   312      49.087  45.658  43.911  1.00 20.00
ATOM   2999  C   VAL   312      45.491  46.195  42.799  1.00 20.00
ATOM   3000  O   VAL   312      44.922  47.244  42.394  1.00 20.00
ATOM   3001  OXT VAL   312      45.095  45.029  42.529  1.00 20.00
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ATOM      3  N   CYS   313      54.063   9.046  61.837  1.00 40.00
ATOM      5  CA  CYS   313      54.050   8.871  60.363  1.00 40.00
ATOM      6  CB  CYS   313      53.300   7.570  60.029  1.00 40.00
ATOM      7  SG  CYS   313      54.210   6.124  60.659  1.00 40.00
ATOM      8  C   CYS   313      53.390  10.060  59.715  1.00 40.00
ATOM      9  O   CYS   313      52.565  10.713  60.344  1.00 40.00
ATOM     10  N   ASN   314      53.749  10.398  58.452  1.00 40.00
ATOM     12  CA  ASN   314      53.183  11.550  57.785  1.00 40.00
ATOM     13  CB  ASN   314      54.130  12.176  56.746  1.00 40.00
ATOM     14  CG  ASN   314      54.433  11.136  55.678  1.00 40.00
ATOM     15  OD1 ASN   314      54.238   9.938  55.880  1.00 40.00
ATOM     16  ND2 ASN   314      54.937  11.606  54.505  1.00 40.00
ATOM     19  C   ASN   314      51.911  11.161  57.091  1.00 40.00
ATOM     20  O   ASN   314      51.514   9.999  57.138  1.00 40.00
ATOM     21  N   GLY   315      51.235  12.143  56.442  1.00 20.00
ATOM     23  CA  GLY   315      49.998  11.903  55.745  1.00 20.00
ATOM     24  C   GLY   315      50.241  10.746  54.839  1.00 20.00
ATOM     25  O   GLY   315      51.148  10.775  54.010  1.00 20.00
ATOM     26  N   ILE   316      49.421   9.689  54.982  1.00 20.00
ATOM     28  CA  ILE   316      49.654   8.506  54.212  1.00 20.00
ATOM     29  CB  ILE   316      49.701   7.266  55.060  1.00 20.00
ATOM     30  CG2 ILE   316      49.810   6.043  54.134  1.00 20.00
ATOM     31  CG1 ILE   316      50.840   7.372  56.089  1.00 20.00
ATOM     32  CD1 ILE   316      50.774   6.314  57.189  1.00 20.00
ATOM     33  C   ILE   316      48.554   8.324  53.222  1.00 20.00
ATOM     34  O   ILE   316      47.383   8.559  53.518  1.00 20.00
ATOM     35  N   GLY   317      48.916   7.913  51.992  1.00 20.00
ATOM     37  CA  GLY   317      47.898   7.677  51.018  1.00 20.00
ATOM     38  C   GLY   317      48.178   6.350  50.401  1.00 20.00
ATOM     39  O   GLY   317      48.942   6.247  49.443  1.00 20.00
ATOM     40  N   ILE   318      47.543   5.290  50.933  1.00 20.00
ATOM     42  CA  ILE   318      47.728   3.986  50.371  1.00 20.00
ATOM     43  CB  ILE   318      47.758   2.881  51.385  1.00 20.00
ATOM     44  CG2 ILE   318      49.016   3.053  52.249  1.00 20.00
ATOM     45  CG1 ILE   318      46.447   2.831  52.178  1.00 20.00
ATOM     46  CD1 ILE   318      46.354   1.602  53.078  1.00 20.00
ATOM     47  C   ILE   318      46.595   3.745  49.429  1.00 20.00
ATOM     48  O   ILE   318      45.691   4.571  49.319  1.00 20.00
ATOM     49  N   GLY   319      46.626   2.611  48.699  1.00 40.00
ATOM     51  CA  GLY   319      45.557   2.342  47.782  1.00 40.00
ATOM     52  C   GLY   319      46.137   2.189  46.416  1.00 40.00
ATOM     53  O   GLY   319      46.896   1.261  46.142  1.00 40.00
ATOM     54  N   GLU   320      45.781   3.123  45.516  1.00 40.00
ATOM     56  CA  GLU   320      46.284   3.084  44.178  1.00 40.00
ATOM     57  CB  GLU   320      47.797   3.351  44.098  1.00 40.00
ATOM     58  CG  GLU   320      48.335   3.435  42.670  1.00 40.00
ATOM     59  CD  GLU   320      49.826   3.732  42.752  1.00 40.00
ATOM     60  OE1 GLU   320      50.461   3.873  41.673  1.00 40.00
ATOM     61  OE2 GLU   320      50.350   3.829  43.894  1.00 40.00
ATOM     62  C   GLU   320      46.002   1.771  43.534  1.00 40.00
ATOM     63  O   GLU   320      46.780   0.825  43.637  1.00 40.00
ATOM     64  N   PHE   321      44.840   1.688  42.861  1.00 60.00
ATOM     66  CA  PHE   321      44.481   0.492  42.166  1.00 60.00
ATOM     67  CB  PHE   321      43.051   0.531  41.598  1.00 60.00
ATOM     68  CG  PHE   321      42.809  -0.724  40.830  1.00 60.00
ATOM     69  CD1 PHE   321      43.173  -0.813  39.504  1.00 60.00
ATOM     70  CD2 PHE   321      42.188  -1.800  41.418  1.00 60.00
ATOM     71  CE1 PHE   321      42.944  -1.958  38.780  1.00 60.00
ATOM     72  CE2 PHE   321      41.947  -2.947  40.697  1.00 60.00
ATOM     73  CZ  PHE   321      42.326  -3.028  39.379  1.00 60.00
ATOM     74  C   PHE   321      45.414   0.351  41.014  1.00 60.00
ATOM     75  O   PHE   321      45.223   0.969  39.967  1.00 60.00
ATOM     76  N   LYS   322      46.461  -0.474  41.190  1.00 60.00
ATOM     78  CA  LYS   322      47.379  -0.713  40.121  1.00 60.00
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Figure 7

A	79	CB	LYS	322	48.815	-0.252	40.428	1.00	60.00
ATOM	80	CG	LYS	322	49.803	-0.503	39.286	1.00	60.00
ATOM	81	CD	LYS	322	49.579	0.390	38.062	1.00	60.00
M	82	CE	LYS	322	48.513	-0.125	37.093	1.00	60.00
ATOM	83	NZ	LYS	322	48.375	0.808	35.950	1.00	60.00
ATOM	87	C	LYS	322	47.420	-2.191	39.932	1.00	60.00
ATOM	88	O	LYS	322	47.746	-2.936	40.855	1.00	60.00
ATOM	89	N	ASP	323	47.051	-2.658	38.726	1.00	60.00
ATOM	91	CA	ASP	323	47.099	-4.062	38.456	1.00	60.00
ATOM	92	CB	ASP	323	46.397	-4.458	37.143	1.00	60.00
ATOM	93	CG	ASP	323	47.108	-3.784	35.978	1.00	60.00
ATOM	94	OD1	ASP	323	47.322	-4.469	34.942	1.00	60.00
ATOM	95	OD2	ASP	323	47.433	-2.574	36.104	1.00	60.00
ATOM	96	C	ASP	323	48.538	-4.441	38.350	1.00	60.00
ATOM	97	O	ASP	323	48.930	-5.553	38.698	1.00	60.00
ATOM	98	N	SER	324	49.371	-3.492	37.882	1.00	60.00
ATOM	100	CA	SER	324	50.760	-3.756	37.658	1.00	60.00
ATOM	101	CB	SER	324	51.544	-2.494	37.259	1.00	60.00
ATOM	102	OG	SER	324	51.058	-1.985	36.026	1.00	60.00
ATOM	104	C	SER	324	51.395	-4.290	38.899	1.00	60.00
ATOM	105	O	SER	324	52.008	-5.357	38.874	1.00	60.00
ATOM	106	N	LEU	325	51.255	-3.578	40.032	1.00	60.00
ATOM	108	CA	LEU	325	51.896	-4.060	41.219	1.00	60.00
ATOM	109	CB	LEU	325	51.804	-3.116	42.430	1.00	60.00
ATOM	110	CG	LEU	325	52.625	-1.823	42.267	1.00	60.00
ATOM	111	CD1	LEU	325	52.077	-0.948	41.128	1.00	60.00
ATOM	112	CD2	LEU	325	52.755	-1.070	43.601	1.00	60.00
ATOM	113	C	LEU	325	51.288	-5.362	41.603	1.00	60.00
ATOM	114	O	LEU	325	50.220	-5.735	41.119	1.00	60.00
ATOM	115	N	SER	326	51.986	-6.105	42.482	1.00	60.00
ATOM	117	CA	SER	326	51.499	-7.384	42.897	1.00	60.00
ATOM	118	CB	SER	326	52.451	-8.095	43.874	1.00	60.00
ATOM	119	OG	SER	326	51.915	-9.354	44.250	1.00	60.00
ATOM	121	C	SER	326	50.202	-7.174	43.599	1.00	60.00
ATOM	122	O	SER	326	49.180	-7.743	43.219	1.00	60.00
ATOM	123	N	ILE	327	50.204	-6.324	44.644	1.00	60.00
ATOM	125	CA	ILE	327	48.983	-6.090	45.352	1.00	60.00
ATOM	126	CB	ILE	327	48.834	-6.950	46.573	1.00	60.00
ATOM	127	CG2	ILE	327	49.917	-6.537	47.583	1.00	60.00
ATOM	128	CG1	ILE	327	47.402	-6.864	47.126	1.00	60.00
ATOM	129	CD1	ILE	327	46.352	-7.480	46.202	1.00	60.00
ATOM	130	C	ILE	327	48.969	-4.668	45.802	1.00	60.00
ATOM	131	O	ILE	327	50.015	-4.078	46.071	1.00	60.00
ATOM	132	N	ASN	328	47.762	-4.072	45.865	1.00	40.00
ATOM	134	CA	ASN	328	47.611	-2.726	46.322	1.00	40.00
ATOM	135	CB	ASN	328	46.295	-2.093	45.841	1.00	40.00
ATOM	136	CG	ASN	328	46.384	-1.981	44.323	1.00	40.00
ATOM	137	OD1	ASN	328	47.466	-1.791	43.771	1.00	40.00
ATOM	138	ND2	ASN	328	45.223	-2.111	43.626	1.00	40.00
ATOM	141	C	ASN	328	47.578	-2.827	47.812	1.00	40.00
ATOM	142	O	ASN	328	47.893	-1.878	48.529	1.00	40.00
ATOM	143	N	ALA	329	47.214	-4.025	48.301	1.00	40.00
ATOM	145	CA	ALA	329	47.117	-4.326	49.698	1.00	40.00
ATOM	146	CB	ALA	329	46.633	-5.761	49.967	1.00	40.00
ATOM	147	C	ALA	329	48.482	-4.197	50.290	1.00	40.00
ATOM	148	O	ALA	329	48.636	-3.841	51.456	1.00	40.00
ATOM	149	N	THR	330	49.518	-4.458	49.476	1.00	40.00
ATOM	151	CA	THR	330	50.871	-4.441	49.946	1.00	40.00
ATOM	152	CB	THR	330	51.875	-4.612	48.845	1.00	40.00
ATOM	153	OG1	THR	330	53.174	-4.807	49.385	1.00	40.00
ATOM	155	CG2	THR	330	51.853	-3.347	47.972	1.00	40.00
ATOM	156	C	THR	330	51.143	-3.117	50.583	1.00	40.00
ATOM	157	O	THR	330	51.963	-3.021	51.493	1.00	40.00
ATOM	158	N	ASN	331	50.459	-2.059	50.112	1.00	40.00

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ATOM    160  CA  ASN   331      50.645  -0.728  50.616  1.00 40.00
ATOM    161  CB  ASN   331      49.784   0.317  49.883  1.00 40.00
ATOM    162  CG  ASN   331      50.411   0.592  48.522  1.00 40.00
ATOM    163  OD1 ASN   331      50.424  -0.259  47.634  1.00 40.00
ATOM    164  ND2 ASN   331      50.947   1.831  48.353  1.00 40.00
ATOM    167  C   ASN   331      50.311  -0.634  52.079  1.00 40.00
ATOM    168  O   ASN   331      50.896   0.175  52.796  1.00 40.00
ATOM    169  N   ILE   332      49.370  -1.468  52.558  1.00 40.00
ATOM    171  CA  ILE   332      48.883  -1.467  53.915  1.00 40.00
ATOM    172  CB  ILE   332      47.753  -2.450  54.108  1.00 40.00
ATOM    173  CG2 ILE   332      47.465  -2.606  55.611  1.00 40.00
ATOM    174  CG1 ILE   332      46.510  -1.984  53.324  1.00 40.00
ATOM    175  CD1 ILE   332      46.687  -1.946  51.808  1.00 40.00
ATOM    176  C   ILE   332      49.982  -1.751  54.903  1.00 40.00
ATOM    177  O   ILE   332      49.872  -1.399  56.076  1.00 40.00
ATOM    178  N   LYS   333      51.066  -2.412  54.462  1.00 40.00
ATOM    180  CA  LYS   333      52.173  -2.772  55.309  1.00 40.00
ATOM    181  CB  LYS   333      53.279  -3.515  54.544  1.00 40.00
ATOM    182  CG  LYS   333      52.838  -4.845  53.933  1.00 40.00
ATOM    183  CD  LYS   333      53.866  -5.413  52.953  1.00 40.00
ATOM    184  CE  LYS   333      53.457  -6.746  52.323  1.00 40.00
ATOM    185  NZ  LYS   333      54.529  -7.228  51.422  1.00 40.00
ATOM    189  C   LYS   333      52.828  -1.565  55.913  1.00 40.00
ATOM    190  O   LYS   333      53.348  -1.628  57.025  1.00 40.00
ATOM    191  N   HIS   334      52.803  -0.423  55.204  1.00 40.00
ATOM    193  CA  HIS   334      53.459   0.777  55.644  1.00 40.00
ATOM    194  CB  HIS   334      53.101   1.980  54.753  1.00 40.00
ATOM    195  CG  HIS   334      53.623   3.291  55.265  1.00 40.00
ATOM    196  CD2 HIS   334      52.952   4.317  55.858  1.00 40.00
ATOM    197  ND1 HIS   334      54.937   3.695  55.190  1.00 40.00
ATOM    199  CE1 HIS   334      54.996   4.935  55.738  1.00 40.00
ATOM    200  NE2 HIS   334      53.816   5.355  56.157  1.00 40.00
ATOM    202  C   HIS   334      53.016   1.117  57.030  1.00 40.00
ATOM    203  O   HIS   334      53.778   1.672  57.818  1.00 40.00
ATOM    204  N   PHE   335      51.753   0.791  57.336  1.00 40.00
ATOM    206  CA  PHE   335      51.061   1.055  58.562  1.00 40.00
ATOM    207  CB  PHE   335      49.554   0.799  58.431  1.00 40.00
ATOM    208  CG  PHE   335      49.102   1.681  57.320  1.00 40.00
ATOM    209  CD1 PHE   335      48.896   1.164  56.062  1.00 40.00
ATOM    210  CD2 PHE   335      49.140   3.047  57.469  1.00 40.00
ATOM    211  CE1 PHE   335      48.627   1.983  54.990  1.00 40.00
ATOM    212  CE2 PHE   335      48.902   3.873  56.397  1.00 40.00
ATOM    213  CZ  PHE   335      48.625   3.345  55.159  1.00 40.00
ATOM    214  C   PHE   335      51.559   0.283  59.744  1.00 40.00
ATOM    215  O   PHE   335      51.268   0.647  60.879  1.00 40.00
ATOM    216  N   LYS   336      52.301  -0.815  59.536  1.00 40.00
ATOM    218  CA  LYS   336      52.650  -1.655  60.647  1.00 40.00
ATOM    219  CB  LYS   336      53.554  -2.830  60.237  1.00 40.00
ATOM    220  CG  LYS   336      52.800  -3.964  59.540  1.00 40.00
ATOM    221  CD  LYS   336      51.765  -4.630  60.450  1.00 40.00
ATOM    222  CE  LYS   336      50.988  -5.769  59.788  1.00 40.00
ATOM    223  NZ  LYS   336      50.020  -6.339  60.752  1.00 40.00
ATOM    227  C   LYS   336      53.325  -0.951  61.793  1.00 40.00
ATOM    228  O   LYS   336      53.026  -1.250  62.946  1.00 40.00
ATOM    229  N   ASN   337      54.284  -0.045  61.530  1.00 40.00
ATOM    231  CA  ASN   337      54.995   0.629  62.589  1.00 40.00
ATOM    232  CB  ASN   337      56.335   1.211  62.109  1.00 40.00
ATOM    233  CG  ASN   337      57.267   0.038  61.842  1.00 40.00
ATOM    234  OD1 ASN   337      57.310  -0.920  62.613  1.00 40.00
ATOM    235  ND2 ASN   337      58.031   0.106  60.719  1.00 40.00
ATOM    238  C   ASN   337      54.274   1.726  63.336  1.00 40.00
ATOM    239  O   ASN   337      54.441   1.867  64.546  1.00 40.00
ATOM    240  N   CYS   338      53.450   2.529  62.634  1.00 20.00
ATOM    242  CA  CYS   338      52.859   3.733  63.159  1.00 20.00
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A	243	CB	CYS	338	52.042	4.491	62.087	1.00	20.00
ATOM	244	SG	CYS	338	52.908	4.575	60.487	1.00	20.00
ATOM	245	C	CYS	338	51.966	3.576	64.354	1.00	20.00
M	246	O	CYS	338	50.994	2.823	64.335	1.00	20.00
ATOM	247	N	THR	339	52.356	4.224	65.473	1.00	20.00
ATOM	249	CA	THR	339	51.526	4.354	66.634	1.00	20.00
ATOM	250	CB	THR	339	52.332	4.553	67.880	1.00	20.00
ATOM	251	OG1	THR	339	51.470	4.672	69.000	1.00	20.00
ATOM	253	CG2	THR	339	53.197	5.812	67.719	1.00	20.00
ATOM	254	C	THR	339	50.613	5.531	66.451	1.00	20.00
ATOM	255	O	THR	339	49.437	5.490	66.809	1.00	20.00
ATOM	256	N	SER	340	51.146	6.642	65.898	1.00	20.00
ATOM	258	CA	SER	340	50.317	7.795	65.714	1.00	20.00
ATOM	259	CB	SER	340	50.454	8.820	66.856	1.00	20.00
ATOM	260	OG	SER	340	51.788	9.301	66.938	1.00	20.00
ATOM	262	C	SER	340	50.677	8.482	64.438	1.00	20.00
ATOM	263	O	SER	340	51.676	9.194	64.362	1.00	20.00
ATOM	264	N	ILE	341	49.850	8.318	63.390	1.00	20.00
ATOM	266	CA	ILE	341	50.200	8.984	62.177	1.00	20.00
ATOM	267	CB	ILE	341	49.518	8.470	60.942	1.00	20.00
ATOM	268	CG2	ILE	341	50.047	7.067	60.638	1.00	20.00
ATOM	269	CG1	ILE	341	47.995	8.562	61.072	1.00	20.00
ATOM	270	CD1	ILE	341	47.273	8.284	59.755	1.00	20.00
ATOM	271	C	ILE	341	49.868	10.426	62.330	1.00	20.00
ATOM	272	O	ILE	341	48.711	10.792	62.521	1.00	20.00
ATOM	273	N	SER	342	50.901	11.287	62.273	1.00	20.00
ATOM	275	CA	SER	342	50.671	12.692	62.381	1.00	20.00
ATOM	276	CB	SER	342	51.889	13.483	62.888	1.00	20.00
ATOM	277	OG	SER	342	52.193	13.107	64.223	1.00	20.00
ATOM	279	C	SER	342	50.364	13.165	61.002	1.00	20.00
ATOM	280	O	SER	342	51.259	13.536	60.243	1.00	20.00
ATOM	281	N	GLY	343	49.065	13.173	60.654	1.00	20.00
ATOM	283	CA	GLY	343	48.661	13.571	59.341	1.00	20.00
ATOM	284	C	GLY	343	47.366	12.873	59.096	1.00	20.00
ATOM	285	O	GLY	343	46.609	12.606	60.026	1.00	20.00
ATOM	286	N	ASP	344	47.073	12.555	57.824	1.00	20.00
ATOM	288	CA	ASP	344	45.833	11.906	57.524	1.00	20.00
ATOM	289	CB	ASP	344	44.961	12.709	56.536	1.00	20.00
ATOM	290	CG	ASP	344	45.728	12.897	55.232	1.00	20.00
ATOM	291	OD1	ASP	344	46.922	12.501	55.179	1.00	20.00
ATOM	292	OD2	ASP	344	45.130	13.455	54.272	1.00	20.00
ATOM	293	C	ASP	344	46.100	10.563	56.933	1.00	20.00
ATOM	294	O	ASP	344	47.197	10.290	56.452	1.00	20.00
ATOM	295	N	LEU	345	45.098	9.664	56.999	1.00	20.00
ATOM	297	CA	LEU	345	45.262	8.362	56.427	1.00	20.00
ATOM	298	CB	LEU	345	45.064	7.222	57.438	1.00	20.00
ATOM	299	CG	LEU	345	45.234	5.831	56.810	1.00	20.00
ATOM	300	CD1	LEU	345	46.611	5.704	56.157	1.00	20.00
ATOM	301	CD2	LEU	345	44.967	4.716	57.834	1.00	20.00
ATOM	302	C	LEU	345	44.237	8.203	55.351	1.00	20.00
ATOM	303	O	LEU	345	43.061	8.494	55.558	1.00	20.00
ATOM	304	N	HIS	346	44.671	7.763	54.152	1.00	20.00
ATOM	306	CA	HIS	346	43.738	7.541	53.085	1.00	20.00
ATOM	307	CB	HIS	346	43.989	8.395	51.827	1.00	20.00
ATOM	308	CG	HIS	346	43.667	9.851	51.988	1.00	20.00
ATOM	309	CD2	HIS	346	42.906	10.487	52.921	1.00	20.00
ATOM	310	ND1	HIS	346	44.071	10.828	51.105	1.00	20.00
ATOM	312	CE1	HIS	346	43.545	11.998	51.546	1.00	20.00
ATOM	313	NE2	HIS	346	42.830	11.841	52.645	1.00	20.00
ATOM	315	C	HIS	346	43.890	6.122	52.650	1.00	20.00
ATOM	316	O	HIS	346	44.995	5.670	52.356	1.00	20.00
ATOM	317	N	ILE	347	42.778	5.366	52.619	1.00	20.00
ATOM	319	CA	ILE	347	42.884	4.018	52.151	1.00	20.00
ATOM	320	CB	ILE	347	42.422	3.010	53.159	1.00	20.00

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ATOM    321  CG2 ILE   347      42.527   1.621  52.511  1.00 20.00
ATOM    322  CG1 ILE   347      43.253   3.143  54.449  1.00 20.00
ATOM    323  CD1 ILE   347      42.665   2.393  55.644  1.00 20.00
ATOM    324  C   ILE   347      42.000   3.938  50.952  1.00 20.00
ATOM    325  O   ILE   347      40.795   3.715  51.052  1.00 20.00
ATOM    326  N   LEU   348      42.607   4.094  49.766  1.00 20.00
ATOM    328  CA  LEU   348      41.882   4.138  48.533  1.00 20.00
ATOM    329  CB  LEU   348      42.700   4.845  47.444  1.00 20.00
ATOM    330  CG  LEU   348      43.043   6.285  47.877  1.00 20.00
ATOM    331  CD1 LEU   348      43.859   7.034  46.817  1.00 20.00
ATOM    332  CD2 LEU   348      41.778   7.053  48.295  1.00 20.00
ATOM    333  C   LEU   348      41.557   2.743  48.110  1.00 20.00
ATOM    334  O   LEU   348      41.948   1.769  48.753  1.00 20.00
ATOM    335  N   PRO   349      40.852   2.625  47.019  1.00 60.00
ATOM    336  CD  PRO   349      40.061   3.714  46.470  1.00 60.00
ATOM    337  CA  PRO   349      40.393   1.344  46.575  1.00 60.00
ATOM    338  CB  PRO   349      39.558   1.614  45.327  1.00 60.00
ATOM    339  CG  PRO   349      39.008   3.034  45.575  1.00 60.00
ATOM    340  C   PRO   349      41.486   0.350  46.425  1.00 60.00
ATOM    341  O   PRO   349      42.349   0.514  45.563  1.00 60.00
ATOM    342  N   VAL   350      41.442  -0.704  47.259  1.00 60.00
ATOM    344  CA  VAL   350      42.426  -1.737  47.213  1.00 60.00
ATOM    345  CB  VAL   350      43.285  -1.798  48.441  1.00 60.00
ATOM    346  CG1 VAL   350      42.379  -2.090  49.649  1.00 60.00
ATOM    347  CG2 VAL   350      44.379  -2.856  48.224  1.00 60.00
ATOM    348  C   VAL   350      41.677  -3.023  47.137  1.00 60.00
ATOM    349  O   VAL   350      40.582  -3.149  47.684  1.00 60.00
ATOM    350  N   ALA   351      42.250  -4.012  46.429  1.00 60.00
ATOM    352  CA  ALA   351      41.609  -5.287  46.311  1.00 60.00
ATOM    353  CB  ALA   351      41.491  -5.785  44.861  1.00 60.00
ATOM    354  C   ALA   351      42.473  -6.255  47.046  1.00 60.00
ATOM    355  O   ALA   351      43.584  -5.918  47.450  1.00 60.00
ATOM    356  N   PHE   352      41.974  -7.487  47.264  1.00 60.00
ATOM    358  CA  PHE   352      42.778  -8.437  47.974  1.00 60.00
ATOM    359  CB  PHE   352      42.087  -9.007  49.226  1.00 60.00
ATOM    360  CG  PHE   352      43.030  -9.963  49.871  1.00 60.00
ATOM    361  CD1 PHE   352      44.096  -9.492  50.603  1.00 60.00
ATOM    362  CD2 PHE   352      42.811 -11.320  49.813  1.00 60.00
ATOM    363  CE1 PHE   352      44.955 -10.359  51.235  1.00 60.00
ATOM    364  CE2 PHE   352      43.661 -12.192  50.452  1.00 60.00
ATOM    365  CZ  PHE   352      44.739 -11.712  51.161  1.00 60.00
ATOM    366  C   PHE   352      43.092  -9.582  47.065  1.00 60.00
ATOM    367  O   PHE   352      42.202 -10.173  46.456  1.00 60.00
ATOM    368  N   ARG   353      44.394  -9.908  46.946  1.00 60.00
ATOM    370  CA  ARG   353      44.828 -10.999  46.123  1.00 60.00
ATOM    371  CB  ARG   353      44.901 -10.663  44.623  1.00 60.00
ATOM    372  CG  ARG   353      43.555 -10.313  43.988  1.00 60.00
ATOM    373  CD  ARG   353      43.617 -10.218  42.462  1.00 60.00
ATOM    374  NE  ARG   353      44.677  -9.228  42.122  1.00 60.00
ATOM    376  CZ  ARG   353      44.731  -8.690  40.869  1.00 60.00
ATOM    377  NH1 ARG   353      43.783  -9.023  39.946  1.00 60.00
ATOM    380  NH2 ARG   353      45.731  -7.821  40.540  1.00 60.00
ATOM    383  C   ARG   353      46.228 -11.284  46.553  1.00 60.00
ATOM    384  O   ARG   353      46.565 -11.176  47.730  1.00 60.00
ATOM    385  N   GLY   354      47.083 -11.675  45.590  1.00 60.00
ATOM    387  CA  GLY   354      48.461 -11.908  45.900  1.00 60.00
ATOM    388  C   GLY   354      48.628 -13.246  46.535  1.00 60.00
ATOM    389  O   GLY   354      49.468 -13.421  47.417  1.00 60.00
ATOM    390  N   ASP   355      47.825 -14.237  46.108  1.00 60.00
ATOM    392  CA  ASP   355      47.984 -15.537  46.687  1.00 60.00
ATOM    393  CB  ASP   355      46.681 -16.153  47.215  1.00 60.00
ATOM    394  CG  ASP   355      45.757 -16.365  46.024  1.00 60.00
ATOM    395  OD1 ASP   355      45.504 -17.551  45.679  1.00 60.00
ATOM    396  OD2 ASP   355      45.289 -15.348  45.446  1.00 60.00
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A[illegible]	397	C	ASP	355	48.470	-16.459	45.620	1.00	60.00
ATOM	398	O	ASP	355	48.219	-16.249	44.435	1.00	60.00
ATOM	399	N	SER	356	49.208	-17.508	46.031	1.00	60.00
M	401	CA	SER	356	49.665	-18.494	45.102	1.00	60.00
A.OM	402	CB	SER	356	51.181	-18.759	45.157	1.00	60.00
ATOM	403	OG	SER	356	51.541	-19.312	46.414	1.00	60.00
ATOM	405	C	SER	356	48.964	-19.745	45.511	1.00	60.00
ATOM	406	O	SER	356	48.464	-19.844	46.630	1.00	60.00
ATOM	407	N	PHE	357	48.891	-20.736	44.605	1.00	60.00
ATOM	409	CA	PHE	357	48.189	-21.935	44.948	1.00	60.00
ATOM	410	CB	PHE	357	47.958	-22.864	43.742	1.00	60.00
ATOM	411	CG	PHE	357	47.190	-24.055	44.203	1.00	60.00
ATOM	412	CD1	PHE	357	47.831	-25.123	44.790	1.00	60.00
ATOM	413	CD2	PHE	357	45.832	-24.125	43.999	1.00	60.00
ATOM	414	CE1	PHE	357	47.123	-26.237	45.175	1.00	60.00
ATOM	415	CE2	PHE	357	45.118	-25.238	44.379	1.00	60.00
ATOM	416	CZ	PHE	357	45.766	-26.298	44.967	1.00	60.00
ATOM	417	C	PHE	357	49.029	-22.664	45.942	1.00	60.00
ATOM	418	O	PHE	357	50.005	-23.320	45.583	1.00	60.00
ATOM	419	N	THR	358	48.674	-22.547	47.236	1.00	60.00
ATOM	421	CA	THR	358	49.444	-23.220	48.238	1.00	60.00
ATOM	422	CB	THR	358	50.377	-22.305	48.975	1.00	60.00
ATOM	423	OG1	THR	358	51.242	-23.055	49.814	1.00	60.00
ATOM	425	CG2	THR	358	49.546	-21.314	49.809	1.00	60.00
ATOM	426	C	THR	358	48.515	-23.828	49.240	1.00	60.00
ATOM	427	O	THR	358	47.512	-23.229	49.627	1.00	60.00
ATOM	428	N	HIS	359	48.825	-25.068	49.661	1.00	60.00
ATOM	430	CA	HIS	359	48.031	-25.756	50.636	1.00	60.00
ATOM	431	CB	HIS	359	48.406	-27.241	50.750	1.00	60.00
ATOM	432	CG	HIS	359	48.261	-27.982	49.456	1.00	60.00
ATOM	433	CD2	HIS	359	47.273	-28.810	49.019	1.00	60.00
ATOM	434	ND1	HIS	359	49.184	-27.927	48.435	1.00	60.00
ATOM	436	CE1	HIS	359	48.713	-28.717	47.439	1.00	60.00
ATOM	437	NE2	HIS	359	47.556	-29.275	47.747	1.00	60.00
ATOM	439	C	HIS	359	48.286	-25.152	51.980	1.00	60.00
ATOM	440	O	HIS	359	47.362	-24.901	52.753	1.00	60.00
ATOM	441	N	THR	360	49.573	-24.886	52.275	1.00	60.00
ATOM	443	CA	THR	360	49.971	-24.398	53.563	1.00	60.00
ATOM	444	CB	THR	360	51.419	-24.013	53.638	1.00	60.00
ATOM	445	OG1	THR	360	51.804	-23.813	54.990	1.00	60.00
ATOM	447	CG2	THR	360	51.624	-22.718	52.833	1.00	60.00
ATOM	448	C	THR	360	49.166	-23.203	53.939	1.00	60.00
ATOM	449	O	THR	360	48.683	-22.445	53.098	1.00	60.00
ATOM	450	N	PRO	361	48.991	-23.059	55.221	1.00	60.00
ATOM	451	CD	PRO	361	48.870	-24.216	56.090	1.00	60.00
ATOM	452	CA	PRO	361	48.265	-21.932	55.724	1.00	60.00
ATOM	453	CB	PRO	361	47.721	-22.343	57.095	1.00	60.00
ATOM	454	CG	PRO	361	48.502	-23.620	57.456	1.00	60.00
ATOM	455	C	PRO	361	49.167	-20.745	55.759	1.00	60.00
ATOM	456	O	PRO	361	50.356	-20.899	56.035	1.00	60.00
ATOM	457	N	PRO	362	48.624	-19.595	55.497	1.00	60.00
ATOM	458	CD	PRO	362	47.213	-19.348	55.739	1.00	60.00
ATOM	459	CA	PRO	362	49.387	-18.382	55.475	1.00	60.00
ATOM	460	CB	PRO	362	48.366	-17.271	55.254	1.00	60.00
ATOM	461	CG	PRO	362	47.104	-17.827	55.939	1.00	60.00
ATOM	462	C	PRO	362	50.049	-18.232	56.803	1.00	60.00
ATOM	463	O	PRO	362	49.509	-18.719	57.795	1.00	60.00
ATOM	464	N	LEU	363	51.229	-17.585	56.840	1.00	60.00
ATOM	466	CA	LEU	363	51.885	-17.368	58.091	1.00	60.00
ATOM	467	CB	LEU	363	53.225	-16.627	57.946	1.00	60.00
ATOM	468	CG	LEU	363	53.937	-16.380	59.289	1.00	60.00
ATOM	469	CD1	LEU	363	54.300	-17.700	59.983	1.00	60.00
ATOM	470	CD2	LEU	363	55.146	-15.448	59.115	1.00	60.00
ATOM	471	C	LEU	363	50.973	-16.498	58.880	1.00	60.00

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ATOM    472  O   LEU   363      50.651 -16.791  60.030  1.00 60.00
ATOM    473  N   ASP   364      50.514 -15.401  58.255  1.00 60.00
ATOM    475  CA  ASP   364      49.614 -14.521  58.928  1.00 60.00
ATOM    476  CB  ASP   364      49.691 -13.063  58.441  1.00 60.00
ATOM    477  CG  ASP   364      51.035 -12.490  58.861  1.00 60.00
ATOM    478  OD1 ASP   364      51.297 -11.302  58.532  1.00 60.00
ATOM    479  OD2 ASP   364      51.820 -13.232  59.511  1.00 60.00
ATOM    480  C   ASP   364      48.249 -15.013  58.601  1.00 60.00
ATOM    481  O   ASP   364      48.075 -16.007  57.898  1.00 60.00
ATOM    482  N   PRO   365      47.273 -14.343  59.135  1.00 60.00
ATOM    483  CD  PRO   365      47.390 -13.790  60.473  1.00 60.00
ATOM    484  CA  PRO   365      45.920 -14.690  58.816  1.00 60.00
ATOM    485  CB  PRO   365      45.060 -14.202  59.985  1.00 60.00
ATOM    486  CG  PRO   365      45.982 -13.264  60.784  1.00 60.00
ATOM    487  C   PRO   365      45.602 -14.043  57.512  1.00 60.00
ATOM    488  O   PRO   365      46.289 -13.094  57.136  1.00 60.00
ATOM    489  N   GLN   366      44.578 -14.538  56.796  1.00 60.00
ATOM    491  CA  GLN   366      44.261 -13.941  55.537  1.00 60.00
ATOM    492  CB  GLN   366      43.136 -14.680  54.789  1.00 60.00
ATOM    493  CG  GLN   366      43.557 -16.094  54.371  1.00 60.00
ATOM    494  CD  GLN   366      42.408 -16.769  53.636  1.00 60.00
ATOM    495  OE1 GLN   366      42.506 -17.940  53.271  1.00 60.00
ATOM    496  NE2 GLN   366      41.297 -16.021  53.404  1.00 60.00
ATOM    499  C   GLN   366      43.854 -12.534  55.822  1.00 60.00
ATOM    500  O   GLN   366      44.212 -11.612  55.090  1.00 60.00
ATOM    501  N   GLU   367      43.102 -12.332  56.920  1.00 60.00
ATOM    503  CA  GLU   367      42.701 -11.010  57.300  1.00 60.00
ATOM    504  CB  GLU   367      41.684 -11.013  58.454  1.00 60.00
ATOM    505  CG  GLU   367      42.187 -11.759  59.692  1.00 60.00
ATOM    506  CD  GLU   367      41.045 -11.857  60.693  1.00 60.00
ATOM    507  OE1 GLU   367      40.612 -10.795  61.212  1.00 60.00
ATOM    508  OE2 GLU   367      40.589 -13.004  60.951  1.00 60.00
ATOM    509  C   GLU   367      43.940 -10.300  57.747  1.00 60.00
ATOM    510  O   GLU   367      44.893 -10.933  58.198  1.00 60.00
ATOM    511  N   LEU   368      43.971  -8.958  57.610  1.00 40.00
ATOM    513  CA  LEU   368      45.148  -8.233  57.992  1.00 40.00
ATOM    514  CB  LEU   368      45.817  -7.526  56.792  1.00 40.00
ATOM    515  CG  LEU   368      47.098  -6.716  57.097  1.00 40.00
ATOM    516  CD1 LEU   368      46.823  -5.435  57.902  1.00 40.00
ATOM    517  CD2 LEU   368      48.171  -7.612  57.734  1.00 40.00
ATOM    518  C   LEU   368      44.735  -7.199  58.981  1.00 40.00
ATOM    519  O   LEU   368      43.798  -6.437  58.752  1.00 40.00
ATOM    520  N   ASP   369      45.427  -7.161  60.132  1.00 40.00
ATOM    522  CA  ASP   369      45.144  -6.135  61.082  1.00 40.00
ATOM    523  CB  ASP   369      45.333  -6.552  62.551  1.00 40.00
ATOM    524  CG  ASP   369      44.269  -7.568  62.932  1.00 40.00
ATOM    525  OD1 ASP   369      44.164  -7.875  64.150  1.00 40.00
ATOM    526  OD2 ASP   369      43.553  -8.056  62.018  1.00 40.00
ATOM    527  C   ASP   369      46.245  -5.196  60.786  1.00 40.00
ATOM    528  O   ASP   369      47.393  -5.629  60.696  1.00 40.00
ATOM    529  N   ILE   370      45.918  -3.906  60.581  1.00 40.00
ATOM    531  CA  ILE   370      46.965  -2.968  60.332  1.00 40.00
ATOM    532  CB  ILE   370      46.459  -1.569  60.186  1.00 40.00
ATOM    533  CG2 ILE   370      47.655  -0.605  60.196  1.00 40.00
ATOM    534  CG1 ILE   370      45.594  -1.485  58.919  1.00 40.00
ATOM    535  CD1 ILE   370      44.814  -0.183  58.792  1.00 40.00
ATOM    536  C   ILE   370      47.813  -3.082  61.542  1.00 40.00
ATOM    537  O   ILE   370      48.973  -3.478  61.441  1.00 40.00
ATOM    538  N   LEU   371      47.230  -2.776  62.718  1.00 40.00
ATOM    540  CA  LEU   371      47.927  -3.049  63.936  1.00 40.00
ATOM    541  CB  LEU   371      49.402  -2.609  63.988  1.00 40.00
ATOM    542  CG  LEU   371      50.110  -3.093  65.267  1.00 40.00
ATOM    543  CD1 LEU   371      50.003  -4.621  65.407  1.00 40.00
ATOM    544  CD2 LEU   371      51.575  -2.632  65.301  1.00 40.00
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ATOM	545	C	LEU	371	47.234	-2.413	65.087	1.00	40.00
ATOM	546	O	LEU	371	46.575	-1.382	64.958	1.00	40.00
ATOM	547	N	LYS	372	47.392	-3.051	66.257	1.00	20.00
ATOM	549	CA	LYS	372	46.865	-2.593	67.503	1.00	20.00
ATOM	550	CB	LYS	372	47.005	-3.637	68.625	1.00	20.00
ATOM	551	CG	LYS	372	46.173	-4.896	68.358	1.00	20.00
ATOM	552	CD	LYS	372	46.478	-6.068	69.293	1.00	20.00
ATOM	553	CE	LYS	372	45.536	-6.144	70.496	1.00	20.00
ATOM	554	NZ	LYS	372	45.826	-7.358	71.292	1.00	20.00
ATOM	558	C	LYS	372	47.650	-1.374	67.857	1.00	20.00
ATOM	559	O	LYS	372	47.230	-0.550	68.665	1.00	20.00
ATOM	560	N	THR	373	48.841	-1.234	67.255	1.00	20.00
ATOM	562	CA	THR	373	49.713	-0.143	67.570	1.00	20.00
ATOM	563	CB	THR	373	50.993	-0.161	66.790	1.00	20.00
ATOM	564	OG1	THR	373	51.913	0.773	67.334	1.00	20.00
ATOM	566	CG2	THR	373	50.677	0.195	65.327	1.00	20.00
ATOM	567	C	THR	373	49.078	1.188	67.308	1.00	20.00
ATOM	568	O	THR	373	49.377	2.153	68.009	1.00	20.00
ATOM	569	N	VAL	374	48.194	1.295	66.295	1.00	20.00
ATOM	571	CA	VAL	374	47.677	2.593	65.946	1.00	20.00
ATOM	572	CB	VAL	374	47.137	2.637	64.544	1.00	20.00
ATOM	573	CG1	VAL	374	46.601	4.051	64.263	1.00	20.00
ATOM	574	CG2	VAL	374	48.245	2.177	63.578	1.00	20.00
ATOM	575	C	VAL	374	46.591	3.087	66.859	1.00	20.00
ATOM	576	O	VAL	374	45.431	2.689	66.736	1.00	20.00
ATOM	577	N	LYS	375	46.980	3.924	67.848	1.00	20.00
ATOM	579	CA	LYS	375	46.084	4.602	68.746	1.00	20.00
ATOM	580	CB	LYS	375	46.752	5.075	70.049	1.00	20.00
ATOM	581	CG	LYS	375	47.091	3.970	71.050	1.00	20.00
ATOM	582	CD	LYS	375	47.814	4.503	72.289	1.00	20.00
ATOM	583	CE	LYS	375	47.964	3.476	73.413	1.00	20.00
ATOM	584	NZ	LYS	375	48.533	4.126	74.615	1.00	20.00
ATOM	588	C	LYS	375	45.439	5.830	68.169	1.00	20.00
ATOM	589	O	LYS	375	44.256	6.079	68.386	1.00	20.00
ATOM	590	N	GLU	376	46.193	6.658	67.419	1.00	20.00
ATOM	592	CA	GLU	376	45.613	7.918	67.049	1.00	20.00
ATOM	593	CB	GLU	376	46.103	9.051	67.971	1.00	20.00
ATOM	594	CG	GLU	376	45.540	10.438	67.665	1.00	20.00
ATOM	595	CD	GLU	376	46.126	11.397	68.691	1.00	20.00
ATOM	596	OE1	GLU	376	45.997	11.108	69.911	1.00	20.00
ATOM	597	OE2	GLU	376	46.716	12.426	68.269	1.00	20.00
ATOM	598	C	GLU	376	45.926	8.309	65.641	1.00	20.00
ATOM	599	O	GLU	376	46.796	7.732	64.994	1.00	20.00
ATOM	600	N	ILE	377	45.148	9.283	65.121	1.00	20.00
ATOM	602	CA	ILE	377	45.362	9.865	63.833	1.00	20.00
ATOM	603	CB	ILE	377	44.403	9.370	62.791	1.00	20.00
ATOM	604	CG2	ILE	377	44.680	10.133	61.485	1.00	20.00
ATOM	605	CG1	ILE	377	44.526	7.844	62.642	1.00	20.00
ATOM	606	CD1	ILE	377	43.402	7.214	61.820	1.00	20.00
ATOM	607	C	ILE	377	45.075	11.311	64.089	1.00	20.00
ATOM	608	O	ILE	377	44.015	11.662	64.599	1.00	20.00
ATOM	609	N	THR	378	46.029	12.183	63.740	1.00	20.00
ATOM	611	CA	THR	378	45.985	13.594	63.994	1.00	20.00
ATOM	612	CB	THR	378	47.317	14.235	63.734	1.00	20.00
ATOM	613	OG1	THR	378	48.316	13.599	64.516	1.00	20.00
ATOM	615	CG2	THR	378	47.249	15.718	64.124	1.00	20.00
ATOM	616	C	THR	378	44.965	14.303	63.159	1.00	20.00
ATOM	617	O	THR	378	44.612	15.442	63.452	1.00	20.00
ATOM	618	N	GLY	379	44.522	13.695	62.044	1.00	20.00
ATOM	620	CA	GLY	379	43.608	14.380	61.171	1.00	20.00
ATOM	621	C	GLY	379	42.325	13.631	61.001	1.00	20.00
ATOM	622	O	GLY	379	41.520	13.523	61.923	1.00	20.00
ATOM	623	N	PHE	380	42.082	13.126	59.775	1.00	20.00
ATOM	625	CA	PHE	380	40.869	12.405	59.515	1.00	20.00

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ATOM    626  CB  PHE   380      39.920  13.116  58.530  1.00 20.00
ATOM    627  CG  PHE   380      40.598  13.264  57.212  1.00 20.00
ATOM    628  CD1 PHE   380      40.528  12.265  56.268  1.00 20.00
ATOM    629  CD2 PHE   380      41.265  14.427  56.902  1.00 20.00
ATOM    630  CE1 PHE   380      41.112  12.426  55.034  1.00 20.00
ATOM    631  CE2 PHE   380      41.860  14.590  55.674  1.00 20.00
ATOM    632  CZ  PHE   380      41.780  13.589  54.736  1.00 20.00
ATOM    633  C   PHE   380      41.216  11.066  58.955  1.00 20.00
ATOM    634  O   PHE   380      42.359  10.824  58.573  1.00 20.00
ATOM    635  N   LEU   381      40.231  10.141  58.942  1.00 20.00
ATOM    637  CA  LEU   381      40.454   8.822  58.422  1.00 20.00
ATOM    638  CB  LEU   381      40.156   7.725  59.462  1.00 20.00
ATOM    639  CG  LEU   381      40.369   6.281  58.972  1.00 20.00
ATOM    640  CD1 LEU   381      41.834   6.032  58.580  1.00 20.00
ATOM    641  CD2 LEU   381      39.866   5.268  60.015  1.00 20.00
ATOM    642  C   LEU   381      39.534   8.629  57.251  1.00 20.00
ATOM    643  O   LEU   381      38.318   8.782  57.368  1.00 20.00
ATOM    644  N   LEU   382      40.096   8.290  56.073  1.00 20.00
ATOM    646  CA  LEU   382      39.283   8.132  54.899  1.00 20.00
ATOM    647  CB  LEU   382      39.642   9.158  53.808  1.00 20.00
ATOM    648  CG  LEU   382      38.818   9.062  52.511  1.00 20.00
ATOM    649  CD1 LEU   382      37.330   9.337  52.761  1.00 20.00
ATOM    650  CD2 LEU   382      39.405   9.975  51.424  1.00 20.00
ATOM    651  C   LEU   382      39.459   6.767  54.312  1.00 20.00
ATOM    652  O   LEU   382      40.548   6.399  53.873  1.00 20.00
ATOM    653  N   ILE   383      38.375   5.968  54.295  1.00 20.00
ATOM    655  CA  ILE   383      38.451   4.677  53.681  1.00 20.00
ATOM    656  CB  ILE   383      38.143   3.540  54.623  1.00 20.00
ATOM    657  CG2 ILE   383      36.747   3.739  55.239  1.00 20.00
ATOM    658  CG1 ILE   383      38.351   2.191  53.916  1.00 20.00
ATOM    659  CD1 ILE   383      38.352   1.000  54.872  1.00 20.00
ATOM    660  C   ILE   383      37.471   4.676  52.553  1.00 20.00
ATOM    661  O   ILE   383      36.259   4.747  52.745  1.00 20.00
ATOM    662  N   GLN   384      37.975   4.608  51.314  1.00 20.00
ATOM    664  CA  GLN   384      37.065   4.622  50.213  1.00 20.00
ATOM    665  CB  GLN   384      37.334   5.758  49.212  1.00 20.00
ATOM    666  CG  GLN   384      36.365   5.786  48.026  1.00 20.00
ATOM    667  CD  GLN   384      36.804   6.908  47.092  1.00 20.00
ATOM    668  OE1 GLN   384      37.864   7.503  47.279  1.00 20.00
ATOM    669  NE2 GLN   384      35.972   7.208  46.058  1.00 20.00
ATOM    672  C   GLN   384      37.241   3.340  49.472  1.00 20.00
ATOM    673  O   GLN   384      38.359   2.852  49.313  1.00 20.00
ATOM    674  N   ALA   385      36.108   2.768  49.020  1.00 20.00
ATOM    676  CA  ALA   385      36.047   1.565  48.240  1.00 20.00
ATOM    677  CB  ALA   385      36.094   1.823  46.723  1.00 20.00
ATOM    678  C   ALA   385      37.093   0.547  48.564  1.00 20.00
ATOM    679  O   ALA   385      38.095   0.433  47.860  1.00 20.00
ATOM    680  N   TRP   386      36.905  -0.206  49.665  1.00 40.00
ATOM    682  CA  TRP   386      37.807  -1.282  49.951  1.00 40.00
ATOM    683  CB  TRP   386      38.698  -1.047  51.187  1.00 40.00
ATOM    684  CG  TRP   386      39.643  -2.188  51.498  1.00 40.00
ATOM    685  CD2 TRP   386      40.808  -2.083  52.333  1.00 40.00
ATOM    686  CE2 TRP   386      41.411  -3.341  52.364  1.00 40.00
ATOM    687  CE3 TRP   386      41.335  -1.026  53.017  1.00 40.00
ATOM    688  CD1 TRP   386      39.602  -3.478  51.060  1.00 40.00
ATOM    689  NE1 TRP   386      40.658  -4.188  51.581  1.00 40.00
ATOM    691  CZ2 TRP   386      42.553  -3.560  53.080  1.00 40.00
ATOM    692  CZ3 TRP   386      42.485  -1.251  53.740  1.00 40.00
ATOM    693  CH2 TRP   386      43.085  -2.492  53.768  1.00 40.00
ATOM    694  C   TRP   386      36.955  -2.481  50.219  1.00 40.00
ATOM    695  O   TRP   386      36.205  -2.513  51.194  1.00 40.00
ATOM    696  N   PRO   387      37.010  -3.458  49.359  1.00 40.00
ATOM    697  CD  PRO   387      37.070  -3.165  47.936  1.00 40.00
ATOM    698  CA  PRO   387      36.218  -4.629  49.623  1.00 40.00
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ATOM    699  CB  PRO   387      35.733  -5.146  48.267  1.00 40.00
ATOM    700  CG  PRO   387      36.669  -4.479  47.248  1.00 40.00
ATOM    701  C   PRO   387      36.983  -5.651  50.398  1.00 40.00
ATOM    702  O   PRO   387      38.205  -5.705  50.273  1.00 40.00
ATOM    703  N   GLU   388      36.281  -6.468  51.211  1.00 60.00
ATOM    705  CA  GLU   388      36.926  -7.544  51.902  1.00 60.00
ATOM    706  CB  GLU   388      38.009  -7.126  52.913  1.00 60.00
ATOM    707  CG  GLU   388      37.503  -6.355  54.129  1.00 60.00
ATOM    708  CD  GLU   388      38.681  -6.251  55.088  1.00 60.00
ATOM    709  OE1 GLU   388      38.438  -6.226  56.323  1.00 60.00
ATOM    710  OE2 GLU   388      39.841  -6.199  54.597  1.00 60.00
ATOM    711  C   GLU   388      35.886  -8.334  52.631  1.00 60.00
ATOM    712  O   GLU   388      34.735  -7.917  52.752  1.00 60.00
ATOM    713  N   ASN   389      36.284  -9.524  53.118  1.00 60.00
ATOM    715  CA  ASN   389      35.397 -10.427  53.793  1.00 60.00
ATOM    716  CB  ASN   389      36.064 -11.789  54.065  1.00 60.00
ATOM    717  CG  ASN   389      35.053 -12.711  54.733  1.00 60.00
ATOM    718  OD1 ASN   389      33.860 -12.668  54.438  1.00 60.00
ATOM    719  ND2 ASN   389      35.546 -13.572  55.664  1.00 60.00
ATOM    722  C   ASN   389      34.935  -9.900  55.114  1.00 60.00
ATOM    723  O   ASN   389      33.736  -9.844  55.382  1.00 60.00
ATOM    724  N   ARG   390      35.880  -9.474  55.972  1.00 60.00
ATOM    726  CA  ARG   390      35.501  -9.094  57.300  1.00 60.00
ATOM    727  CB  ARG   390      36.509  -9.551  58.362  1.00 60.00
ATOM    728  CG  ARG   390      36.820 -11.045  58.294  1.00 60.00
ATOM    729  CD  ARG   390      37.813 -11.498  59.364  1.00 60.00
ATOM    730  NE  ARG   390      38.361 -12.814  58.936  1.00 60.00
ATOM    732  CZ  ARG   390      37.702 -13.969  59.241  1.00 60.00
ATOM    733  NH1 ARG   390      38.230 -15.169  58.863  1.00 60.00
ATOM    736  NH2 ARG   390      36.522 -13.923  59.925  1.00 60.00
ATOM    739  C   ARG   390      35.418  -7.612  57.417  1.00 60.00
ATOM    740  O   ARG   390      35.440  -6.887  56.423  1.00 60.00
ATOM    741  N   THR   391      35.301  -7.131  58.670  1.00 60.00
ATOM    743  CA  THR   391      35.236  -5.722  58.895  1.00 60.00
ATOM    744  CB  THR   391      34.997  -5.337  60.326  1.00 60.00
ATOM    745  OG1 THR   391      36.067  -5.792  61.141  1.00 60.00
ATOM    747  CG2 THR   391      33.669  -5.954  60.793  1.00 60.00
ATOM    748  C   THR   391      36.572  -5.192  58.519  1.00 60.00
ATOM    749  O   THR   391      37.595  -5.622  59.045  1.00 60.00
ATOM    750  N   ASP   392      36.586  -4.236  57.579  1.00 60.00
ATOM    752  CA  ASP   392      37.814  -3.675  57.114  1.00 60.00
ATOM    753  CB  ASP   392      37.609  -2.694  55.949  1.00 60.00
ATOM    754  CG  ASP   392      38.951  -2.481  55.266  1.00 60.00
ATOM    755  OD1 ASP   392      39.929  -3.181  55.641  1.00 60.00
ATOM    756  OD2 ASP   392      39.012  -1.613  54.355  1.00 60.00
ATOM    757  C   ASP   392      38.410  -2.927  58.259  1.00 60.00
ATOM    758  O   ASP   392      39.629  -2.870  58.415  1.00 60.00
ATOM    759  N   LEU   393      37.542  -2.351  59.111  1.00 40.00
ATOM    761  CA  LEU   393      37.993  -1.561  60.212  1.00 40.00
ATOM    762  CB  LEU   393      36.881  -0.757  60.882  1.00 40.00
ATOM    763  CG  LEU   393      36.203   0.250  59.929  1.00 40.00
ATOM    764  CD1 LEU   393      37.198   1.308  59.425  1.00 40.00
ATOM    765  CD2 LEU   393      35.465  -0.465  58.787  1.00 40.00
ATOM    766  C   LEU   393      38.699  -2.424  61.212  1.00 40.00
ATOM    767  O   LEU   393      39.431  -1.924  62.064  1.00 40.00
ATOM    768  N   HIS   394      38.494  -3.755  61.128  1.00 40.00
ATOM    770  CA  HIS   394      39.064  -4.696  62.056  1.00 40.00
ATOM    771  CB  HIS   394      38.835  -6.171  61.670  1.00 40.00
ATOM    772  CG  HIS   394      39.918  -6.759  60.813  1.00 40.00
ATOM    773  CD2 HIS   394      40.944  -7.577  61.173  1.00 40.00
ATOM    774  ND1 HIS   394      40.040  -6.583  59.452  1.00 40.00
ATOM    776  CE1 HIS   394      41.125  -7.298  59.061  1.00 40.00
ATOM    777  NE2 HIS   394      41.708  -7.918  60.071  1.00 40.00
ATOM    779  C   HIS   394      40.542  -4.479  62.140  1.00 40.00
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ATOM    780  O   HIS   394      41.183  -4.881  63.110  1.00 40.00
ATOM    781  N   ALA   395      41.128  -3.850  61.108  1.00 20.00
ATOM    783  CA  ALA   395      42.534  -3.591  61.111  1.00 20.00
  )M    784  CB  ALA   395      43.013  -2.876  59.836  1.00 20.00
ATOM    785  C   ALA   395      42.905  -2.722  62.278  1.00 20.00
ATOM    786  O   ALA   395      43.955  -2.932  62.885  1.00 20.00
ATOM    787  N   PHE   396      42.069  -1.717  62.626  1.00 20.00
ATOM    789  CA  PHE   396      42.434  -0.830  63.705  1.00 20.00
ATOM    790  CB  PHE   396      41.987   0.623  63.471  1.00 20.00
ATOM    791  CG  PHE   396      42.601   1.137  62.215  1.00 20.00
ATOM    792  CD1 PHE   396      41.970   0.936  61.010  1.00 20.00
ATOM    793  CD2 PHE   396      43.750   1.892  62.249  1.00 20.00
ATOM    794  CE1 PHE   396      42.471   1.484  59.854  1.00 20.00
ATOM    795  CE2 PHE   396      44.253   2.448  61.097  1.00 20.00
ATOM    796  CZ  PHE   396      43.604   2.261  59.900  1.00 20.00
ATOM    797  C   PHE   396      41.763  -1.229  64.987  1.00 20.00
ATOM    798  O   PHE   396      40.773  -0.623  65.396  1.00 20.00
ATOM    799  N   GLU   397      42.341  -2.208  65.703  1.00 20.00
ATOM    801  CA  GLU   397      41.757  -2.723  66.905  1.00 20.00
ATOM    802  CB  GLU   397      42.569  -3.905  67.471  1.00 20.00
ATOM    803  CG  GLU   397      41.904  -4.650  68.632  1.00 20.00
ATOM    804  CD  GLU   397      42.496  -4.154  69.944  1.00 20.00
ATOM    805  OE1 GLU   397      42.958  -2.984  69.989  1.00 20.00
ATOM    806  OE2 GLU   397      42.499  -4.948  70.923  1.00 20.00
ATOM    807  C   GLU   397      41.655  -1.675  67.964  1.00 20.00
ATOM    808  O   GLU   397      40.644  -1.605  68.659  1.00 20.00
ATOM    809  N   ASN   398      42.685  -0.827  68.149  1.00 20.00
ATOM    811  CA  ASN   398      42.500   0.116  69.212  1.00 20.00
ATOM    812  CB  ASN   398      43.278  -0.228  70.496  1.00 20.00
ATOM    813  CG  ASN   398      44.748  -0.336  70.160  1.00 20.00
ATOM    814  OD1 ASN   398      45.445   0.664  70.001  1.00 20.00
ATOM    815  ND2 ASN   398      45.231  -1.602  70.058  1.00 20.00
ATOM    818  C   ASN   398      42.762   1.538  68.839  1.00 20.00
ATOM    819  O   ASN   398      43.417   2.273  69.576  1.00 20.00
ATOM    820  N   LEU   399      42.217   1.979  67.692  1.00 20.00
ATOM    822  CA  LEU   399      42.347   3.356  67.321  1.00 20.00
ATOM    823  CB  LEU   399      41.827   3.606  65.897  1.00 20.00
ATOM    824  CG  LEU   399      41.928   5.058  65.406  1.00 20.00
ATOM    825  CD1 LEU   399      43.391   5.505  65.279  1.00 20.00
ATOM    826  CD2 LEU   399      41.127   5.245  64.106  1.00 20.00
ATOM    827  C   LEU   399      41.471   4.100  68.289  1.00 20.00
ATOM    828  O   LEU   399      40.256   3.918  68.277  1.00 20.00
ATOM    829  N   GLU   400      42.091   4.869  69.215  1.00 20.00
ATOM    831  CA  GLU   400      41.431   5.661  70.222  1.00 20.00
ATOM    832  CB  GLU   400      42.356   6.005  71.405  1.00 20.00
ATOM    833  CG  GLU   400      42.782   4.812  72.263  1.00 20.00
ATOM    834  CD  GLU   400      43.606   5.354  73.425  1.00 20.00
ATOM    835  OE1 GLU   400      44.471   6.236  73.178  1.00 20.00
ATOM    836  OE2 GLU   400      43.375   4.898  74.578  1.00 20.00
ATOM    837  C   GLU   400      40.825   6.981  69.817  1.00 20.00
ATOM    838  O   GLU   400      39.679   7.269  70.160  1.00 20.00
ATOM    839  N   ILE   401      41.572   7.832  69.077  1.00 20.00
ATOM    841  CA  ILE   401      41.078   9.168  68.850  1.00 20.00
ATOM    842  CB  ILE   401      41.695  10.146  69.819  1.00 20.00
ATOM    843  CG2 ILE   401      43.157  10.343  69.395  1.00 20.00
ATOM    844  CG1 ILE   401      40.914  11.465  69.932  1.00 20.00
ATOM    845  CD1 ILE   401      39.739  11.393  70.906  1.00 20.00
ATOM    846  C   ILE   401      41.463   9.647  67.479  1.00 20.00
ATOM    847  O   ILE   401      42.510   9.275  66.952  1.00 20.00
ATOM    848  N   ILE   402      40.600  10.483  66.858  1.00 20.00
ATOM    850  CA  ILE   402      40.900  11.079  65.584  1.00 20.00
ATOM    851  CB  ILE   402      39.949  10.655  64.500  1.00 20.00
ATOM    852  CG2 ILE   402      40.278  11.455  63.230  1.00 20.00
ATOM    853  CG1 ILE   402      40.012   9.132  64.295  1.00 20.00
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ATOM    854  CD1 ILE   402      38.867   8.585  63.442  1.00 20.00
ATOM    855  C   ILE   402      40.704  12.546  65.815  1.00 20.00
ATOM    856  O   ILE   402      39.584  13.045  65.775  1.00 20.00
ATOM    857  N   ARG   403      41.806  13.295  65.984  1.00 20.00
ATOM    859  CA  ARG   403      41.738  14.672  66.393  1.00 20.00
ATOM    860  CB  ARG   403      43.121  15.317  66.557  1.00 20.00
ATOM    861  CG  ARG   403      43.868  14.804  67.785  1.00 20.00
ATOM    862  CD  ARG   403      45.126  15.607  68.111  1.00 20.00
ATOM    863  NE  ARG   403      45.666  15.072  69.390  1.00 20.00
ATOM    865  CZ  ARG   403      45.210  15.567  70.578  1.00 20.00
ATOM    866  NH1 ARG   403      45.704  15.080  71.753  1.00 20.00
ATOM    869  NH2 ARG   403      44.258  16.545  70.591  1.00 20.00
ATOM    872  C   ARG   403      40.944  15.560  65.491  1.00 20.00
ATOM    873  O   ARG   403      40.289  16.485  65.964  1.00 20.00
ATOM    874  N   GLY   404      40.997  15.347  64.168  1.00 20.00
ATOM    876  CA  GLY   404      40.235  16.191  63.295  1.00 20.00
ATOM    877  C   GLY   404      40.869  17.541  63.176  1.00 20.00
ATOM    878  O   GLY   404      40.188  18.528  62.898  1.00 20.00
ATOM    879  N   ARG   405      42.199  17.625  63.364  1.00 20.00
ATOM    881  CA  ARG   405      42.834  18.908  63.279  1.00 20.00
ATOM    882  CB  ARG   405      44.355  18.861  63.503  1.00 20.00
ATOM    883  CG  ARG   405      44.950  20.250  63.742  1.00 20.00
ATOM    884  CD  ARG   405      46.470  20.259  63.903  1.00 20.00
ATOM    885  NE  ARG   405      47.048  20.241  62.532  1.00 20.00
ATOM    887  CZ  ARG   405      47.194  21.412  61.846  1.00 20.00
ATOM    888  NH1 ARG   405      46.838  22.594  62.429  1.00 20.00
ATOM    891  NH2 ARG   405      47.689  21.400  60.574  1.00 20.00
ATOM    894  C   ARG   405      42.576  19.416  61.898  1.00 20.00
ATOM    895  O   ARG   405      42.315  20.602  61.697  1.00 20.00
ATOM    896  N   THR   406      42.645  18.516  60.902  1.00 20.00
ATOM    898  CA  THR   406      42.323  18.902  59.561  1.00 20.00
ATOM    899  CB  THR   406      43.479  18.799  58.610  1.00 20.00
ATOM    900  OG1 THR   406      43.939  17.459  58.535  1.00 20.00
ATOM    902  CG2 THR   406      44.604  19.723  59.109  1.00 20.00
ATOM    903  C   THR   406      41.261  17.949  59.121  1.00 20.00
ATOM    904  O   THR   406      41.354  16.748  59.368  1.00 20.00
ATOM    905  N   LYS   407      40.218  18.467  58.449  1.00 20.00
ATOM    907  CA  LYS   407      39.097  17.653  58.078  1.00 20.00
ATOM    908  CB  LYS   407      37.788  18.227  58.638  1.00 20.00
ATOM    909  CG  LYS   407      37.577  19.672  58.180  1.00 20.00
ATOM    910  CD  LYS   407      36.235  20.287  58.571  1.00 20.00
ATOM    911  CE  LYS   407      36.072  21.725  58.076  1.00 20.00
ATOM    912  NZ  LYS   407      37.081  22.597  58.716  1.00 20.00
ATOM    916  C   LYS   407      38.962  17.595  56.591  1.00 20.00
ATOM    917  O   LYS   407      39.427  18.483  55.878  1.00 20.00
ATOM    918  N   GLN   408      38.330  16.518  56.080  1.00 20.00
ATOM    920  CA  GLN   408      38.139  16.441  54.663  1.00 20.00
ATOM    921  CB  GLN   408      38.080  15.016  54.076  1.00 20.00
ATOM    922  CG  GLN   408      36.898  14.167  54.539  1.00 20.00
ATOM    923  CD  GLN   408      36.969  12.853  53.772  1.00 20.00
ATOM    924  OE1 GLN   408      36.014  12.455  53.107  1.00 20.00
ATOM    925  NE2 GLN   408      38.139  12.164  53.857  1.00 20.00
ATOM    928  C   GLN   408      36.847  17.130  54.381  1.00 20.00
ATOM    929  O   GLN   408      36.081  17.408  55.301  1.00 20.00
ATOM    930  N   HIS   409      36.585  17.409  53.086  1.00 20.00
ATOM    932  CA  HIS   409      35.431  18.151  52.662  1.00 20.00
ATOM    933  CB  HIS   409      35.166  18.082  51.145  1.00 20.00
ATOM    934  CG  HIS   409      36.230  18.712  50.294  1.00 20.00
ATOM    935  CD2 HIS   409      37.316  18.149  49.695  1.00 20.00
ATOM    936  ND1 HIS   409      36.251  20.042  49.936  1.00 20.00
ATOM    938  CE1 HIS   409      37.341  20.217  49.146  1.00 20.00
ATOM    939  NE2 HIS   409      38.018  19.097  48.972  1.00 20.00
ATOM    941  C   HIS   409      34.216  17.607  53.323  1.00 20.00
ATOM    942  O   HIS   409      34.102  16.405  53.551  1.00 20.00
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ATOM    943  N   GLY   410      33.280  18.503  53.673  1.00 20.00
ATOM    945  CA  GLY   410      32.100  18.067  54.349  1.00 20.00
ATOM    946  C   GLY   410      32.429  18.116  55.801  1.00 20.00
ATOM    947  O   GLY   410      31.585  17.843  56.654  1.00 20.00
ATOM    948  N   GLN   411      33.681  18.501  56.113  1.00 20.00
ATOM    950  CA  GLN   411      34.103  18.580  57.477  1.00 20.00
ATOM    951  CB  GLN   411      33.207  19.505  58.319  1.00 20.00
ATOM    952  CG  GLN   411      33.226  20.973  57.890  1.00 20.00
ATOM    953  CD  GLN   411      32.231  21.722  58.767  1.00 20.00
ATOM    954  OE1 GLN   411      31.032  21.444  58.750  1.00 20.00
ATOM    955  NE2 GLN   411      32.742  22.699  59.562  1.00 20.00
ATOM    958  C   GLN   411      34.038  17.226  58.105  1.00 20.00
ATOM    959  O   GLN   411      33.609  17.101  59.250  1.00 20.00
ATOM    960  N   PHE   412      34.488  16.174  57.393  1.00 20.00
ATOM    962  CA  PHE   412      34.372  14.865  57.966  1.00 20.00
ATOM    963  CB  PHE   412      33.979  13.774  56.952  1.00 20.00
ATOM    964  CG  PHE   412      32.657  14.127  56.359  1.00 20.00
ATOM    965  CD1 PHE   412      32.590  14.732  55.125  1.00 20.00
ATOM    966  CD2 PHE   412      31.494  13.933  57.068  1.00 20.00
ATOM    967  CE1 PHE   412      31.377  15.086  54.582  1.00 20.00
ATOM    968  CE2 PHE   412      30.279  14.300  56.538  1.00 20.00
ATOM    969  CZ  PHE   412      30.217  14.866  55.287  1.00 20.00
ATOM    970  C   PHE   412      35.665  14.421  58.576  1.00 20.00
ATOM    971  O   PHE   412      36.735  14.549  57.986  1.00 20.00
ATOM    972  N   SER   413      35.579  13.964  59.837  1.00 20.00
ATOM    974  CA  SER   413      36.652  13.395  60.599  1.00 20.00
ATOM    975  CB  SER   413      36.267  13.239  62.073  1.00 20.00
ATOM    976  OG  SER   413      35.611  14.412  62.523  1.00 20.00
ATOM    978  C   SER   413      36.871  12.000  60.127  1.00 20.00
ATOM    979  O   SER   413      38.002  11.534  60.023  1.00 20.00
ATOM    980  N   LEU   414      35.754  11.288  59.881  1.00 20.00
ATOM    982  CA  LEU   414      35.805   9.915  59.483  1.00 20.00
ATOM    983  CB  LEU   414      35.290   8.979  60.592  1.00 20.00
ATOM    984  CG  LEU   414      35.304   7.480  60.252  1.00 20.00
ATOM    985  CD1 LEU   414      36.732   6.966  60.018  1.00 20.00
ATOM    986  CD2 LEU   414      34.543   6.670  61.315  1.00 20.00
ATOM    987  C   LEU   414      34.909   9.756  58.304  1.00 20.00
ATOM    988  O   LEU   414      33.688   9.855  58.414  1.00 20.00
ATOM    989  N   ALA   415      35.501   9.503  57.126  1.00 20.00
ATOM    991  CA  ALA   415      34.678   9.310  55.973  1.00 20.00
ATOM    992  CB  ALA   415      35.070  10.198  54.779  1.00 20.00
ATOM    993  C   ALA   415      34.858   7.893  55.551  1.00 20.00
ATOM    994  O   ALA   415      35.981   7.453  55.314  1.00 20.00
ATOM    995  N   VAL   416      33.750   7.129  55.490  1.00 20.00
ATOM    997  CA  VAL   416      33.822   5.776  55.025  1.00 20.00
ATOM    998  CB  VAL   416      33.376   4.767  56.042  1.00 20.00
ATOM    999  CG1 VAL   416      33.451   3.368  55.405  1.00 20.00
ATOM   1000  CG2 VAL   416      34.245   4.921  57.301  1.00 20.00
ATOM   1001  C   VAL   416      32.869   5.702  53.878  1.00 20.00
ATOM   1002  O   VAL   416      31.655   5.739  54.068  1.00 20.00
ATOM   1003  N   VAL   417      33.392   5.581  52.645  1.00 20.00
ATOM   1005  CA  VAL   417      32.503   5.564  51.522  1.00 20.00
ATOM   1006  CB  VAL   417      32.770   6.667  50.541  1.00 20.00
ATOM   1007  CG1 VAL   417      31.784   6.531  49.369  1.00 20.00
ATOM   1008  CG2 VAL   417      32.682   8.013  51.277  1.00 20.00
ATOM   1009  C   VAL   417      32.669   4.279  50.779  1.00 20.00
ATOM   1010  O   VAL   417      33.789   3.805  50.597  1.00 20.00
ATOM   1011  N   SER   418      31.533   3.706  50.321  1.00 40.00
ATOM   1013  CA  SER   418      31.494   2.482  49.564  1.00 40.00
ATOM   1014  CB  SER   418      31.778   2.690  48.065  1.00 40.00
ATOM   1015  OG  SER   418      33.087   3.207  47.882  1.00 40.00
ATOM   1017  C   SER   418      32.463   1.474  50.101  1.00 40.00
ATOM   1018  O   SER   418      33.596   1.381  49.632  1.00 40.00
ATOM   1019  N   LEU   419      32.040   0.703  51.124  1.00 40.00
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ATOM   1021  CA  LEU   419      32.930  -0.252  51.727  1.00 40.00
ATOM   1022  CB  LEU   419      33.355   0.212  53.133  1.00 40.00
ATOM   1023  CG  LEU   419      34.471  -0.608  53.800  1.00 40.00
ATOM   1024  CD1 LEU   419      35.781  -0.502  53.005  1.00 40.00
ATOM   1025  CD2 LEU   419      34.654  -0.187  55.267  1.00 40.00
ATOM   1026  C   LEU   419      32.191  -1.562  51.860  1.00 40.00
ATOM   1027  O   LEU   419      30.971  -1.567  51.980  1.00 40.00
ATOM   1028  N   ASN   420      32.888  -2.724  51.824  1.00 40.00
ATOM   1030  CA  ASN   420      32.176  -3.970  51.957  1.00 40.00
ATOM   1031  CB  ASN   420      32.676  -5.083  51.022  1.00 40.00
ATOM   1032  CG  ASN   420      32.133  -4.765  49.636  1.00 40.00
ATOM   1033  OD1 ASN   420      32.655  -5.225  48.622  1.00 40.00
ATOM   1034  ND2 ASN   420      31.047  -3.946  49.591  1.00 40.00
ATOM   1037  C   ASN   420      32.296  -4.436  53.366  1.00 40.00
ATOM   1038  O   ASN   420      32.839  -5.503  53.642  1.00 40.00
ATOM   1039  N   ILE   421      31.756  -3.654  54.316  1.00 40.00
ATOM   1041  CA  ILE   421      31.927  -4.069  55.669  1.00 40.00
ATOM   1042  CB  ILE   421      32.813  -3.154  56.450  1.00 40.00
ATOM   1043  CG2 ILE   421      32.914  -3.688  57.888  1.00 40.00
ATOM   1044  CG1 ILE   421      34.165  -3.055  55.728  1.00 40.00
ATOM   1045  CD1 ILE   421      34.783  -4.417  55.417  1.00 40.00
ATOM   1046  C   ILE   421      30.629  -4.187  56.387  1.00 40.00
ATOM   1047  O   ILE   421      29.675  -3.461  56.115  1.00 40.00
ATOM   1048  N   THR   422      30.572  -5.185  57.289  1.00 40.00
ATOM   1050  CA  THR   422      29.453  -5.479  58.131  1.00 40.00
ATOM   1051  CB  THR   422      29.559  -6.840  58.751  1.00 40.00
ATOM   1052  OG1 THR   422      30.720  -6.920  59.564  1.00 40.00
ATOM   1054  CG2 THR   422      29.628  -7.884  57.622  1.00 40.00
ATOM   1055  C   THR   422      29.301  -4.487  59.241  1.00 40.00
ATOM   1056  O   THR   422      28.183  -4.130  59.601  1.00 40.00
ATOM   1057  N   SER   423      30.416  -4.022  59.842  1.00 20.00
ATOM   1059  CA  SER   423      30.266  -3.123  60.951  1.00 20.00
ATOM   1060  CB  SER   423      30.124  -3.861  62.296  1.00 20.00
ATOM   1061  OG  SER   423      29.972  -2.937  63.364  1.00 20.00
ATOM   1063  C   SER   423      31.482  -2.254  61.046  1.00 20.00
ATOM   1064  O   SER   423      32.423  -2.422  60.273  1.00 20.00
ATOM   1065  N   LEU   424      31.436  -1.238  61.938  1.00 20.00
ATOM   1067  CA  LEU   424      32.556  -0.374  62.194  1.00 20.00
ATOM   1068  CB  LEU   424      32.159   0.841  63.054  1.00 20.00
ATOM   1069  CG  LEU   424      31.078   1.743  62.419  1.00 20.00
ATOM   1070  CD1 LEU   424      31.575   2.391  61.116  1.00 20.00
ATOM   1071  CD2 LEU   424      29.741   1.001  62.254  1.00 20.00
ATOM   1072  C   LEU   424      33.616  -1.131  62.947  1.00 20.00
ATOM   1073  O   LEU   424      34.764  -1.191  62.523  1.00 20.00
ATOM   1074  N   GLY   425      33.269  -1.752  64.093  1.00 20.00
ATOM   1076  CA  GLY   425      34.242  -2.537  64.818  1.00 20.00
ATOM   1077  C   GLY   425      35.328  -1.708  65.458  1.00 20.00
ATOM   1078  O   GLY   425      36.307  -2.237  65.980  1.00 20.00
ATOM   1079  N   LEU   426      35.143  -0.381  65.462  1.00 20.00
ATOM   1081  CA  LEU   426      36.012   0.656  65.963  1.00 20.00
ATOM   1082  CB  LEU   426      35.706   2.062  65.412  1.00 20.00
ATOM   1083  CG  LEU   426      36.084   2.249  63.931  1.00 20.00
ATOM   1084  CD1 LEU   426      35.790   3.681  63.458  1.00 20.00
ATOM   1085  CD2 LEU   426      37.542   1.836  63.676  1.00 20.00
ATOM   1086  C   LEU   426      35.965   0.746  67.452  1.00 20.00
ATOM   1087  O   LEU   426      36.277   1.801  67.987  1.00 20.00
ATOM   1088  N   ARG   427      35.524  -0.305  68.168  1.00 20.00
ATOM   1090  CA  ARG   427      35.179  -0.216  69.568  1.00 20.00
ATOM   1091  CB  ARG   427      35.061  -1.583  70.265  1.00 20.00
ATOM   1092  CG  ARG   427      36.373  -2.362  70.329  1.00 20.00
ATOM   1093  CD  ARG   427      36.329  -3.537  71.307  1.00 20.00
ATOM   1094  NE  ARG   427      37.689  -4.143  71.322  1.00 20.00
ATOM   1096  CZ  ARG   427      38.665  -3.598  72.105  1.00 20.00
ATOM   1097  NH1 ARG   427      38.390  -2.515  72.890  1.00 20.00
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ATOM   1100  NH2 ARG   427      39.924  -4.125  72.091  1.00 20.00
ATOM   1103  C   ARG   427      36.081   0.609  70.444  1.00 20.00
ATOM   1104  O   ARG   427      35.606   1.179  71.423  1.00 20.00
   M   1105  N   SER   428      37.393   0.670  70.174  1.00 20.00
ATOM   1107  CA  SER   428      38.285   1.469  70.974  1.00 20.00
ATOM   1108  CB  SER   428      39.760   1.196  70.643  1.00 20.00
ATOM   1109  OG  SER   428      40.020   1.553  69.294  1.00 20.00
ATOM   1111  C   SER   428      38.056   2.952  70.818  1.00 20.00
ATOM   1112  O   SER   428      38.444   3.741  71.677  1.00 20.00
ATOM   1113  N   LEU   429      37.456   3.375  69.690  1.00 20.00
ATOM   1115  CA  LEU   429      37.291   4.759  69.331  1.00 20.00
ATOM   1116  CB  LEU   429      36.679   4.907  67.924  1.00 20.00
ATOM   1117  CG  LEU   429      36.534   6.355  67.423  1.00 20.00
ATOM   1118  CD1 LEU   429      37.911   7.015  67.237  1.00 20.00
ATOM   1119  CD2 LEU   429      35.668   6.419  66.152  1.00 20.00
ATOM   1120  C   LEU   429      36.441   5.523  70.302  1.00 20.00
ATOM   1121  O   LEU   429      35.213   5.440  70.285  1.00 20.00
ATOM   1122  N   LYS   430      37.105   6.242  71.230  1.00 20.00
ATOM   1124  CA  LYS   430      36.429   7.073  72.178  1.00 20.00
ATOM   1125  CB  LYS   430      37.263   7.316  73.436  1.00 20.00
ATOM   1126  CG  LYS   430      37.388   6.040  74.265  1.00 20.00
ATOM   1127  CD  LYS   430      38.410   6.146  75.388  1.00 20.00
ATOM   1128  CE  LYS   430      38.325   4.996  76.391  1.00 20.00
ATOM   1129  NZ  LYS   430      39.167   5.291  77.572  1.00 20.00
ATOM   1133  C   LYS   430      35.960   8.392  71.653  1.00 20.00
ATOM   1134  O   LYS   430      34.829   8.788  71.920  1.00 20.00
ATOM   1135  N   GLU   431      36.797   9.134  70.896  1.00 20.00
ATOM   1137  CA  GLU   431      36.277  10.402  70.477  1.00 20.00
ATOM   1138  CB  GLU   431      36.374  11.497  71.552  1.00 20.00
ATOM   1139  CG  GLU   431      35.636  12.776  71.151  1.00 20.00
ATOM   1140  CD  GLU   431      35.614  13.725  72.339  1.00 20.00
ATOM   1141  OE1 GLU   431      36.713  14.064  72.853  1.00 20.00
ATOM   1142  OE2 GLU   431      34.491  14.125  72.749  1.00 20.00
ATOM   1143  C   GLU   431      36.920  10.936  69.242  1.00 20.00
ATOM   1144  O   GLU   431      38.056  10.606  68.902  1.00 20.00
ATOM   1145  N   ILE   432      36.155  11.771  68.512  1.00 20.00
ATOM   1147  CA  ILE   432      36.674  12.438  67.363  1.00 20.00
ATOM   1148  CB  ILE   432      35.882  12.180  66.111  1.00 20.00
ATOM   1149  CG2 ILE   432      36.343  13.160  65.021  1.00 20.00
ATOM   1150  CG1 ILE   432      36.042  10.697  65.719  1.00 20.00
ATOM   1151  CD1 ILE   432      35.157  10.240  64.561  1.00 20.00
ATOM   1152  C   ILE   432      36.637  13.880  67.732  1.00 20.00
ATOM   1153  O   ILE   432      35.638  14.574  67.562  1.00 20.00
ATOM   1154  N   SER   433      37.801  14.387  68.155  1.00 20.00
ATOM   1156  CA  SER   433      37.934  15.679  68.751  1.00 20.00
ATOM   1157  CB  SER   433      39.413  16.039  68.966  1.00 20.00
ATOM   1158  OG  SER   433      39.525  17.269  69.660  1.00 20.00
ATOM   1160  C   SER   433      37.297  16.746  67.915  1.00 20.00
ATOM   1161  O   SER   433      36.732  17.688  68.465  1.00 20.00
ATOM   1162  N   ASP   434      37.373  16.661  66.574  1.00 20.00
ATOM   1164  CA  ASP   434      36.769  17.708  65.793  1.00 20.00
ATOM   1165  CB  ASP   434      37.778  18.757  65.285  1.00 20.00
ATOM   1166  CG  ASP   434      38.367  19.559  66.437  1.00 20.00
ATOM   1167  OD1 ASP   434      39.564  19.935  66.325  1.00 20.00
ATOM   1168  OD2 ASP   434      37.636  19.820  67.428  1.00 20.00
ATOM   1169  C   ASP   434      36.205  17.125  64.536  1.00 20.00
ATOM   1170  O   ASP   434      36.755  16.164  64.006  1.00 20.00
ATOM   1171  N   GLY   435      35.099  17.712  64.023  1.00 20.00
ATOM   1173  CA  GLY   435      34.518  17.298  62.776  1.00 20.00
ATOM   1174  C   GLY   435      33.489  16.239  63.009  1.00 20.00
ATOM   1175  O   GLY   435      33.406  15.670  64.096  1.00 20.00
ATOM   1176  N   ASP   436      32.666  15.958  61.972  1.00 20.00
ATOM   1178  CA  ASP   436      31.658  14.941  62.091  1.00 20.00
ATOM   1179  CB  ASP   436      30.248  15.361  61.626  1.00 20.00
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ATOM	1180	CG	ASP	436	30.254	15.669	60.138	1.00	20.00
ATOM	1181	OD1	ASP	436	31.256	16.260	59.658	1.00	20.00
ATOM	1182	OD2	ASP	436	29.252	15.318	59.459	1.00	20.00
ATOM	1183	C	ASP	436	32.073	13.745	61.293	1.00	20.00
ATOM	1184	O	ASP	436	33.236	13.617	60.924	1.00	20.00
ATOM	1185	N	VAL	437	31.138	12.805	61.036	1.00	20.00
ATOM	1187	CA	VAL	437	31.480	11.636	60.270	1.00	20.00
ATOM	1188	CB	VAL	437	31.538	10.383	61.101	1.00	20.00
ATOM	1189	CG1	VAL	437	31.609	9.134	60.207	1.00	20.00
ATOM	1190	CG2	VAL	437	32.787	10.510	61.984	1.00	20.00
ATOM	1191	C	VAL	437	30.518	11.447	59.139	1.00	20.00
ATOM	1192	O	VAL	437	29.386	11.919	59.199	1.00	20.00
ATOM	1193	N	ILE	438	30.965	10.802	58.037	1.00	20.00
ATOM	1195	CA	ILE	438	30.073	10.553	56.944	1.00	20.00
ATOM	1196	CB	ILE	438	30.382	11.398	55.726	1.00	20.00
ATOM	1197	CG2	ILE	438	31.787	11.046	55.207	1.00	20.00
ATOM	1198	CG1	ILE	438	29.259	11.328	54.670	1.00	20.00
ATOM	1199	CD1	ILE	438	29.073	9.964	54.005	1.00	20.00
ATOM	1200	C	ILE	438	30.118	9.092	56.609	1.00	20.00
ATOM	1201	O	ILE	438	31.115	8.561	56.122	1.00	20.00
ATOM	1202	N	ILE	439	29.012	8.381	56.877	1.00	20.00
ATOM	1204	CA	ILE	439	29.001	6.988	56.549	1.00	20.00
ATOM	1205	CB	ILE	439	28.507	6.134	57.681	1.00	20.00
ATOM	1206	CG2	ILE	439	28.420	4.677	57.195	1.00	20.00
ATOM	1207	CG1	ILE	439	29.412	6.316	58.910	1.00	20.00
ATOM	1208	CD1	ILE	439	28.821	5.723	60.188	1.00	20.00
ATOM	1209	C	ILE	439	28.042	6.847	55.410	1.00	20.00
ATOM	1210	O	ILE	439	26.831	6.784	55.614	1.00	20.00
ATOM	1211	N	SER	440	28.563	6.770	54.167	1.00	20.00
ATOM	1213	CA	SER	440	27.669	6.726	53.047	1.00	20.00
ATOM	1214	CB	SER	440	27.725	8.001	52.186	1.00	20.00
ATOM	1215	OG	SER	440	26.819	7.899	51.097	1.00	20.00
ATOM	1217	C	SER	440	27.936	5.571	52.133	1.00	20.00
ATOM	1218	O	SER	440	29.056	5.070	52.032	1.00	20.00
ATOM	1219	N	GLY	441	26.867	5.109	51.455	1.00	20.00
ATOM	1221	CA	GLY	441	26.962	4.082	50.458	1.00	20.00
ATOM	1222	C	GLY	441	27.610	2.838	50.970	1.00	20.00
ATOM	1223	O	GLY	441	28.639	2.420	50.440	1.00	20.00
ATOM	1224	N	ASN	442	27.056	2.230	52.037	1.00	20.00
ATOM	1226	CA	ASN	442	27.610	0.991	52.508	1.00	20.00
ATOM	1227	CB	ASN	442	28.298	1.143	53.873	1.00	20.00
ATOM	1228	CG	ASN	442	29.495	2.061	53.665	1.00	20.00
ATOM	1229	OD1	ASN	442	30.454	1.711	52.979	1.00	20.00
ATOM	1230	ND2	ASN	442	29.430	3.282	54.259	1.00	20.00
ATOM	1233	C	ASN	442	26.463	0.049	52.672	1.00	20.00
ATOM	1234	O	ASN	442	25.955	-0.145	53.775	1.00	20.00
ATOM	1235	N	LYS	443	26.091	-0.654	51.589	1.00	20.00
ATOM	1237	CA	LYS	443	24.876	-1.410	51.620	1.00	20.00
ATOM	1238	CB	LYS	443	24.582	-2.098	50.279	1.00	20.00
ATOM	1239	CG	LYS	443	24.381	-1.055	49.178	1.00	20.00
ATOM	1240	CD	LYS	443	23.303	-0.027	49.532	1.00	20.00
ATOM	1241	CE	LYS	443	23.348	1.248	48.686	1.00	20.00
ATOM	1242	NZ	LYS	443	22.704	1.018	47.374	1.00	20.00
ATOM	1246	C	LYS	443	24.824	-2.413	52.734	1.00	20.00
ATOM	1247	O	LYS	443	23.798	-2.535	53.398	1.00	20.00
ATOM	1248	N	ASN	444	25.920	-3.155	52.963	1.00	20.00
ATOM	1250	CA	ASN	444	26.027	-4.165	53.984	1.00	20.00
ATOM	1251	CB	ASN	444	27.114	-5.208	53.675	1.00	20.00
ATOM	1252	CG	ASN	444	26.577	-6.095	52.559	1.00	20.00
ATOM	1253	OD1	ASN	444	25.369	-6.297	52.447	1.00	20.00
ATOM	1254	ND2	ASN	444	27.490	-6.648	51.717	1.00	20.00
ATOM	1257	C	ASN	444	26.247	-3.673	55.387	1.00	20.00
ATOM	1258	O	ASN	444	26.107	-4.446	56.333	1.00	20.00
ATOM	1259	N	LEU	445	26.670	-2.409	55.575	1.00	20.00

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ATOM   1261  CA  LEU   445      27.029  -1.962  56.894  1.00 20.00
ATOM   1262  CB  LEU   445      27.608  -0.533  56.890  1.00 20.00
ATOM   1263  CG  LEU   445      28.021  -0.002  58.276  1.00 20.00
   OM  1264  CD1 LEU   445      29.207  -0.798  58.846  1.00 20.00
ATOM   1265  CD2 LEU   445      28.286   1.512  58.239  1.00 20.00
ATOM   1266  C   LEU   445      25.880  -2.002  57.855  1.00 20.00
ATOM   1267  O   LEU   445      24.803  -1.466  57.601  1.00 20.00
ATOM   1268  N   CYS   446      26.109  -2.656  59.011  1.00 20.00
ATOM   1270  CA  CYS   446      25.129  -2.767  60.051  1.00 20.00
ATOM   1271  CB  CYS   446      24.604  -4.196  60.270  1.00 20.00
ATOM   1272  SG  CYS   446      23.521  -4.750  58.922  1.00 20.00
ATOM   1273  C   CYS   446      25.815  -2.339  61.305  1.00 20.00
ATOM   1274  O   CYS   446      26.913  -1.790  61.261  1.00 20.00
ATOM   1275  N   TYR   447      25.170  -2.551  62.467  1.00 20.00
ATOM   1277  CA  TYR   447      25.788  -2.176  63.704  1.00 20.00
ATOM   1278  CB  TYR   447      27.139  -2.860  63.933  1.00 20.00
ATOM   1279  CG  TYR   447      26.901  -4.315  64.050  1.00 20.00
ATOM   1280  CD1 TYR   447      26.684  -5.079  62.926  1.00 20.00
ATOM   1281  CE1 TYR   447      26.536  -6.440  63.018  1.00 20.00
ATOM   1282  CD2 TYR   447      27.005  -4.920  65.274  1.00 20.00
ATOM   1283  CE2 TYR   447      26.887  -6.280  65.362  1.00 20.00
ATOM   1284  CZ  TYR   447      26.639  -7.040  64.246  1.00 20.00
ATOM   1285  OH  TYR   447      26.509  -8.439  64.357  1.00 20.00
ATOM   1287  C   TYR   447      26.099  -0.718  63.647  1.00 20.00
ATOM   1288  O   TYR   447      27.098  -0.285  64.220  1.00 20.00
ATOM   1289  N   ALA   448      25.354   0.035  62.816  1.00 20.00
ATOM   1291  CA  ALA   448      25.444   1.468  62.731  1.00 20.00
ATOM   1292  CB  ALA   448      25.053   1.995  61.341  1.00 20.00
ATOM   1293  C   ALA   448      24.577   2.186  63.723  1.00 20.00
ATOM   1294  O   ALA   448      24.983   3.172  64.335  1.00 20.00
ATOM   1295  N   ASN   449      23.326   1.702  63.860  1.00 20.00
ATOM   1297  CA  ASN   449      22.283   2.266  64.675  1.00 20.00
ATOM   1298  CB  ASN   449      20.909   1.646  64.371  1.00 20.00
ATOM   1299  CG  ASN   449      20.560   1.977  62.927  1.00 20.00
ATOM   1300  OD1 ASN   449      20.287   1.088  62.122  1.00 20.00
ATOM   1301  ND2 ASN   449      20.574   3.293  62.586  1.00 20.00
ATOM   1304  C   ASN   449      22.569   2.021  66.116  1.00 20.00
ATOM   1305  O   ASN   449      22.047   2.695  67.001  1.00 20.00
ATOM   1306  N   THR   450      23.375   0.983  66.361  1.00 20.00
ATOM   1308  CA  THR   450      23.740   0.473  67.644  1.00 20.00
ATOM   1309  CB  THR   450      24.470  -0.828  67.513  1.00 20.00
ATOM   1310  OG1 THR   450      23.769  -1.689  66.632  1.00 20.00
ATOM   1312  CG2 THR   450      24.492  -1.486  68.896  1.00 20.00
ATOM   1313  C   THR   450      24.647   1.405  68.395  1.00 20.00
ATOM   1314  O   THR   450      24.795   1.253  69.605  1.00 20.00
ATOM   1315  N   ILE   451      25.329   2.350  67.707  1.00 20.00
ATOM   1317  CA  ILE   451      26.316   3.163  68.373  1.00 20.00
ATOM   1318  CB  ILE   451      27.580   3.277  67.555  1.00 20.00
ATOM   1319  CG2 ILE   451      27.299   4.270  66.414  1.00 20.00
ATOM   1320  CG1 ILE   451      28.815   3.653  68.399  1.00 20.00
ATOM   1321  CD1 ILE   451      28.834   5.086  68.923  1.00 20.00
ATOM   1322  C   ILE   451      25.818   4.546  68.693  1.00 20.00
ATOM   1323  O   ILE   451      25.096   5.166  67.913  1.00 20.00
ATOM   1324  N   ASN   452      26.191   5.056  69.889  1.00 20.00
ATOM   1326  CA  ASN   452      25.793   6.369  70.309  1.00 20.00
ATOM   1327  CB  ASN   452      25.558   6.442  71.830  1.00 20.00
ATOM   1328  CG  ASN   452      24.657   7.627  72.151  1.00 20.00
ATOM   1329  OD1 ASN   452      24.663   8.643  71.460  1.00 20.00
ATOM   1330  ND2 ASN   452      23.848   7.489  73.236  1.00 20.00
ATOM   1333  C   ASN   452      26.916   7.303  69.951  1.00 20.00
ATOM   1334  O   ASN   452      27.858   7.507  70.716  1.00 20.00
ATOM   1335  N   TRP   453      26.809   7.922  68.762  1.00 20.00
ATOM   1337  CA  TRP   453      27.799   8.801  68.207  1.00 20.00
ATOM   1338  CB  TRP   453      27.480   9.218  66.759  1.00 20.00
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ATOM   1339  CG  TRP   453      27.480   8.071  65.773  1.00 20.00
ATOM   1340  CD2 TRP   453      28.653   7.348  65.358  1.00 20.00
ATOM   1341  CE2 TRP   453      28.237   6.354  64.473  1.00 20.00
ATOM   1342  CE3 TRP   453      29.967   7.498  65.690  1.00 20.00
ATOM   1343  CD1 TRP   453      26.422   7.468  65.152  1.00 20.00
ATOM   1344  NE1 TRP   453      26.867   6.442  64.354  1.00 20.00
ATOM   1346  CZ2 TRP   453      29.138   5.503  63.898  1.00 20.00
ATOM   1347  CZ3 TRP   453      30.876   6.651  65.095  1.00 20.00
ATOM   1348  CH2 TRP   453      30.468   5.670  64.215  1.00 20.00
ATOM   1349  C   TRP   453      27.873  10.031  69.043  1.00 20.00
ATOM   1350  O   TRP   453      28.849  10.771  68.982  1.00 20.00
ATOM   1351  N   LYS   454      26.814  10.303  69.823  1.00 20.00
ATOM   1353  CA  LYS   454      26.774  11.481  70.637  1.00 20.00
ATOM   1354  CB  LYS   454      25.501  11.532  71.502  1.00 20.00
ATOM   1355  CG  LYS   454      25.282  12.849  72.250  1.00 20.00
ATOM   1356  CD  LYS   454      23.876  12.981  72.840  1.00 20.00
ATOM   1357  CE  LYS   454      23.801  12.650  74.332  1.00 20.00
ATOM   1358  NZ  LYS   454      24.177  11.237  74.560  1.00 20.00
ATOM   1362  C   LYS   454      27.947  11.473  71.563  1.00 20.00
ATOM   1363  O   LYS   454      28.592  12.501  71.763  1.00 20.00
ATOM   1364  N   LYS   455      28.249  10.309  72.167  1.00 20.00
ATOM   1366  CA  LYS   455      29.358  10.234  73.073  1.00 20.00
ATOM   1367  CB  LYS   455      29.457   8.875  73.785  1.00 20.00
ATOM   1368  CG  LYS   455      30.614   8.799  74.783  1.00 20.00
ATOM   1369  CD  LYS   455      30.517   7.613  75.745  1.00 20.00
ATOM   1370  CE  LYS   455      31.670   7.543  76.748  1.00 20.00
ATOM   1371  NZ  LYS   455      31.474   6.401  77.669  1.00 20.00
ATOM   1375  C   LYS   455      30.646  10.448  72.341  1.00 20.00
ATOM   1376  O   LYS   455      31.520  11.181  72.801  1.00 20.00
ATOM   1377  N   LEU   456      30.793   9.802  71.171  1.00 20.00
ATOM   1379  CA  LEU   456      32.005   9.890  70.405  1.00 20.00
ATOM   1380  CB  LEU   456      31.950   8.928  69.195  1.00 20.00
ATOM   1381  CG  LEU   456      33.236   8.741  68.352  1.00 20.00
ATOM   1382  CD1 LEU   456      32.974   7.740  67.215  1.00 20.00
ATOM   1383  CD2 LEU   456      33.819  10.056  67.809  1.00 20.00
ATOM   1384  C   LEU   456      32.207  11.296  69.921  1.00 20.00
ATOM   1385  O   LEU   456      33.299  11.850  70.051  1.00 20.00
ATOM   1386  N   PHE   457      31.152  11.919  69.356  1.00 20.00
ATOM   1388  CA  PHE   457      31.275  13.239  68.804  1.00 20.00
ATOM   1389  CB  PHE   457      30.520  13.432  67.483  1.00 20.00
ATOM   1390  CG  PHE   457      31.040  12.438  66.521  1.00 20.00
ATOM   1391  CD1 PHE   457      32.171  12.700  65.787  1.00 20.00
ATOM   1392  CD2 PHE   457      30.393  11.236  66.379  1.00 20.00
ATOM   1393  CE1 PHE   457      32.660  11.752  64.926  1.00 20.00
ATOM   1394  CE2 PHE   457      30.882  10.287  65.522  1.00 20.00
ATOM   1395  CZ  PHE   457      32.031  10.535  64.819  1.00 20.00
ATOM   1396  C   PHE   457      30.582  14.189  69.714  1.00 20.00
ATOM   1397  O   PHE   457      29.355  14.198  69.791  1.00 20.00
ATOM   1398  N   GLY   458      31.351  14.991  70.462  1.00 40.00
ATOM   1400  CA  GLY   458      30.716  15.995  71.255  1.00 40.00
ATOM   1401  C   GLY   458      30.329  17.121  70.356  1.00 40.00
ATOM   1402  O   GLY   458      29.233  17.673  70.446  1.00 40.00
ATOM   1403  N   THR   459      31.242  17.448  69.423  1.00 40.00
ATOM   1405  CA  THR   459      31.117  18.607  68.594  1.00 40.00
ATOM   1406  CB  THR   459      32.178  18.671  67.530  1.00 40.00
ATOM   1407  OG1 THR   459      32.074  17.559  66.653  1.00 40.00
ATOM   1409  CG2 THR   459      33.557  18.683  68.213  1.00 40.00
ATOM   1410  C   THR   459      29.793  18.691  67.916  1.00 40.00
ATOM   1411  O   THR   459      29.038  19.634  68.147  1.00 40.00
ATOM   1412  N   SER   460      29.448  17.707  67.070  1.00 40.00
ATOM   1414  CA  SER   460      28.205  17.880  66.388  1.00 40.00
ATOM   1415  CB  SER   460      28.307  18.854  65.203  1.00 40.00
ATOM   1416  OG  SER   460      27.047  18.984  64.566  1.00 40.00
ATOM   1418  C   SER   460      27.707  16.589  65.838  1.00 40.00
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ATOM   1419  O   SER   460      28.122  16.158  64.765  1.00 40.00
ATOM   1420  N   GLY   461      26.798  15.935  66.578  1.00 40.00
ATOM   1422  CA  GLY   461      26.202  14.721  66.113  1.00 40.00
ATOM   1423  C   GLY   461      25.299  15.063  64.973  1.00 40.00
ATOM   1424  O   GLY   461      25.091  14.265  64.062  1.00 40.00
ATOM   1425  N   GLN   462      24.725  16.279  65.013  1.00 40.00
ATOM   1427  CA  GLN   462      23.786  16.715  64.020  1.00 40.00
ATOM   1428  CB  GLN   462      23.223  18.115  64.315  1.00 40.00
ATOM   1429  CG  GLN   462      24.287  19.212  64.282  1.00 40.00
ATOM   1430  CD  GLN   462      23.621  20.547  64.584  1.00 40.00
ATOM   1431  OE1 GLN   462      22.443  20.753  64.300  1.00 40.00
ATOM   1432  NE2 GLN   462      24.401  21.484  65.187  1.00 40.00
ATOM   1435  C   GLN   462      24.444  16.755  62.677  1.00 40.00
ATOM   1436  O   GLN   462      23.805  16.489  61.660  1.00 40.00
ATOM   1437  N   LYS   463      25.746  17.092  62.649  1.00 40.00
ATOM   1439  CA  LYS   463      26.507  17.247  61.440  1.00 40.00
ATOM   1440  CB  LYS   463      27.923  17.786  61.702  1.00 40.00
ATOM   1441  CG  LYS   463      28.590  18.361  60.452  1.00 40.00
ATOM   1442  CD  LYS   463      27.908  19.641  59.963  1.00 40.00
ATOM   1443  CE  LYS   463      28.550  20.258  58.720  1.00 40.00
ATOM   1444  NZ  LYS   463      27.801  21.469  58.318  1.00 40.00
ATOM   1448  C   LYS   463      26.660  15.969  60.669  1.00 40.00
ATOM   1449  O   LYS   463      26.753  15.991  59.443  1.00 40.00
ATOM   1450  N   THR   464      26.712  14.816  61.359  1.00 40.00
ATOM   1452  CA  THR   464      26.955  13.574  60.676  1.00 40.00
ATOM   1453  CB  THR   464      26.867  12.373  61.572  1.00 40.00
ATOM   1454  OG1 THR   464      27.293  11.210  60.877  1.00 40.00
ATOM   1456  CG2 THR   464      25.409  12.209  62.037  1.00 40.00
ATOM   1457  C   THR   464      26.008  13.353  59.545  1.00 40.00
ATOM   1458  O   THR   464      24.823  13.670  59.636  1.00 40.00
ATOM   1459  N   LYS   465      26.533  12.820  58.419  1.00 40.00
ATOM   1461  CA  LYS   465      25.666  12.528  57.319  1.00 40.00
ATOM   1462  CB  LYS   465      26.015  13.230  55.998  1.00 40.00
ATOM   1463  CG  LYS   465      24.994  12.891  54.910  1.00 40.00
ATOM   1464  CD  LYS   465      25.020  13.816  53.693  1.00 40.00
ATOM   1465  CE  LYS   465      23.979  13.435  52.638  1.00 40.00
ATOM   1466  NZ  LYS   465      23.968  14.436  51.549  1.00 40.00
ATOM   1470  C   LYS   465      25.706  11.064  57.057  1.00 40.00
ATOM   1471  O   LYS   465      26.759  10.491  56.776  1.00 40.00
ATOM   1472  N   ILE   466      24.532  10.415  57.150  1.00 40.00
ATOM   1474  CA  ILE   466      24.500   9.007  56.923  1.00 40.00
ATOM   1475  CB  ILE   466      24.176   8.233  58.167  1.00 40.00
ATOM   1476  CG2 ILE   466      24.064   6.747  57.789  1.00 40.00
ATOM   1477  CG1 ILE   466      25.226   8.516  59.256  1.00 40.00
ATOM   1478  CD1 ILE   466      24.825   8.003  60.639  1.00 40.00
ATOM   1479  C   ILE   466      23.436   8.713  55.920  1.00 40.00
ATOM   1480  O   ILE   466      22.278   9.088  56.102  1.00 40.00
ATOM   1481  N   ILE   467      23.821   8.046  54.814  1.00 40.00
ATOM   1483  CA  ILE   467      22.874   7.661  53.810  1.00 40.00
ATOM   1484  CB  ILE   467      22.588   8.736  52.798  1.00 40.00
ATOM   1485  CG2 ILE   467      21.923   9.922  53.515  1.00 40.00
ATOM   1486  CG1 ILE   467      23.865   9.111  52.030  1.00 40.00
ATOM   1487  CD1 ILE   467      23.596   9.992  50.811  1.00 40.00
ATOM   1488  C   ILE   467      23.454   6.505  53.058  1.00 40.00
ATOM   1489  O   ILE   467      24.671   6.345  52.991  1.00 40.00
ATOM   1490  N   SER   468      22.575   5.682  52.452  1.00 40.00
ATOM   1492  CA  SER   468      22.961   4.556  51.646  1.00 40.00
ATOM   1493  CB  SER   468      24.002   4.934  50.577  1.00 40.00
ATOM   1494  OG  SER   468      23.458   5.896  49.686  1.00 40.00
ATOM   1496  C   SER   468      23.509   3.382  52.407  1.00 40.00
ATOM   1497  O   SER   468      24.142   2.512  51.810  1.00 40.00
ATOM   1498  N   ASN   469      23.263   3.292  53.729  1.00 20.00
ATOM   1500  CA  ASN   469      23.744   2.155  54.472  1.00 20.00
ATOM   1501  CB  ASN   469      24.112   2.474  55.930  1.00 20.00
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ATOM   1502  CG  ASN   469      25.381   3.315  55.913  1.00 20.00
ATOM   1503  OD1 ASN   469      26.339   3.005  55.205  1.00 20.00
ATOM   1504  ND2 ASN   469      25.388   4.414  56.712  1.00 20.00
ATOM   1507  C   ASN   469      22.672   1.112  54.485  1.00 20.00
ATOM   1508  O   ASN   469      21.660   1.240  53.800  1.00 20.00
ATOM   1509  N   ARG   470      22.877   0.022  55.254  1.00 20.00
ATOM   1511  CA  ARG   470      21.898  -1.026  55.268  1.00 20.00
ATOM   1512  CB  ARG   470      22.443  -2.371  55.776  1.00 20.00
ATOM   1513  CG  ARG   470      21.540  -3.550  55.415  1.00 20.00
ATOM   1514  CD  ARG   470      22.221  -4.913  55.539  1.00 20.00
ATOM   1515  NE  ARG   470      21.220  -5.939  55.132  1.00 20.00
ATOM   1517  CZ  ARG   470      21.018  -6.201  53.807  1.00 20.00
ATOM   1518  NH1 ARG   470      20.128  -7.165  53.429  1.00 20.00
ATOM   1521  NH2 ARG   470      21.699  -5.492  52.859  1.00 20.00
ATOM   1524  C   ARG   470      20.742  -0.619  56.128  1.00 20.00
ATOM   1525  O   ARG   470      20.889   0.183  57.048  1.00 20.00
ATOM   1526  N   GLY   471      19.546  -1.171  55.835  1.00 20.00
ATOM   1528  CA  GLY   471      18.369  -0.820  56.575  1.00 20.00
ATOM   1529  C   GLY   471      18.410  -1.520  57.892  1.00 20.00
ATOM   1530  O   GLY   471      18.635  -2.726  57.968  1.00 20.00
ATOM   1531  N   GLU   472      18.110  -0.768  58.964  1.00 20.00
ATOM   1533  CA  GLU   472      18.175  -1.258  60.308  1.00 20.00
ATOM   1534  CB  GLU   472      17.700  -0.191  61.312  1.00 20.00
ATOM   1535  CG  GLU   472      17.766  -0.618  62.778  1.00 20.00
ATOM   1536  CD  GLU   472      17.265   0.550  63.621  1.00 20.00
ATOM   1537  OE1 GLU   472      17.843   1.662  63.488  1.00 20.00
ATOM   1538  OE2 GLU   472      16.297   0.348  64.401  1.00 20.00
ATOM   1539  C   GLU   472      17.281  -2.449  60.428  1.00 20.00
ATOM   1540  O   GLU   472      17.601  -3.408  61.131  1.00 20.00
ATOM   1541  N   ASN   473      16.126  -2.412  59.741  1.00 20.00
ATOM   1543  CA  ASN   473      15.193  -3.499  59.794  1.00 20.00
ATOM   1544  CB  ASN   473      13.928  -3.214  58.965  1.00 20.00
ATOM   1545  CG  ASN   473      13.138  -2.118  59.669  1.00 20.00
ATOM   1546  OD1 ASN   473      12.431  -2.374  60.643  1.00 20.00
ATOM   1547  ND2 ASN   473      13.264  -0.859  59.169  1.00 20.00
ATOM   1550  C   ASN   473      15.837  -4.727  59.232  1.00 20.00
ATOM   1551  O   ASN   473      15.707  -5.817  59.788  1.00 20.00
ATOM   1552  N   SER   474      16.555  -4.573  58.103  1.00 20.00
ATOM   1554  CA  SER   474      17.194  -5.681  57.451  1.00 20.00
ATOM   1555  CB  SER   474      17.843  -5.283  56.113  1.00 20.00
ATOM   1556  OG  SER   474      18.457  -6.413  55.510  1.00 20.00
ATOM   1558  C   SER   474      18.276  -6.232  58.324  1.00 20.00
ATOM   1559  O   SER   474      18.449  -7.445  58.429  1.00 20.00
ATOM   1560  N   CYS   475      19.036  -5.344  58.987  1.00 20.00
ATOM   1562  CA  CYS   475      20.125  -5.779  59.808  1.00 20.00
ATOM   1563  CB  CYS   475      20.906  -4.613  60.438  1.00 20.00
ATOM   1564  SG  CYS   475      21.836  -3.652  59.208  1.00 20.00
ATOM   1565  C   CYS   475      19.582  -6.621  60.912  1.00 20.00
ATOM   1566  O   CYS   475      20.186  -7.628  61.278  1.00 20.00
ATOM   1567  N   LYS   476      18.409  -6.242  61.459  1.00 60.00
ATOM   1569  CA  LYS   476      17.874  -6.990  62.558  1.00 60.00
ATOM   1570  CB  LYS   476      17.613  -8.468  62.216  1.00 60.00
ATOM   1571  CG  LYS   476      16.317  -8.703  61.436  1.00 60.00
ATOM   1572  CD  LYS   476      15.048  -8.476  62.266  1.00 60.00
ATOM   1573  CE  LYS   476      14.947  -7.089  62.904  1.00 60.00
ATOM   1574  NZ  LYS   476      13.748  -7.017  63.770  1.00 60.00
ATOM   1578  C   LYS   476      18.921  -6.920  63.604  1.00 60.00
ATOM   1579  O   LYS   476      19.139  -7.855  64.372  1.00 60.00
ATOM   1580  N   ALA   477      19.596  -5.764  63.640  1.00 60.00
ATOM   1582  CA  ALA   477      20.675  -5.551  64.538  1.00 60.00
ATOM   1583  CB  ALA   477      21.779  -4.658  63.931  1.00 60.00
ATOM   1584  C   ALA   477      20.208  -4.882  65.785  1.00 60.00
ATOM   1585  O   ALA   477      19.038  -4.543  65.960  1.00 60.00
ATOM   1586  N   THR   478      21.182  -4.797  66.700  1.00 60.00
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ATOM   1588  CA  THR   478      21.298  -4.164  67.976  1.00 60.00
ATOM   1589  CB  THR   478      20.348  -4.676  69.025  1.00 60.00
ATOM   1590  OG1 THR   478      20.460  -6.086  69.145  1.00 60.00
ATOM   1592  CG2 THR   478      18.907  -4.266  68.681  1.00 60.00
ATOM   1593  C   THR   478      22.621  -4.786  68.220  1.00 60.00
ATOM   1594  O   THR   478      22.914  -5.304  69.294  1.00 60.00
ATOM   1595  N   GLY   479      23.468  -4.695  67.178  1.00 60.00
ATOM   1597  CA  GLY   479      24.658  -5.480  67.102  1.00 60.00
ATOM   1598  C   GLY   479      24.076  -6.585  66.277  1.00 60.00
ATOM   1599  O   GLY   479      23.056  -6.365  65.632  1.00 60.00
ATOM   1600  N   GLN   480      24.678  -7.792  66.239  1.00 60.00
ATOM   1602  CA  GLN   480      23.982  -8.847  65.552  1.00 60.00
ATOM   1603  CB  GLN   480      24.733 -10.188  65.586  1.00 60.00
ATOM   1604  CG  GLN   480      24.025 -11.318  64.839  1.00 60.00
ATOM   1605  CD  GLN   480      24.929 -12.541  64.896  1.00 60.00
ATOM   1606  OE1 GLN   480      24.989 -13.330  63.955  1.00 60.00
ATOM   1607  NE2 GLN   480      25.659 -12.704  66.032  1.00 60.00
ATOM   1610  C   GLN   480      22.824  -8.945  66.475  1.00 60.00
ATOM   1611  O   GLN   480      21.664  -9.097  66.095  1.00 60.00
ATOM   1612  N   VAL   481      23.201  -8.820  67.750  1.00 60.00
ATOM   1614  CA  VAL   481      22.411  -8.694  68.923  1.00 60.00
ATOM   1615  CB  VAL   481      21.982 -10.002  69.518  1.00 60.00
ATOM   1616  CG1 VAL   481      23.239 -10.779  69.947  1.00 60.00
ATOM   1617  CG2 VAL   481      21.013  -9.716  70.677  1.00 60.00
ATOM   1618  C   VAL   481      23.529  -8.182  69.755  1.00 60.00
ATOM   1619  O   VAL   481      24.685  -8.456  69.436  1.00 60.00
ATOM   1620  N   CYS   482      23.285  -7.401  70.814  1.00 20.00
ATOM   1622  CA  CYS   482      24.503  -7.039  71.462  1.00 20.00
ATOM   1623  CB  CYS   482      24.576  -5.617  72.037  1.00 20.00
ATOM   1624  SG  CYS   482      26.326  -5.221  72.294  1.00 20.00
ATOM   1625  C   CYS   482      24.696  -8.015  72.582  1.00 20.00
ATOM   1626  O   CYS   482      23.907  -8.945  72.738  1.00 20.00
ATOM   1627  N   HIS   483      25.765  -7.848  73.388  1.00 20.00
ATOM   1629  CA  HIS   483      25.982  -8.790  74.444  1.00 20.00
ATOM   1630  CB  HIS   483      27.387  -8.739  75.065  1.00 20.00
ATOM   1631  CG  HIS   483      27.708 -10.003  75.804  1.00 20.00
ATOM   1632  CD2 HIS   483      28.282 -11.158  75.361  1.00 20.00
ATOM   1633  ND1 HIS   483      27.377 -10.228  77.118  1.00 20.00
ATOM   1635  CE1 HIS   483      27.769 -11.494  77.410  1.00 20.00
ATOM   1636  NE2 HIS   483      28.323 -12.098  76.375  1.00 20.00
ATOM   1638  C   HIS   483      24.956  -8.511  75.490  1.00 20.00
ATOM   1639  O   HIS   483      24.359  -7.436  75.521  1.00 20.00
ATOM   1640  N   ALA   484      24.706  -9.497  76.368  1.00 20.00
ATOM   1642  CA  ALA   484      23.706  -9.332  77.379  1.00 20.00
ATOM   1643  CB  ALA   484      23.553 -10.571  78.276  1.00 20.00
ATOM   1644  C   ALA   484      24.123  -8.198  78.258  1.00 20.00
ATOM   1645  O   ALA   484      23.301  -7.383  78.673  1.00 20.00
ATOM   1646  N   LEU   485      25.432  -8.123  78.554  1.00 20.00
ATOM   1648  CA  LEU   485      25.971  -7.130  79.435  1.00 20.00
ATOM   1649  CB  LEU   485      27.458  -7.364  79.760  1.00 20.00
ATOM   1650  CG  LEU   485      27.723  -8.604  80.636  1.00 20.00
ATOM   1651  CD1 LEU   485      27.110  -8.438  82.033  1.00 20.00
ATOM   1652  CD2 LEU   485      27.254  -9.899  79.959  1.00 20.00
ATOM   1653  C   LEU   485      25.859  -5.731  78.922  1.00 20.00
ATOM   1654  O   LEU   485      25.609  -4.816  79.705  1.00 20.00
ATOM   1655  N   CYS   486      26.059  -5.521  77.605  1.00 20.00
ATOM   1657  CA  CYS   486      26.024  -4.183  77.088  1.00 20.00
ATOM   1658  CB  CYS   486      26.159  -4.089  75.561  1.00 20.00
ATOM   1659  SG  CYS   486      27.793  -4.607  74.972  1.00 20.00
ATOM   1660  C   CYS   486      24.710  -3.584  77.445  1.00 20.00
ATOM   1661  O   CYS   486      23.680  -4.253  77.418  1.00 20.00
ATOM   1662  N   SER   487      24.725  -2.298  77.834  1.00 40.00
ATOM   1664  CA  SER   487      23.489  -1.683  78.191  1.00 40.00
ATOM   1665  CB  SER   487      23.641  -0.401  79.021  1.00 40.00
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ATOM	1666	OG	SER	487	24.221	0.618	78.222	1.00	40.00
ATOM	1668	C	SER	487	22.857	-1.321	76.902	1.00	40.00
ATOM	1669	O	SER	487	23.476	-1.424	75.845	1.00	40.00
ATOM	1670	N	PRO	488	21.639	-0.873	76.994	1.00	40.00
ATOM	1671	CD	PRO	488	20.819	-1.107	78.169	1.00	40.00
ATOM	1672	CA	PRO	488	20.856	-0.523	75.848	1.00	40.00
ATOM	1673	CB	PRO	488	19.425	-0.323	76.356	1.00	40.00
ATOM	1674	CG	PRO	488	19.548	-0.293	77.891	1.00	40.00
ATOM	1675	C	PRO	488	21.442	0.669	75.183	1.00	40.00
ATOM	1676	O	PRO	488	20.909	1.090	74.158	1.00	40.00
ATOM	1677	N	GLU	489	22.526	1.231	75.750	1.00	40.00
ATOM	1679	CA	GLU	489	23.141	2.350	75.112	1.00	40.00
ATOM	1680	CB	GLU	489	24.424	2.824	75.815	1.00	40.00
ATOM	1681	CG	GLU	489	24.146	3.512	77.152	1.00	40.00
ATOM	1682	CD	GLU	489	23.356	4.780	76.856	1.00	40.00
ATOM	1683	OE1	GLU	489	22.242	4.929	77.426	1.00	40.00
ATOM	1684	OE2	GLU	489	23.854	5.615	76.055	1.00	40.00
ATOM	1685	C	GLU	489	23.486	1.912	73.726	1.00	40.00
ATOM	1686	O	GLU	489	23.147	2.591	72.758	1.00	40.00
ATOM	1687	N	GLY	490	24.148	0.746	73.581	1.00	40.00
ATOM	1689	CA	GLY	490	24.436	0.300	72.246	1.00	40.00
ATOM	1690	C	GLY	490	25.782	-0.344	72.202	1.00	40.00
ATOM	1691	O	GLY	490	26.427	-0.520	73.233	1.00	40.00
ATOM	1692	N	CYS	491	26.229	-0.748	70.993	1.00	20.00
ATOM	1694	CA	CYS	491	27.534	-1.322	70.876	1.00	20.00
ATOM	1695	CB	CYS	491	27.666	-2.693	71.547	1.00	20.00
ATOM	1696	SG	CYS	491	26.822	-4.060	70.710	1.00	20.00
ATOM	1697	C	CYS	491	27.974	-1.427	69.448	1.00	20.00
ATOM	1698	O	CYS	491	27.191	-1.256	68.516	1.00	20.00
ATOM	1699	N	TRP	492	29.286	-1.658	69.249	1.00	20.00
ATOM	1701	CA	TRP	492	29.852	-1.751	67.932	1.00	20.00
ATOM	1702	CB	TRP	492	31.383	-1.624	67.949	1.00	20.00
ATOM	1703	CG	TRP	492	31.841	-0.264	68.422	1.00	20.00
ATOM	1704	CD2	TRP	492	31.829	0.923	67.613	1.00	20.00
ATOM	1705	CE2	TRP	492	32.262	1.975	68.421	1.00	20.00
ATOM	1706	CE3	TRP	492	31.478	1.122	66.309	1.00	20.00
ATOM	1707	CD1	TRP	492	32.250	0.120	69.665	1.00	20.00
ATOM	1708	NE1	TRP	492	32.522	1.466	69.675	1.00	20.00
ATOM	1710	CZ2	TRP	492	32.349	3.248	67.934	1.00	20.00
ATOM	1711	CZ3	TRP	492	31.572	2.407	65.820	1.00	20.00
ATOM	1712	CH2	TRP	492	31.998	3.449	66.617	1.00	20.00
ATOM	1713	C	TRP	492	29.484	-3.013	67.207	1.00	20.00
ATOM	1714	O	TRP	492	29.238	-2.994	66.001	1.00	20.00
ATOM	1715	N	GLY	493	29.448	-4.151	67.926	1.00	20.00
ATOM	1717	CA	GLY	493	29.135	-5.416	67.316	1.00	20.00
ATOM	1718	C	GLY	493	28.919	-6.347	68.463	1.00	20.00
ATOM	1719	O	GLY	493	28.646	-5.883	69.565	1.00	20.00
ATOM	1720	N	PRO	494	28.961	-7.638	68.284	1.00	40.00
ATOM	1721	CD	PRO	494	28.323	-8.259	67.136	1.00	40.00
ATOM	1722	CA	PRO	494	28.822	-8.443	69.463	1.00	40.00
ATOM	1723	CB	PRO	494	28.300	-9.802	69.006	1.00	40.00
ATOM	1724	CG	PRO	494	27.573	-9.482	67.689	1.00	40.00
ATOM	1725	C	PRO	494	30.128	-8.514	70.185	1.00	40.00
ATOM	1726	O	PRO	494	31.072	-9.053	69.613	1.00	40.00
ATOM	1727	N	GLU	495	30.195	-8.014	71.436	1.00	40.00
ATOM	1729	CA	GLU	495	31.375	-8.089	72.256	1.00	40.00
ATOM	1730	CB	GLU	495	32.593	-7.287	71.749	1.00	40.00
ATOM	1731	CG	GLU	495	33.353	-7.900	70.573	1.00	40.00
ATOM	1732	CD	GLU	495	34.454	-6.930	70.171	1.00	40.00
ATOM	1733	OE1	GLU	495	35.343	-7.337	69.376	1.00	40.00
ATOM	1734	OE2	GLU	495	34.417	-5.764	70.646	1.00	40.00
ATOM	1735	C	GLU	495	31.004	-7.432	73.546	1.00	40.00
ATOM	1736	O	GLU	495	30.221	-6.486	73.553	1.00	40.00
ATOM	1737	N	PRO	496	31.509	-7.915	74.645	1.00	20.00

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ATOM   1738  CD  PRO   496      31.711  -9.341  74.819  1.00 20.00
ATOM   1739  CA  PRO   496      31.264  -7.251  75.897  1.00 20.00
ATOM   1740  CB  PRO   496      31.515  -8.293  76.991  1.00 20.00
ATOM   1741  CG  PRO   496      32.200  -9.467  76.268  1.00 20.00
ATOM   1742  C   PRO   496      32.127  -6.031  76.014  1.00 20.00
ATOM   1743  O   PRO   496      31.852  -5.174  76.853  1.00 20.00
ATOM   1744  N   ARG   497      33.221  -5.983  75.231  1.00 20.00
ATOM   1746  CA  ARG   497      34.147  -4.887  75.215  1.00 20.00
ATOM   1747  CB  ARG   497      35.506  -5.301  74.623  1.00 20.00
ATOM   1748  CG  ARG   497      35.420  -5.828  73.193  1.00 20.00
ATOM   1749  CD  ARG   497      36.661  -6.603  72.744  1.00 20.00
ATOM   1750  NE  ARG   497      36.424  -8.046  73.041  1.00 20.00
ATOM   1752  CZ  ARG   497      36.759  -8.573  74.256  1.00 20.00
ATOM   1753  NH1 ARG   497      37.298  -7.778  75.225  1.00 20.00
ATOM   1756  NH2 ARG   497      36.552  -9.900  74.501  1.00 20.00
ATOM   1759  C   ARG   497      33.629  -3.696  74.461  1.00 20.00
ATOM   1760  O   ARG   497      33.927  -2.551  74.796  1.00 20.00
ATOM   1761  N   ASP   498      32.856  -3.946  73.391  1.00 20.00
ATOM   1763  CA  ASP   498      32.360  -2.918  72.516  1.00 20.00
ATOM   1764  CB  ASP   498      31.966  -3.444  71.128  1.00 20.00
ATOM   1765  CG  ASP   498      30.893  -4.496  71.291  1.00 20.00
ATOM   1766  OD1 ASP   498      30.029  -4.348  72.195  1.00 20.00
ATOM   1767  OD2 ASP   498      30.949  -5.482  70.511  1.00 20.00
ATOM   1768  C   ASP   498      31.265  -2.044  73.055  1.00 20.00
ATOM   1769  O   ASP   498      31.035  -0.965  72.509  1.00 20.00
ATOM   1770  N   CYS   499      30.544  -2.499  74.102  1.00 20.00
ATOM   1772  CA  CYS   499      29.422  -1.807  74.694  1.00 20.00
ATOM   1773  CB  CYS   499      29.165  -2.202  76.162  1.00 20.00
ATOM   1774  SG  CYS   499      29.015  -3.986  76.458  1.00 20.00
ATOM   1775  C   CYS   499      29.589  -0.312  74.732  1.00 20.00
ATOM   1776  O   CYS   499      30.701   0.208  74.795  1.00 20.00
ATOM   1777  N   VAL   500      28.468   0.426  74.575  1.00 20.00
ATOM   1779  CA  VAL   500      28.473   1.851  74.753  1.00 20.00
ATOM   1780  CB  VAL   500      27.278   2.529  74.157  1.00 20.00
ATOM   1781  CG1 VAL   500      27.349   4.028  74.498  1.00 20.00
ATOM   1782  CG2 VAL   500      27.267   2.235  72.648  1.00 20.00
ATOM   1783  C   VAL   500      28.452   2.106  76.226  1.00 20.00
ATOM   1784  O   VAL   500      29.131   3.004  76.723  1.00 20.00
ATOM   1785  N   SER   501      27.643   1.306  76.956  1.00 20.00
ATOM   1787  CA  SER   501      27.519   1.440  78.381  1.00 20.00
ATOM   1788  CB  SER   501      26.337   2.321  78.819  1.00 20.00
ATOM   1789  OG  SER   501      26.279   2.402  80.235  1.00 20.00
ATOM   1791  C   SER   501      27.309   0.062  78.932  1.00 20.00
ATOM   1792  O   SER   501      27.178  -0.900  78.175  1.00 20.00
ATOM   1793  N   CYS   502      27.269  -0.068  80.277  1.00 20.00
ATOM   1795  CA  CYS   502      27.190  -1.365  80.887  1.00 20.00
ATOM   1796  CB  CYS   502      28.384  -1.609  81.830  1.00 20.00
ATOM   1797  SG  CYS   502      28.554  -3.311  82.433  1.00 20.00
ATOM   1798  C   CYS   502      25.908  -1.495  81.653  1.00 20.00
ATOM   1799  O   CYS   502      25.412  -0.529  82.231  1.00 20.00
ATOM   1800  N   ARG   503      25.307  -2.704  81.621  1.00 20.00
ATOM   1802  CA  ARG   503      24.084  -2.958  82.327  1.00 20.00
ATOM   1803  CB  ARG   503      23.441  -4.308  81.965  1.00 20.00
ATOM   1804  CG  ARG   503      22.036  -4.476  82.549  1.00 20.00
ATOM   1805  CD  ARG   503      21.326  -5.747  82.079  1.00 20.00
ATOM   1806  NE  ARG   503      21.250  -5.684  80.591  1.00 20.00
ATOM   1808  CZ  ARG   503      20.221  -5.027  79.980  1.00 20.00
ATOM   1809  NH1 ARG   503      19.253  -4.425  80.731  1.00 20.00
ATOM   1812  NH2 ARG   503      20.160  -4.971  78.618  1.00 20.00
ATOM   1815  C   ARG   503      24.343  -2.949  83.798  1.00 20.00
ATOM   1816  O   ARG   503      23.570  -2.388  84.573  1.00 20.00
ATOM   1817  N   ASN   504      25.466  -3.564  84.211  1.00 20.00
ATOM   1819  CA  ASN   504      25.811  -3.647  85.600  1.00 20.00
ATOM   1820  CB  ASN   504      26.210  -5.061  86.059  1.00 20.00
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ATOM	1821	CG	ASN	504	24.945	-5.909	86.120	1.00	20.00
ATOM	1822	OD1	ASN	504	24.548	-6.522	85.131	1.00	20.00
ATOM	1823	ND2	ASN	504	24.293	-5.950	87.313	1.00	20.00
ATOM	1826	C	ASN	504	26.980	-2.740	85.824	1.00	20.00
ATOM	1827	O	ASN	504	26.865	-1.522	85.689	1.00	20.00
ATOM	1828	N	VAL	505	28.139	-3.314	86.200	1.00	20.00
ATOM	1830	CA	VAL	505	29.288	-2.505	86.489	1.00	20.00
ATOM	1831	CB	VAL	505	29.963	-2.869	87.780	1.00	20.00
ATOM	1832	CG1	VAL	505	28.979	-2.620	88.935	1.00	20.00
ATOM	1833	CG2	VAL	505	30.445	-4.325	87.684	1.00	20.00
ATOM	1834	C	VAL	505	30.314	-2.635	85.410	1.00	20.00
ATOM	1835	O	VAL	505	30.472	-3.695	84.808	1.00	20.00
ATOM	1836	N	SER	506	31.038	-1.534	85.132	1.00	20.00
ATOM	1838	CA	SER	506	32.047	-1.574	84.117	1.00	20.00
ATOM	1839	CB	SER	506	32.071	-0.323	83.220	1.00	20.00
ATOM	1840	OG	SER	506	33.101	-0.437	82.250	1.00	20.00
ATOM	1842	C	SER	506	33.370	-1.667	84.795	1.00	20.00
ATOM	1843	O	SER	506	33.630	-0.956	85.765	1.00	20.00
ATOM	1844	N	ARG	507	34.236	-2.583	84.319	1.00	20.00
ATOM	1846	CA	ARG	507	35.518	-2.700	84.940	1.00	20.00
ATOM	1847	CB	ARG	507	35.551	-3.770	86.044	1.00	20.00
ATOM	1848	CG	ARG	507	36.846	-3.786	86.857	1.00	20.00
ATOM	1849	CD	ARG	507	38.033	-4.429	86.137	1.00	20.00
ATOM	1850	NE	ARG	507	39.153	-4.497	87.119	1.00	20.00
ATOM	1852	CZ	ARG	507	40.019	-3.451	87.258	1.00	20.00
ATOM	1853	NH1	ARG	507	41.011	-3.511	88.194	1.00	20.00
ATOM	1856	NH2	ARG	507	39.896	-2.347	86.465	1.00	20.00
ATOM	1859	C	ARG	507	36.547	-3.076	83.922	1.00	20.00
ATOM	1860	O	ARG	507	36.361	-4.008	83.140	1.00	20.00
ATOM	1861	N	GLY	508	37.671	-2.337	83.903	1.00	20.00
ATOM	1863	CA	GLY	508	38.761	-2.667	83.032	1.00	20.00
ATOM	1864	C	GLY	508	38.308	-2.741	81.610	1.00	20.00
ATOM	1865	O	GLY	508	38.630	-3.693	80.902	1.00	20.00
ATOM	1866	N	ARG	509	37.533	-1.743	81.151	1.00	20.00
ATOM	1868	CA	ARG	509	37.133	-1.717	79.773	1.00	20.00
ATOM	1869	CB	ARG	509	38.342	-1.804	78.826	1.00	20.00
ATOM	1870	CG	ARG	509	39.300	-0.620	78.975	1.00	20.00
ATOM	1871	CD	ARG	509	40.611	-0.784	78.205	1.00	20.00
ATOM	1872	NE	ARG	509	40.319	-0.592	76.758	1.00	20.00
ATOM	1874	CZ	ARG	509	41.257	-0.011	75.954	1.00	20.00
ATOM	1875	NH1	ARG	509	41.009	0.154	74.622	1.00	20.00
ATOM	1878	NH2	ARG	509	42.441	0.412	76.486	1.00	20.00
ATOM	1881	C	ARG	509	36.214	-2.859	79.461	1.00	20.00
ATOM	1882	O	ARG	509	35.901	-3.104	78.297	1.00	20.00
ATOM	1883	N	GLU	510	35.726	-3.579	80.491	1.00	20.00
ATOM	1885	CA	GLU	510	34.853	-4.686	80.217	1.00	20.00
ATOM	1886	CB	GLU	510	35.456	-6.027	80.669	1.00	20.00
ATOM	1887	CG	GLU	510	36.723	-6.393	79.890	1.00	20.00
ATOM	1888	CD	GLU	510	37.447	-7.508	80.630	1.00	20.00
ATOM	1889	OE1	GLU	510	37.664	-8.583	80.009	1.00	20.00
ATOM	1890	OE2	GLU	510	37.801	-7.298	81.821	1.00	20.00
ATOM	1891	C	GLU	510	33.589	-4.481	80.984	1.00	20.00
ATOM	1892	O	GLU	510	33.600	-3.976	82.105	1.00	20.00
ATOM	1893	N	CYS	511	32.451	-4.875	80.385	1.00	20.00
ATOM	1895	CA	CYS	511	31.191	-4.703	81.042	1.00	20.00
ATOM	1896	CB	CYS	511	30.037	-4.512	80.039	1.00	20.00
ATOM	1897	SG	CYS	511	28.372	-4.452	80.762	1.00	20.00
ATOM	1898	C	CYS	511	30.961	-5.930	81.858	1.00	20.00
ATOM	1899	O	CYS	511	30.691	-7.003	81.320	1.00	20.00
ATOM	1900	N	VAL	512	31.079	-5.786	83.195	1.00	20.00
ATOM	1902	CA	VAL	512	30.909	-6.884	84.104	1.00	20.00
ATOM	1903	CB	VAL	512	31.969	-6.991	85.164	1.00	20.00
ATOM	1904	CG1	VAL	512	33.231	-7.611	84.562	1.00	20.00
ATOM	1905	CG2	VAL	512	32.239	-5.583	85.710	1.00	20.00

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ATOM   1906  C   VAL   512      29.591  -6.838  84.803  1.00 20.00
ATOM   1907  O   VAL   512      29.045  -5.775  85.096  1.00 20.00
ATOM   1908  N   ASP   513      29.025  -8.039  85.028  1.00 20.00
ATOM   1910  CA  ASP   513      27.799  -8.215  85.747  1.00 20.00
ATOM   1911  CB  ASP   513      27.233  -9.641  85.627  1.00 20.00
ATOM   1912  CG  ASP   513      28.270 -10.614  86.169  1.00 20.00
ATOM   1913  OD1 ASP   513      28.030 -11.193  87.262  1.00 20.00
ATOM   1914  OD2 ASP   513      29.313 -10.800  85.487  1.00 20.00
ATOM   1915  C   ASP   513      28.029  -7.927  87.193  1.00 20.00
ATOM   1916  O   ASP   513      27.143  -7.429  87.887  1.00 20.00
ATOM   1917  N   LYS   514      29.224  -8.282  87.700  1.00 20.00
ATOM   1919  CA  LYS   514      29.519  -8.023  89.077  1.00 20.00
ATOM   1920  CB  LYS   514      29.130  -9.178  90.019  1.00 20.00
ATOM   1921  CG  LYS   514      29.727 -10.535  89.641  1.00 20.00
ATOM   1922  CD  LYS   514      31.238 -10.640  89.842  1.00 20.00
ATOM   1923  CE  LYS   514      31.789 -12.028  89.510  1.00 20.00
ATOM   1924  NZ  LYS   514      31.203 -13.034  90.424  1.00 20.00
ATOM   1928  C   LYS   514      30.987  -7.772  89.197  1.00 20.00
ATOM   1929  O   LYS   514      31.771  -8.128  88.318  1.00 20.00
ATOM   1930  N   CYS   515      31.388  -7.130  90.309  1.00 20.00
ATOM   1932  CA  CYS   515      32.760  -6.793  90.544  1.00 20.00
ATOM   1933  CB  CYS   515      32.987  -6.056  91.874  1.00 20.00
ATOM   1934  SG  CYS   515      32.657  -4.275  91.855  1.00 20.00
ATOM   1935  C   CYS   515      33.608  -8.019  90.651  1.00 20.00
ATOM   1936  O   CYS   515      33.193  -9.045  91.187  1.00 20.00
ATOM   1937  N   LYS   516      34.854  -7.916  90.148  1.00 20.00
ATOM   1939  CA  LYS   516      35.779  -9.006  90.231  1.00 20.00
ATOM   1940  CB  LYS   516      36.980  -8.859  89.281  1.00 20.00
ATOM   1941  CG  LYS   516      36.574  -8.714  87.813  1.00 20.00
ATOM   1942  CD  LYS   516      35.721  -9.868  87.279  1.00 20.00
ATOM   1943  CE  LYS   516      36.519 -11.130  86.944  1.00 20.00
ATOM   1944  NZ  LYS   516      35.616 -12.169  86.398  1.00 20.00
ATOM   1948  C   LYS   516      36.308  -8.986  91.632  1.00 20.00
ATOM   1949  O   LYS   516      36.045  -8.054  92.389  1.00 20.00
ATOM   1950  N   LEU   517      37.070 -10.024  92.024  1.00 20.00
ATOM   1952  CA  LEU   517      37.576 -10.086  93.364  1.00 20.00
ATOM   1953  CB  LEU   517      38.331 -11.391  93.662  1.00 20.00
ATOM   1954  CG  LEU   517      37.452 -12.646  93.499  1.00 20.00
ATOM   1955  CD1 LEU   517      38.242 -13.929  93.807  1.00 20.00
ATOM   1956  CD2 LEU   517      36.158 -12.536  94.320  1.00 20.00
ATOM   1957  C   LEU   517      38.532  -8.949  93.545  1.00 20.00
ATOM   1958  O   LEU   517      39.091  -8.440  92.575  1.00 20.00
ATOM   1959  N   LEU   518      38.719  -8.513  94.809  1.00 20.00
ATOM   1961  CA  LEU   518      39.625  -7.448  95.142  1.00 20.00
ATOM   1962  CB  LEU   518      40.947  -7.494  94.355  1.00 20.00
ATOM   1963  CG  LEU   518      41.918  -6.351  94.714  1.00 20.00
ATOM   1964  CD1 LEU   518      42.433  -6.480  96.156  1.00 20.00
ATOM   1965  CD2 LEU   518      43.044  -6.226  93.676  1.00 20.00
ATOM   1966  C   LEU   518      38.997  -6.114  94.879  1.00 20.00
ATOM   1967  O   LEU   518      39.208  -5.171  95.640  1.00 20.00
ATOM   1968  N   GLU   519      38.191  -5.992  93.804  1.00 20.00
ATOM   1970  CA  GLU   519      37.604  -4.713  93.517  1.00 20.00
ATOM   1971  CB  GLU   519      37.515  -4.360  92.020  1.00 20.00
ATOM   1972  CG  GLU   519      38.842  -3.943  91.381  1.00 20.00
ATOM   1973  CD  GLU   519      39.585  -5.191  90.933  1.00 20.00
ATOM   1974  OE1 GLU   519      38.935  -6.078  90.320  1.00 20.00
ATOM   1975  OE2 GLU   519      40.814  -5.272  91.196  1.00 20.00
ATOM   1976  C   GLU   519      36.208  -4.674  94.044  1.00 20.00
ATOM   1977  O   GLU   519      35.528  -5.696  94.136  1.00 20.00
ATOM   1978  N   GLY   520      35.758  -3.463  94.422  1.00 20.00
ATOM   1980  CA  GLY   520      34.439  -3.272  94.938  1.00 20.00
ATOM   1981  C   GLY   520      33.813  -2.189  94.136  1.00 20.00
ATOM   1982  O   GLY   520      34.491  -1.278  93.667  1.00 20.00
ATOM   1983  N   GLU   521      32.483  -2.262  93.968  1.00 40.00
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ATOM	1985	CA	GLU	521	31.802	-1.288	93.176	1.00	40.00
ATOM	1986	CB	GLU	521	30.416	-1.771	92.716	1.00	40.00
ATOM	1987	CG	GLU	521	29.514	-2.180	93.882	1.00	40.00
ATOM	1988	CD	GLU	521	28.220	-2.746	93.314	1.00	40.00
ATOM	1989	OE1	GLU	521	27.535	-3.502	94.053	1.00	40.00
ATOM	1990	OE2	GLU	521	27.901	-2.435	92.135	1.00	40.00
ATOM	1991	C	GLU	521	31.612	-0.046	93.973	1.00	40.00
ATOM	1992	O	GLU	521	31.258	-0.082	95.150	1.00	40.00
ATOM	1993	N	PRO	522	31.876	1.066	93.349	1.00	40.00
ATOM	1994	CD	PRO	522	33.036	1.177	92.484	1.00	40.00
ATOM	1995	CA	PRO	522	31.617	2.298	94.026	1.00	40.00
ATOM	1996	CB	PRO	522	32.447	3.373	93.318	1.00	40.00
ATOM	1997	CG	PRO	522	33.044	2.661	92.089	1.00	40.00
ATOM	1998	C	PRO	522	30.143	2.511	94.004	1.00	40.00
ATOM	1999	O	PRO	522	29.528	2.289	92.962	1.00	40.00
ATOM	2000	N	ARG	523	29.558	2.927	95.142	1.00	60.00
ATOM	2002	CA	ARG	523	28.138	3.104	95.212	1.00	60.00
ATOM	2003	CB	ARG	523	27.632	3.334	96.647	1.00	60.00
ATOM	2004	CG	ARG	523	27.668	2.065	97.500	1.00	60.00
ATOM	2005	CD	ARG	523	26.622	1.037	97.064	1.00	60.00
ATOM	2006	NE	ARG	523	26.744	-0.152	97.951	1.00	60.00
ATOM	2008	CZ	ARG	523	25.823	-1.155	97.856	1.00	60.00
ATOM	2009	NH1	ARG	523	24.792	-1.047	96.968	1.00	60.00
ATOM	2012	NH2	ARG	523	25.934	-2.264	98.645	1.00	60.00
ATOM	2015	C	ARG	523	27.691	4.256	94.375	1.00	60.00
ATOM	2016	O	ARG	523	26.770	4.121	93.570	1.00	60.00
ATOM	2017	N	GLU	524	28.341	5.425	94.525	1.00	60.00
ATOM	2019	CA	GLU	524	27.889	6.552	93.767	1.00	60.00
ATOM	2020	CB	GLU	524	28.307	7.917	94.338	1.00	60.00
ATOM	2021	CG	GLU	524	29.821	8.130	94.358	1.00	60.00
ATOM	2022	CD	GLU	524	30.077	9.592	94.694	1.00	60.00
ATOM	2023	OE1	GLU	524	29.169	10.425	94.430	1.00	60.00
ATOM	2024	OE2	GLU	524	31.183	9.896	95.214	1.00	60.00
ATOM	2025	C	GLU	524	28.463	6.463	92.398	1.00	60.00
ATOM	2026	O	GLU	524	29.462	5.782	92.170	1.00	60.00
ATOM	2027	N	PHE	525	27.807	7.140	91.438	1.00	60.00
ATOM	2029	CA	PHE	525	28.296	7.136	90.096	1.00	60.00
ATOM	2030	CB	PHE	525	27.511	6.173	89.180	1.00	60.00
ATOM	2031	CG	PHE	525	26.062	6.520	89.262	1.00	60.00
ATOM	2032	CD1	PHE	525	25.327	6.139	90.361	1.00	60.00
ATOM	2033	CD2	PHE	525	25.421	7.158	88.224	1.00	60.00
ATOM	2034	CE1	PHE	525	23.986	6.428	90.447	1.00	60.00
ATOM	2035	CE2	PHE	525	24.079	7.449	88.302	1.00	60.00
ATOM	2036	CZ	PHE	525	23.361	7.094	89.419	1.00	60.00
ATOM	2037	C	PHE	525	28.221	8.522	89.541	1.00	60.00
ATOM	2038	O	PHE	525	27.144	9.036	89.244	1.00	60.00
ATOM	2039	N	VAL	526	29.385	9.185	89.416	1.00	60.00
ATOM	2041	CA	VAL	526	29.371	10.481	88.812	1.00	60.00
ATOM	2042	CB	VAL	526	30.667	11.230	88.964	1.00	60.00
ATOM	2043	CG1	VAL	526	31.810	10.425	88.324	1.00	60.00
ATOM	2044	CG2	VAL	526	30.481	12.633	88.360	1.00	60.00
ATOM	2045	C	VAL	526	29.111	10.214	87.369	1.00	60.00
ATOM	2046	O	VAL	526	28.324	10.904	86.722	1.00	60.00
ATOM	2047	N	GLU	527	29.766	9.165	86.840	1.00	60.00
ATOM	2049	CA	GLU	527	29.567	8.755	85.486	1.00	60.00
ATOM	2050	CB	GLU	527	30.877	8.509	84.718	1.00	60.00
ATOM	2051	CG	GLU	527	31.745	7.401	85.318	1.00	60.00
ATOM	2052	CD	GLU	527	32.996	7.277	84.460	1.00	60.00
ATOM	2053	OE1	GLU	527	33.118	8.051	83.473	1.00	60.00
ATOM	2054	OE2	GLU	527	33.850	6.407	84.782	1.00	60.00
ATOM	2055	C	GLU	527	28.852	7.454	85.613	1.00	60.00
ATOM	2056	O	GLU	527	28.059	7.264	86.534	1.00	60.00
ATOM	2057	N	ASN	528	29.098	6.517	84.682	1.00	60.00
ATOM	2059	CA	ASN	528	28.438	5.254	84.795	1.00	60.00

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ATOM   2060  CB  ASN   528      28.583   4.372  83.545  1.00 60.00
ATOM   2061  CG  ASN   528      27.745   5.007  82.446  1.00 60.00
ATOM   2062  OD1 ASN   528      28.080   6.064  81.915  1.00 60.00
ATOM   2063  ND2 ASN   528      26.613   4.339  82.093  1.00 60.00
ATOM   2066  C   ASN   528      29.058   4.542  85.951  1.00 60.00
ATOM   2067  O   ASN   528      30.106   4.946  86.451  1.00 60.00
ATOM   2068  N   SER   529      28.404   3.462  86.420  1.00 60.00
ATOM   2070  CA  SER   529      28.932   2.745  87.541  1.00 60.00
ATOM   2071  CB  SER   529      27.912   1.823  88.230  1.00 60.00
ATOM   2072  OG  SER   529      26.889   2.597  88.837  1.00 60.00
ATOM   2074  C   SER   529      30.065   1.899  87.074  1.00 60.00
ATOM   2075  O   SER   529      30.100   1.453  85.928  1.00 60.00
ATOM   2076  N   GLU   530      31.040   1.679  87.972  1.00 40.00
ATOM   2078  CA  GLU   530      32.187   0.891  87.648  1.00 40.00
ATOM   2079  CB  GLU   530      33.402   1.722  87.198  1.00 40.00
ATOM   2080  CG  GLU   530      33.230   2.428  85.852  1.00 40.00
ATOM   2081  CD  GLU   530      34.477   3.269  85.618  1.00 40.00
ATOM   2082  OE1 GLU   530      34.663   3.755  84.470  1.00 40.00
ATOM   2083  OE2 GLU   530      35.262   3.437  86.590  1.00 40.00
ATOM   2084  C   GLU   530      32.595   0.225  88.914  1.00 40.00
ATOM   2085  O   GLU   530      31.996   0.441  89.966  1.00 40.00
ATOM   2086  N   CYS   531      33.630  -0.629  88.833  1.00 20.00
ATOM   2088  CA  CYS   531      34.103  -1.267  90.016  1.00 20.00
ATOM   2089  CB  CYS   531      34.350  -2.774  89.869  1.00 20.00
ATOM   2090  SG  CYS   531      34.511  -3.530  91.504  1.00 20.00
ATOM   2091  C   CYS   531      35.424  -0.624  90.264  1.00 20.00
ATOM   2092  O   CYS   531      36.142  -0.277  89.328  1.00 20.00
ATOM   2093  N   ILE   532      35.769  -0.436  91.548  1.00 20.00
ATOM   2095  CA  ILE   532      36.989   0.225  91.890  1.00 20.00
ATOM   2096  CB  ILE   532      36.762   1.494  92.659  1.00 20.00
ATOM   2097  CG2 ILE   532      36.068   1.136  93.983  1.00 20.00
ATOM   2098  CG1 ILE   532      38.073   2.277  92.821  1.00 20.00
ATOM   2099  CD1 ILE   532      37.862   3.702  93.330  1.00 20.00
ATOM   2100  C   ILE   532      37.797  -0.698  92.746  1.00 20.00
ATOM   2101  O   ILE   532      37.286  -1.694  93.251  1.00 20.00
ATOM   2102  N   GLN   533      39.099  -0.398  92.911  1.00 20.00
ATOM   2104  CA  GLN   533      39.970  -1.243  93.677  1.00 20.00
ATOM   2105  CB  GLN   533      41.456  -1.010  93.368  1.00 20.00
ATOM   2106  CG  GLN   533      41.913   0.404  93.730  1.00 20.00
ATOM   2107  CD  GLN   533      43.389   0.531  93.386  1.00 20.00
ATOM   2108  OE1 GLN   533      44.031  -0.438  92.983  1.00 20.00
ATOM   2109  NE2 GLN   533      43.948   1.759  93.553  1.00 20.00
ATOM   2112  C   GLN   533      39.798  -0.994  95.138  1.00 20.00
ATOM   2113  O   GLN   533      39.414   0.096  95.558  1.00 20.00
ATOM   2114  N   CYS   534      40.071  -2.031  95.955  1.00 20.00
ATOM   2116  CA  CYS   534      40.010  -1.852  97.371  1.00 20.00
ATOM   2117  CB  CYS   534      39.102  -2.844  98.131  1.00 20.00
ATOM   2118  SG  CYS   534      37.326  -2.688  97.744  1.00 20.00
ATOM   2119  C   CYS   534      41.410  -2.018  97.894  1.00 20.00
ATOM   2120  O   CYS   534      42.283  -2.538  97.200  1.00 20.00
ATOM   2121  N   HIS   535      41.663  -1.554  99.138  1.00 20.00
ATOM   2123  CA  HIS   535      42.975  -1.624  99.726  1.00 20.00
ATOM   2124  CB  HIS   535      43.142  -0.690 100.943  1.00 20.00
ATOM   2125  CG  HIS   535      44.548  -0.614 101.466  1.00 20.00
ATOM   2126  CD2 HIS   535      45.604   0.126 101.031  1.00 20.00
ATOM   2127  ND1 HIS   535      45.030  -1.377 102.507  1.00 20.00
ATOM   2129  CE1 HIS   535      46.342  -1.063 102.649  1.00 20.00
ATOM   2130  NE2 HIS   535      46.737  -0.155 101.775  1.00 20.00
ATOM   2132  C   HIS   535      43.233  -3.033 100.155  1.00 20.00
ATOM   2133  O   HIS   535      42.305  -3.815 100.356  1.00 20.00
ATOM   2134  N   PRO   536      44.486  -3.387 100.264  1.00 20.00
ATOM   2135  CD  PRO   536      45.537  -2.747  99.494  1.00 20.00
ATOM   2136  CA  PRO   536      44.852  -4.717 100.662  1.00 20.00
ATOM   2137  CB  PRO   536      46.357  -4.843 100.391  1.00 20.00
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ATOM   2138  CG  PRO   536      46.816  -3.419 100.015  1.00 20.00
ATOM   2139  C   PRO   536      44.427  -5.022 102.064  1.00 20.00
ATOM   2140  O   PRO   536      44.167  -6.187 102.364  1.00 20.00
ATOM   2141  N   GLU   537      44.390  -4.005 102.944  1.00 20.00
ATOM   2143  CA  GLU   537      43.977  -4.177 104.307  1.00 20.00
ATOM   2144  CB  GLU   537      44.378  -2.999 105.211  1.00 20.00
ATOM   2145  CG  GLU   537      45.885  -2.933 105.478  1.00 20.00
ATOM   2146  CD  GLU   537      46.253  -4.093 106.397  1.00 20.00
ATOM   2147  OE1 GLU   537      45.370  -4.525 107.186  1.00 20.00
ATOM   2148  OE2 GLU   537      47.420  -4.562 106.324  1.00 20.00
ATOM   2149  C   GLU   537      42.503  -4.368 104.422  1.00 20.00
ATOM   2150  O   GLU   537      42.021  -5.109 105.278  1.00 20.00
ATOM   2151  N   CYS   538      41.750  -3.673 103.557  1.00 20.00
ATOM   2153  CA  CYS   538      40.321  -3.717 103.554  1.00 20.00
ATOM   2154  CB  CYS   538      39.797  -3.005 102.292  1.00 20.00
ATOM   2155  SG  CYS   538      37.999  -2.970 102.127  1.00 20.00
ATOM   2156  C   CYS   538      39.911  -5.156 103.539  1.00 20.00
ATOM   2157  O   CYS   538      40.518  -5.975 102.854  1.00 20.00
ATOM   2158  N   LEU   539      38.889  -5.507 104.347  1.00 60.00
ATOM   2160  CA  LEU   539      38.409  -6.852 104.428  1.00 60.00
ATOM   2161  CB  LEU   539      38.406  -7.409 105.860  1.00 60.00
ATOM   2162  CG  LEU   539      37.889  -8.855 105.959  1.00 60.00
ATOM   2163  CD1 LEU   539      38.825  -9.831 105.231  1.00 60.00
ATOM   2164  CD2 LEU   539      37.635  -9.253 107.421  1.00 60.00
ATOM   2165  C   LEU   539      36.994  -6.842 103.954  1.00 60.00
ATOM   2166  O   LEU   539      36.240  -5.889 104.147  1.00 60.00
ATOM   2167  N   PRO   540      36.662  -7.905 103.289  1.00 60.00
ATOM   2168  CD  PRO   540      37.663  -8.584 102.484  1.00 60.00
ATOM   2169  CA  PRO   540      35.343  -8.046 102.736  1.00 60.00
ATOM   2170  CB  PRO   540      35.489  -8.938 101.512  1.00 60.00
ATOM   2171  CG  PRO   540      36.865  -9.605 101.667  1.00 60.00
ATOM   2172  C   PRO   540      34.342  -8.599 103.690  1.00 60.00
ATOM   2173  O   PRO   540      34.718  -9.251 104.661  1.00 60.00
ATOM   2174  N   GLN   541      33.050  -8.358 103.404  1.00 60.00
ATOM   2176  CA  GLN   541      31.990  -8.912 104.186  1.00 60.00
ATOM   2177  CB  GLN   541      30.807  -7.956 104.410  1.00 60.00
ATOM   2178  CG  GLN   541      31.077  -6.867 105.446  1.00 60.00
ATOM   2179  CD  GLN   541      31.039  -7.529 106.816  1.00 60.00
ATOM   2180  OE1 GLN   541      31.871  -8.379 107.132  1.00 60.00
ATOM   2181  NE2 GLN   541      30.039  -7.140 107.650  1.00 60.00
ATOM   2184  C   GLN   541      31.472 -10.050 103.379  1.00 60.00
ATOM   2185  O   GLN   541      32.239 -10.843 102.837  1.00 60.00
ATOM   2186  N   ALA   542      30.135 -10.148 103.275  1.00 60.00
ATOM   2188  CA  ALA   542      29.543 -11.216 102.532  1.00 60.00
ATOM   2189  CB  ALA   542      28.010 -11.108 102.452  1.00 60.00
ATOM   2190  C   ALA   542      30.081 -11.120 101.144  1.00 60.00
ATOM   2191  O   ALA   542      30.434 -12.127 100.533  1.00 60.00
ATOM   2192  N   MET   543      30.177  -9.886 100.617  1.00 60.00
ATOM   2194  CA  MET   543      30.686  -9.713  99.290  1.00 60.00
ATOM   2195  CB  MET   543      30.785  -8.239  98.861  1.00 60.00
ATOM   2196  CG  MET   543      31.247  -8.054  97.416  1.00 60.00
ATOM   2197  SD  MET   543      30.011  -8.524  96.170  1.00 60.00
ATOM   2198  CE  MET   543      28.880  -7.154  96.548  1.00 60.00
ATOM   2199  C   MET   543      32.060 -10.297  99.248  1.00 60.00
ATOM   2200  O   MET   543      32.648 -10.610 100.282  1.00 60.00
ATOM   2201  N   ASN   544      32.598 -10.480  98.026  1.00 60.00
ATOM   2203  CA  ASN   544      33.905 -11.044  97.865  1.00 60.00
ATOM   2204  CB  ASN   544      34.265 -11.292  96.389  1.00 60.00
ATOM   2205  CG  ASN   544      34.181  -9.971  95.639  1.00 60.00
ATOM   2206  OD1 ASN   544      35.191  -9.411  95.218  1.00 60.00
ATOM   2207  ND2 ASN   544      32.934  -9.453  95.470  1.00 60.00
ATOM   2210  C   ASN   544      34.920 -10.129  98.468  1.00 60.00
ATOM   2211  O   ASN   544      35.778 -10.570  99.231  1.00 60.00
ATOM   2212  N   ILE   545      34.851  -8.826  98.131  1.00 60.00
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ATOM   2214  CA  ILE   545      35.738  -7.858  98.706  1.00 60.00
ATOM   2215  CB  ILE   545      36.858  -7.450  97.791  1.00 60.00
ATOM   2216  CG2 ILE   545      36.259  -6.690  96.596  1.00 60.00
ATOM   2217  CG1 ILE   545      37.926  -6.670  98.574  1.00 60.00
ATOM   2218  CD1 ILE   545      38.669  -7.527  99.599  1.00 60.00
ATOM   2219  C   ILE   545      34.872  -6.670  98.974  1.00 60.00
ATOM   2220  O   ILE   545      34.027  -6.327  98.149  1.00 60.00
ATOM   2221  N   THR   546      35.013  -6.003 100.138  1.00 60.00
ATOM   2223  CA  THR   546      34.063  -4.943 100.276  1.00 60.00
ATOM   2224  CB  THR   546      32.913  -5.316 101.162  1.00 60.00
ATOM   2225  OG1 THR   546      32.278  -6.482 100.657  1.00 60.00
ATOM   2227  CG2 THR   546      31.908  -4.155 101.168  1.00 60.00
ATOM   2228  C   THR   546      34.655  -3.679 100.798  1.00 60.00
ATOM   2229  O   THR   546      35.273  -3.653 101.862  1.00 60.00
ATOM   2230  N   CYS   547      34.478  -2.587 100.028  1.00 20.00
ATOM   2232  CA  CYS   547      34.910  -1.291 100.451  1.00 20.00
ATOM   2233  CB  CYS   547      36.397  -0.993 100.138  1.00 20.00
ATOM   2234  SG  CYS   547      36.804  -0.821  98.370  1.00 20.00
ATOM   2235  C   CYS   547      34.054  -0.301  99.741  1.00 20.00
ATOM   2236  O   CYS   547      33.714  -0.488  98.574  1.00 20.00
ATOM   2237  N   THR   548      33.658   0.777 100.443  1.00 20.00
ATOM   2239  CA  THR   548      32.823   1.753  99.812  1.00 20.00
ATOM   2240  CB  THR   548      32.286   2.785 100.761  1.00 20.00
ATOM   2241  OG1 THR   548      31.326   3.597 100.100  1.00 20.00
ATOM   2243  CG2 THR   548      33.444   3.643 101.295  1.00 20.00
ATOM   2244  C   THR   548      33.588   2.446  98.731  1.00 20.00
ATOM   2245  O   THR   548      33.071   2.659  97.635  1.00 20.00
ATOM   2246  N   GLY   549      34.860   2.795  99.006  1.00 20.00
ATOM   2248  CA  GLY   549      35.646   3.490  98.029  1.00 20.00
ATOM   2249  C   GLY   549      37.075   3.158  98.301  1.00 20.00
ATOM   2250  O   GLY   549      37.389   2.474  99.273  1.00 20.00
ATOM   2251  N   ARG   550      37.987   3.642  97.439  1.00 40.00
ATOM   2253  CA  ARG   550      39.369   3.329  97.635  1.00 40.00
ATOM   2254  CB  ARG   550      40.252   3.660  96.418  1.00 40.00
ATOM   2255  CG  ARG   550      40.302   5.146  96.055  1.00 40.00
ATOM   2256  CD  ARG   550      40.796   5.399  94.628  1.00 40.00
ATOM   2257  NE  ARG   550      41.174   6.836  94.522  1.00 40.00
ATOM   2259  CZ  ARG   550      42.474   7.204  94.715  1.00 40.00
ATOM   2260  NH1 ARG   550      43.427   6.249  94.930  1.00 40.00
ATOM   2263  NH2 ARG   550      42.824   8.522  94.685  1.00 40.00
ATOM   2266  C   ARG   550      39.863   4.106  98.812  1.00 40.00
ATOM   2267  O   ARG   550      39.578   5.294  98.953  1.00 40.00
ATOM   2268  N   GLY   551      40.613   3.430  99.704  1.00 40.00
ATOM   2270  CA  GLY   551      41.142   4.071 100.872  1.00 40.00
ATOM   2271  C   GLY   551      40.981   3.097 101.997  1.00 40.00
ATOM   2272  O   GLY   551      40.006   2.350 102.054  1.00 40.00
ATOM   2273  N   PRO   552      41.932   3.085 102.888  1.00 20.00
ATOM   2274  CD  PRO   552      43.306   3.313 102.469  1.00 20.00
ATOM   2275  CA  PRO   552      41.863   2.176 104.002  1.00 20.00
ATOM   2276  CB  PRO   552      43.276   2.098 104.570  1.00 20.00
ATOM   2277  CG  PRO   552      44.168   2.400 103.355  1.00 20.00
ATOM   2278  C   PRO   552      40.827   2.555 105.015  1.00 20.00
ATOM   2279  O   PRO   552      40.513   1.735 105.877  1.00 20.00
ATOM   2280  N   ASP   553      40.354   3.812 104.987  1.00 20.00
ATOM   2282  CA  ASP   553      39.319   4.262 105.875  1.00 20.00
ATOM   2283  CB  ASP   553      39.206   5.796 105.947  1.00 20.00
ATOM   2284  CG  ASP   553      38.294   6.152 107.117  1.00 20.00
ATOM   2285  OD1 ASP   553      37.963   7.359 107.264  1.00 20.00
ATOM   2286  OD2 ASP   553      37.920   5.225 107.883  1.00 20.00
ATOM   2287  C   ASP   553      37.996   3.743 105.403  1.00 20.00
ATOM   2288  O   ASP   553      37.059   3.556 106.176  1.00 20.00
ATOM   2289  N   ASN   554      37.896   3.535 104.081  1.00 20.00
ATOM   2291  CA  ASN   554      36.688   3.161 103.405  1.00 20.00
ATOM   2292  CB  ASN   554      36.819   3.236 101.872  1.00 20.00
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ATOM	2293	CG	ASN	554	36.906	4.697	101.440	1.00	20.00
ATOM	2294	OD1	ASN	554	36.433	5.049	100.361	1.00	20.00
ATOM	2295	ND2	ASN	554	37.526	5.567	102.283	1.00	20.00
ATOM	2298	C	ASN	554	36.198	1.788	103.736	1.00	20.00
ATOM	2299	O	ASN	554	35.006	1.510	103.612	1.00	20.00
ATOM	2300	N	CYS	555	37.096	0.882	104.155	1.00	20.00
ATOM	2302	CA	CYS	555	36.709	-0.487	104.278	1.00	20.00
ATOM	2303	CB	CYS	555	37.838	-1.410	104.693	1.00	20.00
ATOM	2304	SG	CYS	555	37.418	-3.035	104.055	1.00	20.00
ATOM	2305	C	CYS	555	35.503	-0.772	105.127	1.00	20.00
ATOM	2306	O	CYS	555	35.108	0.013	105.987	1.00	20.00
ATOM	2307	N	ILE	556	34.806	-1.877	104.783	1.00	20.00
ATOM	2309	CA	ILE	556	33.694	-2.389	105.529	1.00	20.00
ATOM	2310	CB	ILE	556	32.844	-3.320	104.721	1.00	20.00
ATOM	2311	CG2	ILE	556	31.910	-4.052	105.694	1.00	20.00
ATOM	2312	CG1	ILE	556	32.088	-2.530	103.635	1.00	20.00
ATOM	2313	CD1	ILE	556	32.991	-1.832	102.621	1.00	20.00
ATOM	2314	C	ILE	556	34.192	-3.107	106.749	1.00	20.00
ATOM	2315	O	ILE	556	33.569	-3.044	107.807	1.00	20.00
ATOM	2316	N	GLN	557	35.331	-3.827	106.620	1.00	20.00
ATOM	2318	CA	GLN	557	35.888	-4.574	107.717	1.00	20.00
ATOM	2319	CB	GLN	557	35.398	-6.031	107.749	1.00	20.00
ATOM	2320	CG	GLN	557	35.950	-6.848	108.917	1.00	20.00
ATOM	2321	CD	GLN	557	35.315	-6.317	110.194	1.00	20.00
ATOM	2322	OE1	GLN	557	35.729	-5.293	110.735	1.00	20.00
ATOM	2323	NE2	GLN	557	34.271	-7.033	110.688	1.00	20.00
ATOM	2326	C	GLN	557	37.382	-4.600	107.564	1.00	20.00
ATOM	2327	O	GLN	557	37.912	-4.188	106.540	1.00	20.00
ATOM	2328	N	CYS	558	38.134	-5.090	108.568	1.00	20.00
ATOM	2330	CA	CYS	558	39.559	-5.011	108.413	1.00	20.00
ATOM	2331	CB	CYS	558	40.210	-4.242	109.577	1.00	20.00
ATOM	2332	SG	CYS	558	41.972	-3.888	109.346	1.00	20.00
ATOM	2333	C	CYS	558	40.134	-6.394	108.333	1.00	20.00
ATOM	2334	O	CYS	558	39.608	-7.331	108.930	1.00	20.00
ATOM	2335	N	ALA	559	41.202	-6.562	107.523	1.00	20.00
ATOM	2337	CA	ALA	559	41.859	-7.831	107.368	1.00	20.00
ATOM	2338	CB	ALA	559	42.906	-7.830	106.242	1.00	20.00
ATOM	2339	C	ALA	559	42.574	-8.172	108.632	1.00	20.00
ATOM	2340	O	ALA	559	42.555	-9.314	109.090	1.00	20.00
ATOM	2341	N	HIS	560	43.214	-7.155	109.234	1.00	20.00
ATOM	2343	CA	HIS	560	44.004	-7.333	110.413	1.00	20.00
ATOM	2344	CB	HIS	560	45.392	-6.679	110.300	1.00	20.00
ATOM	2345	CG	HIS	560	46.258	-7.335	109.265	1.00	20.00
ATOM	2346	CD2	HIS	560	47.279	-8.222	109.413	1.00	20.00
ATOM	2347	ND1	HIS	560	46.127	-7.137	107.907	1.00	20.00
ATOM	2349	CE1	HIS	560	47.068	-7.908	107.307	1.00	20.00
ATOM	2350	NE2	HIS	560	47.792	-8.585	108.180	1.00	20.00
ATOM	2352	C	HIS	560	43.278	-6.659	111.530	1.00	20.00
ATOM	2353	O	HIS	560	42.187	-7.077	111.915	1.00	20.00
ATOM	2354	N	TYR	561	43.886	-5.602	112.101	1.00	20.00
ATOM	2356	CA	TYR	561	43.280	-4.944	113.218	1.00	20.00
ATOM	2357	CB	TYR	561	44.253	-4.731	114.387	1.00	20.00
ATOM	2358	CG	TYR	561	44.768	-6.077	114.759	1.00	20.00
ATOM	2359	CD1	TYR	561	45.838	-6.609	114.078	1.00	20.00
ATOM	2360	CE1	TYR	561	46.328	-7.852	114.398	1.00	20.00
ATOM	2361	CD2	TYR	561	44.182	-6.812	115.764	1.00	20.00
ATOM	2362	CE2	TYR	561	44.670	-8.055	116.091	1.00	20.00
ATOM	2363	CZ	TYR	561	45.744	-8.576	115.408	1.00	20.00
ATOM	2364	OH	TYR	561	46.253	-9.847	115.746	1.00	20.00
ATOM	2366	C	TYR	561	42.788	-3.592	112.823	1.00	20.00
ATOM	2367	O	TYR	561	43.405	-2.896	112.019	1.00	20.00
ATOM	2368	N	ILE	562	41.644	-3.183	113.406	1.00	20.00
ATOM	2370	CA	ILE	562	41.077	-1.904	113.085	1.00	20.00
ATOM	2371	CB	ILE	562	39.577	-1.918	113.043	1.00	20.00

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ATOM   2372  CG2 ILE   562      39.101  -0.478 112.787  1.00 20.00
ATOM   2373  CG1 ILE   562      39.067  -2.929 112.004  1.00 20.00
ATOM   2374  CD1 ILE   562      37.575  -3.238 112.135  1.00 20.00
ATOM   2375  C   ILE   562      41.455  -0.963 114.180  1.00 20.00
ATOM   2376  O   ILE   562      41.281  -1.264 115.360  1.00 20.00
ATOM   2377  N   ASP   563      42.010   0.207 113.817  1.00 20.00
ATOM   2379  CA  ASP   563      42.386   1.150 114.825  1.00 20.00
ATOM   2380  CB  ASP   563      43.880   1.091 115.205  1.00 20.00
ATOM   2381  CG  ASP   563      44.724   1.403 113.981  1.00 20.00
ATOM   2382  OD1 ASP   563      44.203   1.239 112.847  1.00 20.00
ATOM   2383  OD2 ASP   563      45.905   1.802 114.161  1.00 20.00
ATOM   2384  C   ASP   563      42.058   2.534 114.384  1.00 20.00
ATOM   2385  O   ASP   563      42.380   2.940 113.269  1.00 20.00
ATOM   2386  N   GLY   564      41.419   3.312 115.279  1.00 20.00
ATOM   2388  CA  GLY   564      40.994   4.620 114.891  1.00 20.00
ATOM   2389  C   GLY   564      40.076   4.323 113.755  1.00 20.00
ATOM   2390  O   GLY   564      39.370   3.320 113.749  1.00 20.00
ATOM   2391  N   PRO   565      40.053   5.164 112.786  1.00 20.00
ATOM   2392  CD  PRO   565      39.999   6.582 113.110  1.00 20.00
ATOM   2393  CA  PRO   565      39.193   4.835 111.684  1.00 20.00
ATOM   2394  CB  PRO   565      38.720   6.167 111.103  1.00 20.00
ATOM   2395  CG  PRO   565      38.849   7.155 112.272  1.00 20.00
ATOM   2396  C   PRO   565      39.914   4.021 110.669  1.00 20.00
ATOM   2397  O   PRO   565      39.330   3.776 109.616  1.00 20.00
ATOM   2398  N   HIS   566      41.161   3.590 110.938  1.00 20.00
ATOM   2400  CA  HIS   566      41.857   2.923 109.880  1.00 20.00
ATOM   2401  CB  HIS   566      43.245   3.513 109.586  1.00 20.00
ATOM   2402  CG  HIS   566      43.183   4.857 108.927  1.00 20.00
ATOM   2403  CD2 HIS   566      42.946   5.175 107.625  1.00 20.00
ATOM   2404  ND1 HIS   566      43.342   6.056 109.584  1.00 20.00
ATOM   2406  CE1 HIS   566      43.198   7.033 108.654  1.00 20.00
ATOM   2407  NE2 HIS   566      42.955   6.547 107.449  1.00 20.00
ATOM   2409  C   HIS   566      42.052   1.463 110.093  1.00 20.00
ATOM   2410  O   HIS   566      42.131   0.968 111.216  1.00 20.00
ATOM   2411  N   CYS   567      42.132   0.741 108.961  1.00 20.00
ATOM   2413  CA  CYS   567      42.335  -0.671 108.965  1.00 20.00
ATOM   2414  CB  CYS   567      41.714  -1.325 107.712  1.00 20.00
ATOM   2415  SG  CYS   567      42.066  -3.090 107.483  1.00 20.00
ATOM   2416  C   CYS   567      43.819  -0.844 108.966  1.00 20.00
ATOM   2417  O   CYS   567      44.481  -0.582 107.963  1.00 20.00
ATOM   2418  N   VAL   568      44.384  -1.275 110.117  1.00 20.00
ATOM   2420  CA  VAL   568      45.807  -1.419 110.192  1.00 20.00
ATOM   2421  CB  VAL   568      46.459  -0.634 111.294  1.00 20.00
ATOM   2422  CG1 VAL   568      47.967  -0.920 111.276  1.00 20.00
ATOM   2423  CG2 VAL   568      46.188   0.853 111.019  1.00 20.00
ATOM   2424  C   VAL   568      46.191  -2.866 110.262  1.00 20.00
ATOM   2425  O   VAL   568      45.432  -3.715 110.728  1.00 20.00
ATOM   2426  N   LYS   569      47.374  -3.176 109.694  1.00 20.00
ATOM   2428  CA  LYS   569      47.951  -4.488 109.640  1.00 20.00
ATOM   2429  CB  LYS   569      49.216  -4.537 108.767  1.00 20.00
ATOM   2430  CG  LYS   569      50.380  -3.748 109.372  1.00 20.00
ATOM   2431  CD  LYS   569      51.739  -4.059 108.741  1.00 20.00
ATOM   2432  CE  LYS   569      51.942  -3.404 107.375  1.00 20.00
ATOM   2433  NZ  LYS   569      53.302  -3.698 106.869  1.00 20.00
ATOM   2437  C   LYS   569      48.373  -4.943 111.002  1.00 20.00
ATOM   2438  O   LYS   569      48.320  -6.133 111.312  1.00 20.00
ATOM   2439  N   THR   570      48.869  -4.007 111.834  1.00 20.00
ATOM   2441  CA  THR   570      49.301  -4.370 113.153  1.00 20.00
ATOM   2442  CB  THR   570      50.768  -4.685 113.237  1.00 20.00
ATOM   2443  OG1 THR   570      51.085  -5.252 114.500  1.00 20.00
ATOM   2445  CG2 THR   570      51.560  -3.385 113.022  1.00 20.00
ATOM   2446  C   THR   570      49.043  -3.196 114.041  1.00 20.00
ATOM   2447  O   THR   570      48.887  -2.073 113.571  1.00 20.00
ATOM   2448  N   CYS   571      49.001  -3.415 115.365  1.00 20.00
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ATOM	2450	CA	CYS	571	48.677	-2.326	116.236	1.00	20.00
ATOM	2451	CB	CYS	571	48.297	-2.778	117.655	1.00	20.00
ATOM	2452	SG	CYS	571	46.798	-3.800	117.635	1.00	20.00
ATOM	2453	C	CYS	571	49.804	-1.347	116.339	1.00	20.00
ATOM	2454	O	CYS	571	50.985	-1.688	116.291	1.00	20.00
ATOM	2455	N	PRO	572	49.410	-0.109	116.467	1.00	20.00
ATOM	2456	CD	PRO	572	48.187	0.334	115.816	1.00	20.00
ATOM	2457	CA	PRO	572	50.361	0.959	116.601	1.00	20.00
ATOM	2458	CB	PRO	572	49.585	2.247	116.339	1.00	20.00
ATOM	2459	CG	PRO	572	48.435	1.798	115.422	1.00	20.00
ATOM	2460	C	PRO	572	50.958	0.895	117.971	1.00	20.00
ATOM	2461	O	PRO	572	50.380	0.244	118.840	1.00	20.00
ATOM	2462	N	ALA	573	52.112	1.553	118.188	1.00	20.00
ATOM	2464	CA	ALA	573	52.753	1.489	119.469	1.00	20.00
ATOM	2465	CB	ALA	573	54.133	2.167	119.501	1.00	20.00
ATOM	2466	C	ALA	573	51.895	2.147	120.503	1.00	20.00
ATOM	2467	O	ALA	573	51.194	3.120	120.229	1.00	20.00
ATOM	2468	N	GLY	574	51.916	1.586	121.729	1.00	20.00
ATOM	2470	CA	GLY	574	51.186	2.136	122.834	1.00	20.00
ATOM	2471	C	GLY	574	49.808	1.556	122.845	1.00	20.00
ATOM	2472	O	GLY	574	49.070	1.709	123.817	1.00	20.00
ATOM	2473	N	VAL	575	49.425	0.868	121.753	1.00	20.00
ATOM	2475	CA	VAL	575	48.121	0.274	121.693	1.00	20.00
ATOM	2476	CB	VAL	575	47.314	0.725	120.509	1.00	20.00
ATOM	2477	CG1	VAL	575	46.002	-0.078	120.470	1.00	20.00
ATOM	2478	CG2	VAL	575	47.105	2.245	120.612	1.00	20.00
ATOM	2479	C	VAL	575	48.343	-1.194	121.542	1.00	20.00
ATOM	2480	O	VAL	575	49.335	-1.621	120.954	1.00	20.00
ATOM	2481	N	MET	576	47.427	-2.014	122.094	1.00	20.00
ATOM	2483	CA	MET	576	47.607	-3.428	121.978	1.00	20.00
ATOM	2484	CB	MET	576	47.818	-4.162	123.311	1.00	20.00
ATOM	2485	CG	MET	576	48.045	-5.662	123.110	1.00	20.00
ATOM	2486	SD	MET	576	49.614	-6.061	122.282	1.00	20.00
ATOM	2487	CE	MET	576	49.204	-7.800	121.961	1.00	20.00
ATOM	2488	C	MET	576	46.416	-4.041	121.335	1.00	20.00
ATOM	2489	O	MET	576	45.309	-3.507	121.390	1.00	20.00
ATOM	2490	N	GLY	577	46.635	-5.196	120.684	1.00	20.00
ATOM	2492	CA	GLY	577	45.556	-5.868	120.037	1.00	20.00
ATOM	2493	C	GLY	577	44.786	-6.565	121.098	1.00	20.00
ATOM	2494	O	GLY	577	45.342	-7.317	121.898	1.00	20.00
ATOM	2495	N	GLU	578	43.466	-6.324	121.130	1.00	40.00
ATOM	2497	CA	GLU	578	42.669	-6.989	122.105	1.00	40.00
ATOM	2498	CB	GLU	578	41.196	-6.551	122.069	1.00	40.00
ATOM	2499	CG	GLU	578	40.554	-6.705	120.691	1.00	40.00
ATOM	2500	CD	GLU	578	39.200	-6.015	120.734	1.00	40.00
ATOM	2501	OE1	GLU	578	38.692	-5.780	121.862	1.00	40.00
ATOM	2502	OE2	GLU	578	38.658	-5.709	119.638	1.00	40.00
ATOM	2503	C	GLU	578	42.767	-8.436	121.768	1.00	40.00
ATOM	2504	O	GLU	578	42.470	-8.837	120.643	1.00	40.00
ATOM	2505	N	ASN	579	43.221	-9.250	122.741	1.00	40.00
ATOM	2507	CA	ASN	579	43.379	-10.652	122.497	1.00	40.00
ATOM	2508	CB	ASN	579	43.876	-11.428	123.731	1.00	40.00
ATOM	2509	CG	ASN	579	45.318	-11.027	124.006	1.00	40.00
ATOM	2510	OD1	ASN	579	45.789	-11.102	125.141	1.00	40.00
ATOM	2511	ND2	ASN	579	46.041	-10.587	122.942	1.00	40.00
ATOM	2514	C	ASN	579	42.032	-11.186	122.157	1.00	40.00
ATOM	2515	O	ASN	579	41.839	-11.805	121.113	1.00	40.00
ATOM	2516	N	ASN	580	41.051	-10.939	123.042	1.00	60.00
ATOM	2518	CA	ASN	580	39.724	-11.401	122.781	1.00	60.00
ATOM	2519	CB	ASN	580	39.352	-12.684	123.545	1.00	60.00
ATOM	2520	CG	ASN	580	40.171	-13.837	122.979	1.00	60.00
ATOM	2521	OD1	ASN	580	40.127	-14.129	121.785	1.00	60.00
ATOM	2522	ND2	ASN	580	40.949	-14.516	123.865	1.00	60.00
ATOM	2525	C	ASN	580	38.812	-10.328	123.263	1.00	60.00

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ATOM   2526  O   ASN   580      39.232  -9.411 123.968  1.00 60.00
ATOM   2527  N   THR   581      37.530 -10.406 122.869  1.00 60.00
ATOM   2529  CA  THR   581      36.598  -9.428 123.333  1.00 60.00
ATOM   2530  CB  THR   581      35.565  -9.040 122.316  1.00 60.00
ATOM   2531  OG1 THR   581      36.188  -8.483 121.168  1.00 60.00
ATOM   2533  CG2 THR   581      34.606  -8.019 122.953  1.00 60.00
ATOM   2534  C   THR   581      35.871 -10.061 124.467  1.00 60.00
ATOM   2535  O   THR   581      35.253 -11.113 124.311  1.00 60.00
ATOM   2536  N   LEU   582      35.949  -9.440 125.656  1.00 60.00
ATOM   2538  CA  LEU   582      35.234  -9.983 126.768  1.00 60.00
ATOM   2539  CB  LEU   582      35.778  -9.531 128.134  1.00 60.00
ATOM   2540  CG  LEU   582      35.012 -10.111 129.338  1.00 60.00
ATOM   2541  CD1 LEU   582      35.132 -11.644 129.400  1.00 60.00
ATOM   2542  CD2 LEU   582      35.449  -9.427 130.643  1.00 60.00
ATOM   2543  C   LEU   582      33.850  -9.457 126.615  1.00 60.00
ATOM   2544  O   LEU   582      33.652  -8.300 126.247  1.00 60.00
ATOM   2545  N   VAL   583      32.841 -10.305 126.882  1.00 60.00
ATOM   2547  CA  VAL   583      31.499  -9.852 126.695  1.00 60.00
ATOM   2548  CB  VAL   583      30.462 -10.907 126.944  1.00 60.00
ATOM   2549  CG1 VAL   583      29.073 -10.265 126.789  1.00 60.00
ATOM   2550  CG2 VAL   583      30.715 -12.079 125.980  1.00 60.00
ATOM   2551  C   VAL   583      31.241  -8.720 127.629  1.00 60.00
ATOM   2552  O   VAL   583      31.685  -8.722 128.776  1.00 60.00
ATOM   2553  N   TRP   584      30.519  -7.702 127.128  1.00 60.00
ATOM   2555  CA  TRP   584      30.185  -6.554 127.914  1.00 60.00
ATOM   2556  CB  TRP   584      31.011  -5.309 127.545  1.00 60.00
ATOM   2557  CG  TRP   584      30.852  -4.141 128.493  1.00 60.00
ATOM   2558  CD2 TRP   584      31.646  -2.948 128.430  1.00 60.00
ATOM   2559  CE2 TRP   584      31.259  -2.139 129.496  1.00 60.00
ATOM   2560  CE3 TRP   584      32.627  -2.561 127.561  1.00 60.00
ATOM   2561  CD1 TRP   584      30.038  -4.008 129.578  1.00 60.00
ATOM   2562  NE1 TRP   584      30.266  -2.799 130.191  1.00 60.00
ATOM   2564  CZ2 TRP   584      31.844  -0.923 129.710  1.00 60.00
ATOM   2565  CZ3 TRP   584      33.218  -1.337 127.780  1.00 60.00
ATOM   2566  CH2 TRP   584      32.833  -0.533 128.833  1.00 60.00
ATOM   2567  C   TRP   584      28.765  -6.301 127.534  1.00 60.00
ATOM   2568  O   TRP   584      28.044  -7.238 127.193  1.00 60.00
ATOM   2569  N   LYS   585      28.305  -5.038 127.602  1.00 60.00
ATOM   2571  CA  LYS   585      26.959  -4.800 127.178  1.00 60.00
ATOM   2572  CB  LYS   585      26.533  -3.325 127.263  1.00 60.00
ATOM   2573  CG  LYS   585      26.441  -2.801 128.696  1.00 60.00
ATOM   2574  CD  LYS   585      26.260  -1.285 128.778  1.00 60.00
ATOM   2575  CE  LYS   585      27.256  -0.509 127.914  1.00 60.00
ATOM   2576  NZ  LYS   585      28.639  -0.882 128.280  1.00 60.00
ATOM   2580  C   LYS   585      26.950  -5.188 125.739  1.00 60.00
ATOM   2581  O   LYS   585      26.086  -5.936 125.287  1.00 60.00
ATOM   2582  N   TYR   586      27.950  -4.691 124.988  1.00 60.00
ATOM   2584  CA  TYR   586      28.085  -5.043 123.609  1.00 60.00
ATOM   2585  CB  TYR   586      27.690  -3.915 122.638  1.00 60.00
ATOM   2586  CG  TYR   586      28.454  -2.688 122.991  1.00 60.00
ATOM   2587  CD1 TYR   586      29.742  -2.502 122.545  1.00 60.00
ATOM   2588  CE1 TYR   586      30.421  -1.346 122.848  1.00 60.00
ATOM   2589  CD2 TYR   586      27.853  -1.698 123.734  1.00 60.00
ATOM   2590  CE2 TYR   586      28.527  -0.541 124.039  1.00 60.00
ATOM   2591  CZ  TYR   586      29.814  -0.364 123.594  1.00 60.00
ATOM   2592  OH  TYR   586      30.511   0.821 123.910  1.00 60.00
ATOM   2594  C   TYR   586      29.514  -5.422 123.390  1.00 60.00
ATOM   2595  O   TYR   586      30.384  -5.086 124.192  1.00 60.00
ATOM   2596  N   ALA   587      29.789  -6.164 122.299  1.00 60.00
ATOM   2598  CA  ALA   587      31.126  -6.622 122.057  1.00 60.00
ATOM   2599  CB  ALA   587      31.191  -8.068 121.539  1.00 60.00
ATOM   2600  C   ALA   587      31.792  -5.762 121.035  1.00 60.00
ATOM   2601  O   ALA   587      31.219  -4.793 120.541  1.00 60.00
ATOM   2602  N   ASP   588      33.053  -6.109 120.713  1.00 60.00
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ATOM	2604	CA	ASP	588	33.809	-5.378	119.742	1.00	60.00
ATOM	2605	CB	ASP	588	35.298	-5.256	120.109	1.00	60.00
ATOM	2606	CG	ASP	588	35.393	-4.378	121.349	1.00	60.00
ATOM	2607	OD1	ASP	588	34.698	-3.327	121.383	1.00	60.00
ATOM	2608	OD2	ASP	588	36.148	-4.754	122.286	1.00	60.00
ATOM	2609	C	ASP	588	33.720	-6.146	118.465	1.00	60.00
ATOM	2610	O	ASP	588	33.563	-7.366	118.473	1.00	60.00
ATOM	2611	N	ALA	589	33.802	-5.442	117.320	1.00	60.00
ATOM	2613	CA	ALA	589	33.704	-6.126	116.067	1.00	60.00
ATOM	2614	CB	ALA	589	32.786	-5.424	115.050	1.00	60.00
ATOM	2615	C	ALA	589	35.061	-6.195	115.453	1.00	60.00
ATOM	2616	O	ALA	589	35.884	-5.296	115.622	1.00	60.00
ATOM	2617	N	GLY	590	35.329	-7.298	114.730	1.00	60.00
ATOM	2619	CA	GLY	590	36.583	-7.458	114.058	1.00	60.00
ATOM	2620	C	GLY	590	37.680	-7.372	115.064	1.00	60.00
ATOM	2621	O	GLY	590	37.439	-7.336	116.269	1.00	60.00
ATOM	2622	N	HIS	591	38.932	-7.335	114.574	1.00	60.00
ATOM	2624	CA	HIS	591	40.055	-7.246	115.456	1.00	60.00
ATOM	2625	CB	HIS	591	41.328	-7.879	114.871	1.00	60.00
ATOM	2626	CG	HIS	591	41.115	-9.292	114.411	1.00	60.00
ATOM	2627	CD2	HIS	591	40.894	-9.768	113.156	1.00	60.00
ATOM	2628	ND1	HIS	591	41.088	-10.392	115.240	1.00	60.00
ATOM	2630	CE1	HIS	591	40.855	-11.471	114.449	1.00	60.00
ATOM	2631	NE2	HIS	591	40.731	-11.142	113.176	1.00	60.00
ATOM	2633	C	HIS	591	40.311	-5.785	115.616	1.00	60.00
ATOM	2634	O	HIS	591	40.255	-5.028	114.649	1.00	60.00
ATOM	2635	N	VAL	592	40.576	-5.339	116.859	1.00	40.00
ATOM	2637	CA	VAL	592	40.795	-3.939	117.059	1.00	40.00
ATOM	2638	CB	VAL	592	39.588	-3.239	117.628	1.00	40.00
ATOM	2639	CG1	VAL	592	39.887	-1.741	117.821	1.00	40.00
ATOM	2640	CG2	VAL	592	38.401	-3.505	116.688	1.00	40.00
ATOM	2641	C	VAL	592	41.929	-3.781	118.019	1.00	40.00
ATOM	2642	O	VAL	592	42.264	-4.696	118.769	1.00	40.00
ATOM	2643	N	CYS	593	42.565	-2.597	117.989	1.00	20.00
ATOM	2645	CA	CYS	593	43.667	-2.310	118.848	1.00	20.00
ATOM	2646	CB	CYS	593	44.810	-1.588	118.120	1.00	20.00
ATOM	2647	SG	CYS	593	45.453	-2.575	116.742	1.00	20.00
ATOM	2648	C	CYS	593	43.150	-1.376	119.893	1.00	20.00
ATOM	2649	O	CYS	593	42.462	-0.405	119.583	1.00	20.00
ATOM	2650	N	HIS	594	43.460	-1.661	121.173	1.00	20.00
ATOM	2652	CA	HIS	594	42.998	-0.809	122.227	1.00	20.00
ATOM	2653	CB	HIS	594	42.101	-1.511	123.263	1.00	20.00
ATOM	2654	CG	HIS	594	40.743	-1.878	122.739	1.00	20.00
ATOM	2655	CD2	HIS	594	40.271	-3.063	122.262	1.00	20.00
ATOM	2656	ND1	HIS	594	39.677	-1.007	122.698	1.00	20.00
ATOM	2658	CE1	HIS	594	38.622	-1.700	122.200	1.00	20.00
ATOM	2659	NE2	HIS	594	38.935	-2.953	121.920	1.00	20.00
ATOM	2661	C	HIS	594	44.178	-0.267	122.972	1.00	20.00
ATOM	2662	O	HIS	594	45.251	-0.867	122.987	1.00	20.00
ATOM	2663	N	LEU	595	43.994	0.898	123.625	1.00	20.00
ATOM	2665	CA	LEU	595	45.068	1.563	124.306	1.00	20.00
ATOM	2666	CB	LEU	595	44.724	3.014	124.684	1.00	20.00
ATOM	2667	CG	LEU	595	45.878	3.792	125.340	1.00	20.00
ATOM	2668	CD1	LEU	595	47.067	3.945	124.376	1.00	20.00
ATOM	2669	CD2	LEU	595	45.390	5.145	125.882	1.00	20.00
ATOM	2670	C	LEU	595	45.454	0.813	125.533	1.00	20.00
ATOM	2671	O	LEU	595	44.630	0.164	126.176	1.00	20.00
ATOM	2672	N	CYS	596	46.758	0.870	125.863	1.00	20.00
ATOM	2674	CA	CYS	596	47.264	0.207	127.023	1.00	20.00
ATOM	2675	CB	CYS	596	48.515	-0.637	126.706	1.00	20.00
ATOM	2676	SG	CYS	596	49.102	-1.717	128.046	1.00	20.00
ATOM	2677	C	CYS	596	47.623	1.323	127.945	1.00	20.00
ATOM	2678	O	CYS	596	48.193	2.327	127.521	1.00	20.00
ATOM	2679	N	HIS	597	47.271	1.201	129.238	1.00	20.00

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ATOM   2681  CA  HIS   597      47.588   2.296 130.103  1.00 20.00
ATOM   2682  CB  HIS   597      47.048   2.169 131.538  1.00 20.00
ATOM   2683  CG  HIS   597      47.173   3.456 132.300  1.00 20.00
ATOM   2684  CD2 HIS   597      46.290   4.484 132.432  1.00 20.00
ATOM   2685  ND1 HIS   597      48.302   3.843 132.988  1.00 20.00
ATOM   2687  CE1 HIS   597      48.046   5.072 133.502  1.00 20.00
ATOM   2688  NE2 HIS   597      46.837   5.503 133.190  1.00 20.00
ATOM   2690  C   HIS   597      49.072   2.360 130.162  1.00 20.00
ATOM   2691  O   HIS   597      49.764   1.360 129.977  1.00 20.00
ATOM   2692  N   PRO   598      49.579   3.531 130.393  1.00 20.00
ATOM   2693  CD  PRO   598      48.912   4.745 129.963  1.00 20.00
ATOM   2694  CA  PRO   598      51.001   3.693 130.432  1.00 20.00
ATOM   2695  CB  PRO   598      51.263   5.199 130.329  1.00 20.00
ATOM   2696  CG  PRO   598      49.870   5.853 130.423  1.00 20.00
ATOM   2697  C   PRO   598      51.602   3.024 131.623  1.00 20.00
ATOM   2698  O   PRO   598      52.811   2.794 131.617  1.00 20.00
ATOM   2699  N   ASN   599      50.801   2.740 132.668  1.00 20.00
ATOM   2701  CA  ASN   599      51.344   2.085 133.822  1.00 20.00
ATOM   2702  CB  ASN   599      50.402   2.076 135.045  1.00 20.00
ATOM   2703  CG  ASN   599      49.235   1.134 134.789  1.00 20.00
ATOM   2704  OD1 ASN   599      48.184   1.517 134.280  1.00 20.00
ATOM   2705  ND2 ASN   599      49.442  -0.161 135.149  1.00 20.00
ATOM   2708  C   ASN   599      51.666   0.659 133.500  1.00 20.00
ATOM   2709  O   ASN   599      52.704   0.136 133.906  1.00 20.00
ATOM   2710  N   CYS   600      50.788  -0.012 132.731  1.00 20.00
ATOM   2712  CA  CYS   600      50.992  -1.409 132.501  1.00 20.00
ATOM   2713  CB  CYS   600      49.842  -2.099 131.762  1.00 20.00
ATOM   2714  SG  CYS   600      50.052  -3.899 131.760  1.00 20.00
ATOM   2715  C   CYS   600      52.221  -1.614 131.694  1.00 20.00
ATOM   2716  O   CYS   600      52.686  -0.712 130.998  1.00 20.00
ATOM   2717  N   THR   601      52.793  -2.827 131.802  1.00 20.00
ATOM   2719  CA  THR   601      53.970  -3.148 131.063  1.00 20.00
ATOM   2720  CB  THR   601      55.171  -3.395 131.927  1.00 20.00
ATOM   2721  OG1 THR   601      56.342  -3.487 131.129  1.00 20.00
ATOM   2723  CG2 THR   601      54.952  -4.707 132.700  1.00 20.00
ATOM   2724  C   THR   601      53.703  -4.418 130.327  1.00 20.00
ATOM   2725  O   THR   601      52.841  -5.208 130.709  1.00 20.00
ATOM   2726  N   TYR   602      54.441  -4.621 129.223  1.00 20.00
ATOM   2728  CA  TYR   602      54.362  -5.817 128.443  1.00 20.00
ATOM   2729  CB  TYR   602      54.867  -7.057 129.202  1.00 20.00
ATOM   2730  CG  TYR   602      56.329  -6.858 129.410  1.00 20.00
ATOM   2731  CD1 TYR   602      56.796  -6.184 130.515  1.00 20.00
ATOM   2732  CE1 TYR   602      58.142  -5.949 130.676  1.00 20.00
ATOM   2733  CD2 TYR   602      57.227  -7.268 128.452  1.00 20.00
ATOM   2734  CE2 TYR   602      58.573  -7.031 128.605  1.00 20.00
ATOM   2735  CZ  TYR   602      59.034  -6.373 129.720  1.00 20.00
ATOM   2736  OH  TYR   602      60.414  -6.121 129.872  1.00 20.00
ATOM   2738  C   TYR   602      53.006  -6.118 127.884  1.00 20.00
ATOM   2739  O   TYR   602      52.663  -7.285 127.710  1.00 20.00
ATOM   2740  N   GLY   603      52.193  -5.088 127.573  1.00 20.00
ATOM   2742  CA  GLY   603      50.950  -5.364 126.904  1.00 20.00
ATOM   2743  C   GLY   603      49.741  -5.200 127.771  1.00 20.00
ATOM   2744  O   GLY   603      49.831  -5.132 128.996  1.00 20.00
ATOM   2745  N   CYS   604      48.564  -5.116 127.110  1.00 20.00
ATOM   2747  CA  CYS   604      47.299  -5.006 127.778  1.00 20.00
ATOM   2748  CB  CYS   604      46.694  -3.589 127.763  1.00 20.00
ATOM   2749  SG  CYS   604      47.402  -2.388 128.930  1.00 20.00
ATOM   2750  C   CYS   604      46.311  -5.849 127.031  1.00 20.00
ATOM   2751  O   CYS   604      46.297  -5.866 125.800  1.00 20.00
ATOM   2752  N   THR   605      45.467  -6.601 127.765  1.00 20.00
ATOM   2754  CA  THR   605      44.432  -7.348 127.116  1.00 20.00
ATOM   2755  CB  THR   605      43.712  -8.300 128.033  1.00 20.00
ATOM   2756  OG1 THR   605      42.795  -9.093 127.292  1.00 20.00
ATOM   2758  CG2 THR   605      42.979  -7.508 129.129  1.00 20.00
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ATOM	2759	C	THR	605	43.453	-6.350	126.590	1.00	20.00
ATOM	2760	O	THR	605	42.937	-6.487	125.482	1.00	20.00
ATOM	2761	N	GLY	606	43.191	-5.295	127.388	1.00	20.00
ATOM	2763	CA	GLY	606	42.260	-4.280	126.998	1.00	20.00
ATOM	2764	C	GLY	606	42.606	-3.041	127.757	1.00	20.00
ATOM	2765	O	GLY	606	43.364	-3.061	128.725	1.00	20.00
ATOM	2766	N	PRO	607	42.027	-1.958	127.325	1.00	40.00
ATOM	2767	CD	PRO	607	40.706	-2.007	126.719	1.00	40.00
ATOM	2768	CA	PRO	607	42.301	-0.674	127.908	1.00	40.00
ATOM	2769	CB	PRO	607	41.315	0.279	127.244	1.00	40.00
ATOM	2770	CG	PRO	607	40.092	-0.622	126.987	1.00	40.00
ATOM	2771	C	PRO	607	42.024	-0.743	129.374	1.00	40.00
ATOM	2772	O	PRO	607	41.162	-1.522	129.776	1.00	40.00
ATOM	2773	N	GLY	608	42.749	0.046	130.191	1.00	40.00
ATOM	2775	CA	GLY	608	42.462	0.063	131.595	1.00	40.00
ATOM	2776	C	GLY	608	43.620	-0.455	132.383	1.00	40.00
ATOM	2777	O	GLY	608	44.459	-1.200	131.881	1.00	40.00
ATOM	2778	N	LEU	609	43.675	-0.047	133.666	1.00	20.00
ATOM	2780	CA	LEU	609	44.685	-0.468	134.593	1.00	20.00
ATOM	2781	CB	LEU	609	44.536	0.218	135.962	1.00	20.00
ATOM	2782	CG	LEU	609	45.581	-0.222	137.005	1.00	20.00
ATOM	2783	CD1	LEU	609	47.002	0.209	136.609	1.00	20.00
ATOM	2784	CD2	LEU	609	45.180	0.238	138.415	1.00	20.00
ATOM	2785	C	LEU	609	44.529	-1.936	134.820	1.00	20.00
ATOM	2786	O	LEU	609	45.510	-2.671	134.926	1.00	20.00
ATOM	2787	N	GLU	610	43.268	-2.394	134.896	1.00	20.00
ATOM	2789	CA	GLU	610	42.951	-3.768	135.153	1.00	20.00
ATOM	2790	CB	GLU	610	41.439	-4.034	135.267	1.00	20.00
ATOM	2791	CG	GLU	610	40.784	-3.454	136.522	1.00	20.00
ATOM	2792	CD	GLU	610	40.474	-1.986	136.274	1.00	20.00
ATOM	2793	OE1	GLU	610	40.013	-1.657	135.149	1.00	20.00
ATOM	2794	OE2	GLU	610	40.693	-1.174	137.212	1.00	20.00
ATOM	2795	C	GLU	610	43.449	-4.617	134.033	1.00	20.00
ATOM	2796	O	GLU	610	43.861	-5.757	134.241	1.00	20.00
ATOM	2797	N	GLY	611	43.438	-4.066	132.809	1.00	20.00
ATOM	2799	CA	GLY	611	43.816	-4.811	131.648	1.00	20.00
ATOM	2800	C	GLY	611	45.192	-5.340	131.856	1.00	20.00
ATOM	2801	O	GLY	611	45.560	-6.368	131.291	1.00	20.00
ATOM	2802	N	CYS	612	46.004	-4.617	132.648	1.00	20.00
ATOM	2804	CA	CYS	612	47.344	-5.054	132.897	1.00	20.00
ATOM	2805	CB	CYS	612	48.076	-4.190	133.927	1.00	20.00
ATOM	2806	SG	CYS	612	49.864	-4.351	133.729	1.00	20.00
ATOM	2807	C	CYS	612	47.272	-6.451	133.421	1.00	20.00
ATOM	2808	O	CYS	612	46.224	-6.915	133.873	1.00	20.00
ATOM	2809	N	PRO	613	48.373	-7.149	133.341	1.00	60.00
ATOM	2810	CD	PRO	613	49.228	-6.991	132.183	1.00	60.00
ATOM	2811	CA	PRO	613	48.378	-8.500	133.834	1.00	60.00
ATOM	2812	CB	PRO	613	49.563	-9.188	133.157	1.00	60.00
ATOM	2813	CG	PRO	613	49.734	-8.405	131.846	1.00	60.00
ATOM	2814	C	PRO	613	48.448	-8.547	135.319	1.00	60.00
ATOM	2815	O	PRO	613	48.851	-7.567	135.934	1.00	60.00
ATOM	2816	N	THR	614	48.042	-9.690	135.912	1.00	60.00
ATOM	2818	CA	THR	614	48.080	-9.856	137.334	1.00	60.00
ATOM	2819	CB	THR	614	46.716	-9.892	137.960	1.00	60.00
ATOM	2820	OG1	THR	614	46.814	-9.809	139.377	1.00	60.00
ATOM	2822	CG2	THR	614	46.026	-11.203	137.550	1.00	60.00
ATOM	2823	C	THR	614	48.711	-11.188	137.572	1.00	60.00
ATOM	2824	O	THR	614	49.329	-11.761	136.676	1.00	60.00
ATOM	2825	N	ASN	615	48.591	-11.704	138.810	1.00	60.00
ATOM	2827	CA	ASN	615	49.141	-12.989	139.110	1.00	60.00
ATOM	2828	CB	ASN	615	48.878	-13.439	140.557	1.00	60.00
ATOM	2829	CG	ASN	615	49.650	-12.521	141.491	1.00	60.00
ATOM	2830	OD1	ASN	615	49.126	-12.068	142.508	1.00	60.00
ATOM	2831	ND2	ASN	615	50.933	-12.237	141.141	1.00	60.00

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ATOM   2834  C   ASN  615      48.428 -13.952 138.225  1.00 60.00
ATOM   2835  O   ASN  615      49.035 -14.838 137.625  1.00 60.00
ATOM   2836  N   GLY  616      47.099 -13.780 138.110  1.00 60.00
ATOM   2838  CA  GLY  616      46.324 -14.672 137.308  1.00 60.00
ATOM   2839  C   GLY  616      45.593 -15.544 138.269  1.00 60.00
ATOM   2840  O   GLY  616      45.794 -15.467 139.480  1.00 60.00
ATOM   2841  N   PRO  617      44.734 -16.368 137.747  1.00 60.00
ATOM   2842  CD  PRO  617      43.932 -15.954 136.607  1.00 60.00
ATOM   2843  CA  PRO  617      44.008 -17.246 138.618  1.00 60.00
ATOM   2844  CB  PRO  617      42.801 -17.730 137.819  1.00 60.00
ATOM   2845  CG  PRO  617      42.545 -16.582 136.827  1.00 60.00
ATOM   2846  C   PRO  617      44.910 -18.336 139.081  1.00 60.00
ATOM   2847  O   PRO  617      45.878 -18.646 138.387  1.00 60.00
ATOM   2848  N   LYS  618      44.622 -18.921 140.257  1.00 60.00
ATOM   2850  CA  LYS  618      45.463 -19.964 140.754  1.00 60.00
ATOM   2851  CB  LYS  618      44.979 -20.535 142.097  1.00 60.00
ATOM   2852  CG  LYS  618      44.979 -19.536 143.255  1.00 60.00
ATOM   2853  CD  LYS  618      44.189 -20.044 144.463  1.00 60.00
ATOM   2854  CE  LYS  618      42.726 -20.355 144.136  1.00 60.00
ATOM   2855  NZ  LYS  618      42.066 -20.995 145.296  1.00 60.00
ATOM   2859  C   LYS  618      45.382 -21.073 139.764  1.00 60.00
ATOM   2860  O   LYS  618      46.397 -21.621 139.338  1.00 60.00
ATOM   2861  N   ILE  619      44.147 -21.416 139.355  1.00 60.00
ATOM   2863  CA  ILE  619      43.985 -22.494 138.432  1.00 60.00
ATOM   2864  CB  ILE  619      42.708 -23.256 138.630  1.00 60.00
ATOM   2865  CG2 ILE  619      42.592 -24.284 137.493  1.00 60.00
ATOM   2866  CG1 ILE  619      42.667 -23.878 140.036  1.00 60.00
ATOM   2867  CD1 ILE  619      43.798 -24.870 140.301  1.00 60.00
ATOM   2868  C   ILE  619      43.939 -21.931 137.055  1.00 60.00
ATOM   2869  O   ILE  619      42.903 -21.468 136.579  1.00 60.00
ATOM   2870  N   PRO  620      45.064 -21.962 136.408  1.00 60.00
ATOM   2871  CD  PRO  620      46.133 -22.886 136.747  1.00 60.00
ATOM   2872  CA  PRO  620      45.150 -21.499 135.056  1.00 60.00
ATOM   2873  CB  PRO  620      46.580 -21.807 134.621  1.00 60.00
ATOM   2874  CG  PRO  620      46.929 -23.064 135.443  1.00 60.00
ATOM   2875  C   PRO  620      44.167 -22.326 134.296  1.00 60.00
ATOM   2876  O   PRO  620      43.890 -23.448 134.719  1.00 60.00
ATOM   2877  N   SER  621      43.605 -21.796 133.195  1.00 60.00
ATOM   2879  CA  SER  621      42.673 -22.575 132.437  1.00 60.00
ATOM   2880  CB  SER  621      41.697 -21.723 131.609  1.00 60.00
ATOM   2881  OG  SER  621      40.848 -20.982 132.473  1.00 60.00
ATOM   2883  C   SER  621      43.486 -23.423 131.466  1.00 60.00
ATOM   2884  O   SER  621      44.310 -22.836 130.715  1.00 60.00
ATOM   2885  OXT SER  621      43.293 -24.669 131.461  1.00 60.00
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ATOM	240	N	LEU	25	50.889	2.127	50.184	1.00	40.00
ATOM	242	CA	LEU	25	52.244	2.155	50.646	1.00	40.00
ATOM	243	CB	LEU	25	53.260	1.846	49.534	1.00	40.00
ATOM	244	CG	LEU	25	53.122	0.432	48.944	1.00	40.00
ATOM	245	CD1	LEU	25	51.761	0.244	48.255	1.00	40.00
ATOM	246	CD2	LEU	25	54.305	0.103	48.021	1.00	40.00
ATOM	247	C	LEU	25	52.535	3.540	51.127	1.00	40.00
ATOM	248	O	LEU	25	53.309	3.726	52.063	1.00	40.00
ATOM	249	N	SER	26	51.919	4.552	50.489	1.00	40.00
ATOM	251	CA	SER	26	52.128	5.925	50.853	1.00	40.00
ATOM	252	CB	SER	26	51.479	6.924	49.885	1.00	40.00
ATOM	253	OG	SER	26	52.186	6.916	48.654	1.00	40.00
ATOM	255	C	SER	26	51.646	6.179	52.249	1.00	40.00
ATOM	256	O	SER	26	52.061	7.144	52.888	1.00	40.00
ATOM	257	N	LEU	27	50.743	5.316	52.751	1.00	40.00
ATOM	259	CA	LEU	27	50.199	5.423	54.077	1.00	40.00
ATOM	260	CB	LEU	27	49.203	4.300	54.426	1.00	40.00
ATOM	261	CG	LEU	27	47.799	4.468	53.815	1.00	40.00
ATOM	262	CD1	LEU	27	47.097	5.687	54.425	1.00	40.00
ATOM	263	CD2	LEU	27	47.820	4.503	52.280	1.00	40.00
ATOM	264	C	LEU	27	51.282	5.372	55.114	1.00	40.00
ATOM	265	O	LEU	27	51.125	5.920	56.202	1.00	40.00
ATOM	266	N	GLN	28	52.404	4.695	54.814	1.00	40.00
ATOM	268	CA	GLN	28	53.475	4.531	55.757	1.00	40.00
ATOM	269	CB	GLN	28	54.656	3.726	55.191	1.00	40.00
ATOM	270	CG	GLN	28	55.794	3.551	56.199	1.00	40.00
ATOM	271	CD	GLN	28	56.903	2.750	55.531	1.00	40.00
ATOM	272	OE1	GLN	28	57.466	3.169	54.524	1.00	40.00
ATOM	273	NE2	GLN	28	57.222	1.561	56.110	1.00	40.00
ATOM	276	C	GLN	28	54.028	5.843	56.214	1.00	40.00
ATOM	277	O	GLN	28	54.444	5.978	57.363	1.00	40.00
ATOM	278	N	ARG	29	54.025	6.858	55.334	1.00	40.00
ATOM	280	CA	ARG	29	54.608	8.130	55.649	1.00	40.00
ATOM	281	CB	ARG	29	54.373	9.157	54.531	1.00	40.00
ATOM	282	CG	ARG	29	54.975	10.528	54.816	1.00	40.00
ATOM	283	CD	ARG	29	54.807	11.506	53.653	1.00	40.00
ATOM	284	NE	ARG	29	55.608	10.980	52.511	1.00	40.00
ATOM	286	CZ	ARG	29	55.054	10.093	51.634	1.00	40.00
ATOM	287	NH1	ARG	29	53.754	9.702	51.785	1.00	40.00
ATOM	290	NH2	ARG	29	55.800	9.597	50.603	1.00	40.00
ATOM	293	C	ARG	29	53.987	8.647	56.906	1.00	40.00
ATOM	294	O	ARG	29	54.629	9.325	57.707	1.00	40.00
ATOM	295	N	MET	30	52.697	8.347	57.100	1.00	40.00
ATOM	297	CA	MET	30	51.985	8.770	58.264	1.00	40.00
ATOM	298	CB	MET	30	50.510	8.341	58.207	1.00	40.00
ATOM	299	CG	MET	30	49.715	8.969	57.061	1.00	40.00
ATOM	300	SD	MET	30	49.219	10.693	57.345	1.00	40.00
ATOM	301	CE	MET	30	47.920	10.259	58.538	1.00	40.00
ATOM	302	C	MET	30	52.545	8.139	59.503	1.00	40.00
ATOM	303	O	MET	30	52.717	8.798	60.525	1.00	40.00
ATOM	304	N	PHE	31	52.864	6.835	59.432	1.00	40.00
ATOM	306	CA	PHE	31	53.208	6.092	60.610	1.00	40.00
ATOM	307	CB	PHE	31	53.368	4.587	60.332	1.00	40.00
ATOM	308	CG	PHE	31	53.702	3.932	61.628	1.00	40.00
ATOM	309	CD1	PHE	31	52.704	3.584	62.509	1.00	40.00
ATOM	310	CD2	PHE	31	55.009	3.671	61.966	1.00	40.00
ATOM	311	CE1	PHE	31	53.005	2.991	63.712	1.00	40.00
ATOM	312	CE2	PHE	31	55.316	3.078	63.169	1.00	40.00
ATOM	313	CZ	PHE	31	54.313	2.738	64.045	1.00	40.00
ATOM	314	C	PHE	31	54.443	6.531	61.331	1.00	40.00
ATOM	315	O	PHE	31	54.430	6.668	62.553	1.00	40.00
ATOM	316	N	ASN	32	55.545	6.784	60.607	1.00	40.00
ATOM	318	CA	ASN	32	56.765	7.029	61.316	1.00	40.00
ATOM	319	CB	ASN	32	57.986	7.127	60.383	1.00	40.00

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ATOM    320  CG  ASN    32      57.792   8.311  59.452  1.00 40.00
ATOM    321  OD1 ASN    32      56.702   8.526  58.926  1.00 40.00
ATOM    322  ND2 ASN    32      58.877   9.105  59.244  1.00 40.00
ATOM    325  C   ASN    32      56.761   8.237  62.192  1.00 40.00
ATOM    326  O   ASN    32      57.023   8.132  63.389  1.00 40.00
ATOM    327  N   ASN    33      56.425   9.425  61.661  1.00 40.00
ATOM    329  CA  ASN    33      56.577  10.527  62.559  1.00 40.00
ATOM    330  CB  ASN    33      57.776  11.425  62.207  1.00 40.00
ATOM    331  CG  ASN    33      59.052  10.651  62.509  1.00 40.00
ATOM    332  OD1 ASN    33      59.275  10.223  63.640  1.00 40.00
ATOM    333  ND2 ASN    33      59.912  10.462  61.473  1.00 40.00
ATOM    336  C   ASN    33      55.379  11.408  62.585  1.00 40.00
ATOM    337  O   ASN    33      55.411  12.515  62.049  1.00 40.00
ATOM    338  N   CYS    34      54.275  10.950  63.200  1.00 20.00
ATOM    340  CA  CYS    34      53.212  11.894  63.322  1.00 20.00
ATOM    341  CB  CYS    34      52.404  12.098  62.032  1.00 20.00
ATOM    342  SG  CYS    34      51.433  13.629  62.113  1.00 20.00
ATOM    343  C   CYS    34      52.283  11.462  64.407  1.00 20.00
ATOM    344  O   CYS    34      51.356  10.688  64.175  1.00 20.00
ATOM    345  N   GLU    35      52.542  11.933  65.642  1.00 20.00
ATOM    347  CA  GLU    35      51.663  11.649  66.735  1.00 20.00
ATOM    348  CB  GLU    35      52.196  12.161  68.084  1.00 20.00
ATOM    349  CG  GLU    35      53.439  11.425  68.585  1.00 20.00
ATOM    350  CD  GLU    35      53.851  12.052  69.908  1.00 20.00
ATOM    351  OE1 GLU    35      54.873  11.593  70.485  1.00 20.00
ATOM    352  OE2 GLU    35      53.151  12.998  70.357  1.00 20.00
ATOM    353  C   GLU    35      50.420  12.415  66.450  1.00 20.00
ATOM    354  O   GLU    35      49.309  11.913  66.609  1.00 20.00
ATOM    355  N   VAL    36      50.591  13.679  66.015  1.00 20.00
ATOM    357  CA  VAL    36      49.445  14.482  65.726  1.00 20.00
ATOM    358  CB  VAL    36      49.255  15.619  66.686  1.00 20.00
ATOM    359  CG1 VAL    36      48.015  16.421  66.256  1.00 20.00
ATOM    360  CG2 VAL    36      49.162  15.045  68.110  1.00 20.00
ATOM    361  C   VAL    36      49.603  15.077  64.369  1.00 20.00
ATOM    362  O   VAL    36      50.572  15.778  64.091  1.00 20.00
ATOM    363  N   VAL    37      48.640  14.818  63.471  1.00 20.00
ATOM    365  CA  VAL    37      48.745  15.411  62.175  1.00 20.00
ATOM    366  CB  VAL    37      47.997  14.656  61.101  1.00 20.00
ATOM    367  CG1 VAL    37      48.665  13.282  60.929  1.00 20.00
ATOM    368  CG2 VAL    37      46.508  14.540  61.476  1.00 20.00
ATOM    369  C   VAL    37      48.173  16.787  62.307  1.00 20.00
ATOM    370  O   VAL    37      47.002  16.964  62.634  1.00 20.00
ATOM    371  N   LEU    38      49.011  17.816  62.095  1.00 20.00
ATOM    373  CA  LEU    38      48.538  19.164  62.179  1.00 20.00
ATOM    374  CB  LEU    38      49.664  20.181  62.438  1.00 20.00
ATOM    375  CG  LEU    38      49.181  21.640  62.533  1.00 20.00
ATOM    376  CD1 LEU    38      48.220  21.843  63.715  1.00 20.00
ATOM    377  CD2 LEU    38      50.372  22.614  62.561  1.00 20.00
ATOM    378  C   LEU    38      47.938  19.486  60.856  1.00 20.00
ATOM    379  O   LEU    38      48.632  19.915  59.936  1.00 20.00
ATOM    380  N   GLY    39      46.610  19.300  60.738  1.00 20.00
ATOM    382  CA  GLY    39      45.961  19.543  59.485  1.00 20.00
ATOM    383  C   GLY    39      44.916  18.486  59.339  1.00 20.00
ATOM    384  O   GLY    39      44.326  18.039  60.319  1.00 20.00
ATOM    385  N   ASN    40      44.648  18.054  58.094  1.00 20.00
ATOM    387  CA  ASN    40      43.645  17.052  57.888  1.00 20.00
ATOM    388  CB  ASN    40      42.481  17.526  57.002  1.00 20.00
ATOM    389  CG  ASN    40      43.047  17.898  55.638  1.00 20.00
ATOM    390  OD1 ASN    40      43.930  18.747  55.527  1.00 20.00
ATOM    391  ND2 ASN    40      42.529  17.239  54.568  1.00 20.00
ATOM    394  C   ASN    40      44.258  15.858  57.225  1.00 20.00
ATOM    395  O   ASN    40      45.323  15.950  56.618  1.00 20.00
ATOM    396  N   LEU    41      43.591  14.697  57.360  1.00 20.00
ATOM    398  CA  LEU    41      44.106  13.504  56.750  1.00 20.00
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A	399	CB	LEU	41	44.427	12.413	57.790	1.00	20.00
ATOM	400	CG	LEU	41	44.993	11.095	57.223	1.00	20.00
ATOM	401	CD1	LEU	41	43.917	10.281	56.495	1.00	20.00
M	402	CD2	LEU	41	46.240	11.344	56.360	1.00	20.00
ATOM	403	C	LEU	41	43.081	13.013	55.786	1.00	20.00
ATOM	404	O	LEU	41	41.903	12.890	56.121	1.00	20.00
ATOM	405	N	GLU	42	43.503	12.746	54.530	1.00	20.00
ATOM	407	CA	GLU	42	42.576	12.236	53.573	1.00	20.00
ATOM	408	CB	GLU	42	42.343	13.151	52.357	1.00	20.00
ATOM	409	CG	GLU	42	41.341	12.557	51.362	1.00	20.00
ATOM	410	CD	GLU	42	41.171	13.525	50.199	1.00	20.00
ATOM	411	OE1	GLU	42	41.827	14.601	50.222	1.00	20.00
ATOM	412	OE2	GLU	42	40.384	13.201	49.271	1.00	20.00
ATOM	413	C	GLU	42	43.131	10.961	53.033	1.00	20.00
ATOM	414	O	GLU	42	44.302	10.892	52.659	1.00	20.00
ATOM	415	N	ILE	43	42.304	9.899	53.011	1.00	20.00
ATOM	417	CA	ILE	43	42.752	8.662	52.445	1.00	20.00
ATOM	418	CB	ILE	43	42.741	7.524	53.424	1.00	20.00
ATOM	419	CG2	ILE	43	43.059	6.230	52.657	1.00	20.00
ATOM	420	CG1	ILE	43	43.718	7.804	54.578	1.00	20.00
ATOM	421	CD1	ILE	43	45.176	7.902	54.129	1.00	20.00
ATOM	422	C	ILE	43	41.784	8.327	51.358	1.00	20.00
ATOM	423	O	ILE	43	40.727	7.756	51.616	1.00	20.00
ATOM	424	N	THR	44	42.126	8.643	50.096	1.00	20.00
ATOM	426	CA	THR	44	41.172	8.389	49.058	1.00	20.00
ATOM	427	CB	THR	44	40.818	9.607	48.256	1.00	20.00
ATOM	428	OG1	THR	44	39.737	9.316	47.382	1.00	20.00
ATOM	430	CG2	THR	44	42.053	10.050	47.453	1.00	20.00
ATOM	431	C	THR	44	41.667	7.354	48.098	1.00	20.00
ATOM	432	O	THR	44	42.868	7.121	47.968	1.00	20.00
ATOM	433	N	TYR	45	40.704	6.690	47.429	1.00	20.00
ATOM	435	CA	TYR	45	40.919	5.707	46.405	1.00	20.00
ATOM	436	CB	TYR	45	41.028	6.314	44.994	1.00	20.00
ATOM	437	CG	TYR	45	39.706	6.904	44.639	1.00	20.00
ATOM	438	CD1	TYR	45	38.687	6.101	44.182	1.00	20.00
ATOM	439	CE1	TYR	45	37.480	6.645	43.808	1.00	20.00
ATOM	440	CD2	TYR	45	39.503	8.263	44.708	1.00	20.00
ATOM	441	CE2	TYR	45	38.298	8.812	44.337	1.00	20.00
ATOM	442	CZ	TYR	45	37.284	8.002	43.884	1.00	20.00
ATOM	443	OH	TYR	45	36.051	8.560	43.489	1.00	20.00
ATOM	445	C	TYR	45	42.127	4.854	46.623	1.00	20.00
ATOM	446	O	TYR	45	43.049	4.867	45.811	1.00	20.00
ATOM	447	N	VAL	46	42.169	4.080	47.723	1.00	20.00
ATOM	449	CA	VAL	46	43.301	3.215	47.895	1.00	20.00
ATOM	450	CB	VAL	46	44.235	3.641	48.988	1.00	20.00
ATOM	451	CG1	VAL	46	43.474	3.627	50.320	1.00	20.00
ATOM	452	CG2	VAL	46	45.461	2.713	48.965	1.00	20.00
ATOM	453	C	VAL	46	42.811	1.841	48.220	1.00	20.00
ATOM	454	O	VAL	46	41.745	1.678	48.813	1.00	20.00
ATOM	455	N	GLN	47	43.573	0.802	47.815	1.00	20.00
ATOM	457	CA	GLN	47	43.130	-0.533	48.099	1.00	20.00
ATOM	458	CB	GLN	47	42.333	-1.150	46.940	1.00	20.00
ATOM	459	CG	GLN	47	41.063	-0.367	46.607	1.00	20.00
ATOM	460	CD	GLN	47	40.429	-1.005	45.381	1.00	20.00
ATOM	461	OE1	GLN	47	39.658	-1.958	45.483	1.00	20.00
ATOM	462	NE2	GLN	47	40.771	-0.468	44.180	1.00	20.00
ATOM	465	C	GLN	47	44.309	-1.426	48.332	1.00	20.00
ATOM	466	O	GLN	47	45.210	-1.490	47.501	1.00	20.00
ATOM	467	N	ARG	48	44.353	-2.119	49.490	1.00	20.00
ATOM	469	CA	ARG	48	45.386	-3.099	49.670	1.00	20.00
ATOM	470	CB	ARG	48	46.828	-2.580	49.817	1.00	20.00
ATOM	471	CG	ARG	48	47.112	-1.831	51.115	1.00	20.00
ATOM	472	CD	ARG	48	48.611	-1.746	51.417	1.00	20.00
ATOM	473	NE	ARG	48	49.145	-3.137	51.474	1.00	20.00

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ATOM    475  CZ  ARG    48      50.483  -3.358  51.318  1.00 20.00
ATOM    476  NH1 ARG    48      50.973  -4.631  51.348  1.00 20.00
ATOM    479  NH2 ARG    48      51.331  -2.307  51.125  1.00 20.00
ATOM    482  C   ARG    48      45.108  -3.855  50.928  1.00 20.00
ATOM    483  O   ARG    48      44.103  -3.633  51.600  1.00 20.00
ATOM    484  N   ASN    49      46.020  -4.783  51.272  1.00 20.00
ATOM    486  CA  ASN    49      45.864  -5.613  52.430  1.00 20.00
ATOM    487  CB  ASN    49      46.987  -6.657  52.557  1.00 20.00
ATOM    488  CG  ASN    49      46.858  -7.627  51.393  1.00 20.00
ATOM    489  OD1 ASN    49      45.806  -8.228  51.183  1.00 20.00
ATOM    490  ND2 ASN    49      47.957  -7.781  50.607  1.00 20.00
ATOM    493  C   ASN    49      45.891  -4.796  53.682  1.00 20.00
ATOM    494  O   ASN    49      44.996  -4.901  54.518  1.00 20.00
ATOM    495  N   TYR    50      46.917  -3.937  53.835  1.00 20.00
ATOM    497  CA  TYR    50      47.034  -3.184  55.049  1.00 20.00
ATOM    498  CB  TYR    50      48.313  -2.332  55.148  1.00 20.00
ATOM    499  CG  TYR    50      49.476  -3.249  55.318  1.00 20.00
ATOM    500  CD1 TYR    50      49.774  -3.761  56.559  1.00 20.00
ATOM    501  CE1 TYR    50      50.869  -4.574  56.740  1.00 20.00
ATOM    502  CD2 TYR    50      50.301  -3.547  54.258  1.00 20.00
ATOM    503  CE2 TYR    50      51.398  -4.359  54.433  1.00 20.00
ATOM    504  CZ  TYR    50      51.683  -4.873  55.675  1.00 20.00
ATOM    505  OH  TYR    50      52.810  -5.702  55.857  1.00 20.00
ATOM    507  C   TYR    50      45.871  -2.269  55.220  1.00 20.00
ATOM    508  O   TYR    50      45.151  -1.960  54.272  1.00 20.00
ATOM    509  N   ASP    51      45.658  -1.829  56.476  1.00 40.00
ATOM    511  CA  ASP    51      44.594  -0.929  56.799  1.00 40.00
ATOM    512  CB  ASP    51      43.591  -1.486  57.825  1.00 40.00
ATOM    513  CG  ASP    51      42.761  -2.572  57.151  1.00 40.00
ATOM    514  OD1 ASP    51      42.891  -2.734  55.908  1.00 40.00
ATOM    515  OD2 ASP    51      41.978  -3.250  57.869  1.00 40.00
ATOM    516  C   ASP    51      45.238   0.271  57.414  1.00 40.00
ATOM    517  O   ASP    51      46.447   0.299  57.629  1.00 40.00
ATOM    518  N   LEU    52      44.426   1.306  57.692  1.00 40.00
ATOM    520  CA  LEU    52      44.875   2.544  58.259  1.00 40.00
ATOM    521  CB  LEU    52      43.795   3.638  58.253  1.00 40.00
ATOM    522  CG  LEU    52      44.316   5.001  58.745  1.00 40.00
ATOM    523  CD1 LEU    52      45.417   5.540  57.819  1.00 40.00
ATOM    524  CD2 LEU    52      43.167   6.001  58.947  1.00 40.00
ATOM    525  C   LEU    52      45.316   2.310  59.672  1.00 40.00
ATOM    526  O   LEU    52      46.083   3.086  60.238  1.00 40.00
ATOM    527  N   SER    53      44.838   1.207  60.272  1.00 40.00
ATOM    529  CA  SER    53      45.077   0.879  61.649  1.00 40.00
ATOM    530  CB  SER    53      44.492  -0.484  62.049  1.00 40.00
ATOM    531  OG  SER    53      45.162  -1.527  61.355  1.00 40.00
ATOM    533  C   SER    53      46.536   0.824  61.965  1.00 40.00
ATOM    534  O   SER    53      46.923   1.047  63.111  1.00 40.00
ATOM    535  N   PHE    54      47.391   0.535  60.967  1.00 40.00
ATOM    537  CA  PHE    54      48.788   0.373  61.250  1.00 40.00
ATOM    538  CB  PHE    54      49.665   0.050  60.021  1.00 40.00
ATOM    539  CG  PHE    54      49.742   1.221  59.103  1.00 40.00
ATOM    540  CD1 PHE    54      50.664   2.219  59.322  1.00 40.00
ATOM    541  CD2 PHE    54      48.995   1.254  57.950  1.00 40.00
ATOM    542  CE1 PHE    54      50.813   3.247  58.419  1.00 40.00
ATOM    543  CE2 PHE    54      49.127   2.284  57.049  1.00 40.00
ATOM    544  CZ  PHE    54      50.040   3.284  57.283  1.00 40.00
ATOM    545  C   PHE    54      49.319   1.607  61.908  1.00 40.00
ATOM    546  O   PHE    54      50.271   1.519  62.680  1.00 40.00
ATOM    547  N   LEU    55      48.738   2.790  61.609  1.00 40.00
ATOM    549  CA  LEU    55      49.180   4.002  62.248  1.00 40.00
ATOM    550  CB  LEU    55      48.495   5.271  61.707  1.00 40.00
ATOM    551  CG  LEU    55      48.790   5.573  60.228  1.00 40.00
ATOM    552  CD1 LEU    55      50.281   5.855  60.008  1.00 40.00
ATOM    553  CD2 LEU    55      48.248   4.478  59.299  1.00 40.00
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Annexure A

AUSTRALIA

Patents Act 1990

COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

PROVISIONAL SPECIFICATION

Invention Title:

EGF family receptor agonists and antagonists

The invention is described in the following statement:

EGF FAMILY RECEPTOR AGONISTS AND ANTAGONISTS

Field of the Invention

This invention relates to the field of receptor structure and receptor/ligand interactions. In particular it relates to the field of using receptor structure to predict the structure of related receptors and to use the determined structures and predicted structures to select and screen for agonists and antagonists of the polypeptide ligands.

Background of the Invention

Insulin is the peptide hormone that regulates glucose uptake and metabolism. The two types of diabetes are associated with either an inability to produce insulin because of destruction of the pancreatic islet cells (Homo-Delarche, F. & Boitard, C.,1996, Immunol. Today 10: 456-460) or poor glucose metabolism resulting from either insulin resistance at the target tissues, inadequate insulin secretion by the islets or faulty liver function (Taylor, S. I., et al., 1994, Diabetes, 43: 735-740).

Insulin-like growth factors-1 and 2 (IGF-1 and 2) are structurally related to insulin but are more important in tissue growth and development than in metabolism. They are primarily produced in the liver in response to growth hormone but are also produced in most other tissues where they function as paracrine/autocrine regulators. The IGFs are strong mitogens and are involved in numerous physiological states and certain cancers (Baserga, R., 1996, TibTech 14: 150-152).

Epidermal growth factor (EGF) is a small polypeptide cytokine that is unrelated to the insulin/IGF family. It stimulates marked proliferation of epithelial tissues and is a member of a larger family of structurally related cytokines such as transforming growth factor α, amphiregulin, betacellulin, heparin-binding EGF and some viral gene products. Abnormal EGF family signalling is a characteristic of certain cancers (Soler, C. & Carpenter, G., 1994 In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197; Walker, F. & Burgess, A. W., 1994, In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp198-201).

Each of these growth factors mediate their biological actions through binding to the corresponding receptor. The IR, IGF-1R and insulin receptor-related receptor (IRR), for which the ligand is not known, are closely related to each other and are referred to as the insulin receptor subfamily. There is a

large body of information now available concerning the primary structure of these insulin receptor subfamily members (Ebina, Y., et al., 1985 Cell 40: 747-758; Ullrich, A., et al., 1985, Nature 313: 756-761; Ullrich, A. et al., 1986, EMBO J 5: 2503-2512; Shier, P. & Watt, V. M., 1989, J. Biol. Chem. 264: 14605-14608) and the identification of some of their functional domains (for reviews see De Meyts, P. 1994, Diabetologia 37: 135-148; Lee, J. & Pilch, P. F. 1994 Amer. J. Physiol. 266: C319-C334.; Schaffer, L. 1994, Eur. J. Biochem. 221: 1127-1132). IGF-1R, IR and IRR are members of the tyrosine kinase receptor superfamily and are closely related to the epidermal growth factor receptor (EGFR) subfamily, with which they share significant sequence identity in the extracellular region as well as in the cytoplasmic kinase domains (Ullrich, A. et al., 1984 Nature 309: 418-425; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). Both the insulin and EGF receptor subfamilies have a similar arrangement of two homologous domains (L1 and L2) separated by a cys-rich region of approximately 160 amino acids containing 22-24 cys residues (Bajaj, M., et al., 1987 Biochim. Biophys. Acta 916: 220-226; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). The C-terminal portion of the IGF-1R ectodomain (residues 463 to 906) is comprised of four domains: a connecting domain, two fibronectin type 3 (Fn3) repeats, and an insert domain (O'Bryan, J. P., et al., 1991 Mol Cell Biol 11: 5016-5031); the C-terminal portion of the EGFR ectodomain (residues 477-621) consists solely of a second cys-rich region containing 20 cys residues (Ullrich, A. et al., 1984, Nature 309: 418-425).

Little is known about the secondary, tertiary and quaternary structure of the ectodomains of these receptor subfamilies. Unlike the members of the EGFR subfamily which are transmembrane monomers which dimerise on binding ligand, the IR subfamily members are homodimers, held together by disulphide bonds. The extracellular region of the IR/IGF-1R/IRR monomers contains an α-chain (~ 703 to 735 amino acid residues) and 192-196 residues of the ß-chain. There is a ~23 residue transmembrane segment, followed by the cytoplasmic portion (354 to 408 amino acids) which contains the catalytic tyrosine kinase domain flanked by juxtamembrane and C-tail regulatory regions and is responsible for mediating all receptor-specific functions (White, M. F. & Kahn, C. R. 1994 J. Biol. Chem. 269: 1-4). Chemical analyses of the receptor suggest that the α-chains are linked to the ß-chains

via a single disulphide bond with the IR dimer being formed by at least two α-α disulphide linkages (Finn, F. M., et al., 1990, Proc. Natl. Acad. Sci. 87: 419-423; Chiacchia, K. B., 1991, Biochem. Biophys. Res. Commun. 176, 1178-1182; Schaffer, L. & Ljungqvist, L., 1992, Biochem. Biophys. Res. Comm. 189: 650-653; Sparrow, L. G., et al., 1997, J. Biol. Chem. 47: 29460-29467).

Although the 3D structures of the ligands EGF, TGF-alpha (Hommel, U., et al., 1992, J. Mol. Biol. 227:271-282), insulin (Dodson, E. J., et al., 1983, Biopolymers 22:281-291), IGF-1 (Sato, A., et al., 1993, Int J Peptide Protein Res 41:433-440) and IGF-2 (Torres, A. M., et al.,1995, J. Mol. Biol. 248:385-401) are known and numerous analytical and functional studies of ligand binding to EGFR (Soler, C. & Carpenter, G., 1994 In Nicola (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197), IGF-1R and IR (see De Meyts, P., 1994 Diabetologia, 37:135-148) have been carried out, the mechanisms of ligand binding and subsequent transmembrane signalling have not been resolved.

Ligand-induced, receptor-mediated phosphorylation is the signalling mechanism by which most cytokines, polypeptide hormones and membrane-anchored ligands exert their biological effects. The primary kinase may be part of the intracellular portion of the transmembrane receptor protein as in the tyrosine kinase receptors (for review see Yarden, Y., et al., 1988, Ann. Rev. Biochem. 57:443-478) or the Ser/Thr kinase receptors (Alevizopoulos, A. & Mermod, N., 1997, BioEssays, 19:581-591) or be non-covalently associated with the cytoplasmic tail of the transmembrane protein(s) making up the receptor complex as in the case of the haemopoietic growth factor receptors (Stahl, N., et al., 1995, Science 267:1349-1353). The end result is the same, ligand binding leads to receptor dimerization or oligomerization or a conformational change in pre-existing receptor dimers or oligomers resulting in activation by transphosphorylation, of the covalently attached or non-covalently associated protein kinase domains (Hunter, T., 1995, Cell, 80:225-236).

Many oncogenes have been shown to be homologous to growth factors, growth factor receptors or molecules in the signal transduction pathways (Baserga. R.,1994 Cell, 79:927-930; Hunter, T., 1997 Cell, 88:333-346). One of the best examples is v-Erb (related to the EGFR). Since overexpression of a number of growth factor receptors results in ligand-dependent transformation an alternate strategy for oncogenes is to regulate

the expression of growth factor receptors or their ligands or to directly bind to the receptors to stimulate the same effect (Baserga, R., 1994 Cell, 79:927-930). Examples are v-Src, which activates IGF-1 R intracellularly; c-Myb, which transforms cells by enhancing the expression of IGF1R and SV40 T antigen which interacts with the IGF-1R and enhances the secretion of IGF-1 (see Baserga, R.,1994 Cell, 79:927-930 for review). Cells in which the IGF-1 receptor has been knocked out cannot be transformed by SV40 T antigen. If oncogenes activate growth factors and their receptors then tumour suppressor genes should have the opposite effect. One good example of this is WT1, the Wilm's tumour suppressor gene which suppresses the expression of IGF-1R (Drummond, J. A., et al., 1992, Science, 257:275-277). Cells that are driven to proliferate by oncogenes undergo massive apotosis when growth factor receptors are ablated since unlike normal cells, they appear unable to withdraw from the cell-cycle and enter into the G0 phase (Baserga, R.,1994 Cell, 79:927-930).

The insulin-like growth factor-1 receptor (IGF-1R) is one of several growth-factor receptors that regulate the proliferation of mammalian cells. However, its ubiquitousness and certain unique aspects of its function make IGF-1R an ideal target for therapeutic interventions against abnormal growth, with very little effect on normal cells (see Baserga, R., 1996 TIBTECH, 14:150-152). The receptor is activated by IGF1, IGF2 and insulin and plays a major role in cellular proliferation in at least three ways: it is essential for optimal growth of cells in vitro and in vivo; several cell types require IGF-1R to maintain the transformed state and activated IGF-1R has a protective effect against apoptotic cell death (Baserga, R., 1996 TIBTECH, 14:150-152). These properties alone make it an ideal target for therapeutic interventions. Transgenic experiments have shown that IGF-1R is not an absolute requirement for cell growth but is essential for the establishment of the transformed state (Baserga, R.,1994 Cell, 79: 927-930). In several cases (human glioblastoma, human melanoma; human breast carcinoma; human lung carcinoma; human ovaraian carcinoma; human rhabdomyosarcoma; mouse melanoma, mouse leukaemia; rat glioblastoma; rat rhabdomyosarcoma; hamster mesothelioma) the transformed phenotype can be reversed by decreasing the expression of IGF-1R using antisense to IGF-1R (Baserga. R., 1996 TIBTECH 14:150-152); or interfering with its function by antibodies to IGF-1R (human breast carcinoma; human rhabdomyosarcoma)

or by dominant negatives of IGF-1R (rat glioblastoma; Baserga, R.,1996 TIBTECH 14:150-152).

Three effects are observed when the function of IGF-1R is impaired: tumour cells undergo massive apoptosis which results in inhibition of tumourogenesis; surviving tumour cells are eliminated by a specific immune response; and such a host response can cause a regression of an established wild-type tumour (Resnicoff, M., et al., 1995, Cancer Res. 54:2218-2222). These effects, plus the fact that interference of IGF-1R function has a limited effect on normal cells (partial inhibition of growth without apoptosis) makes IGF-1R a unique target for therapeutic interventions (Baserga, R., 1996 TIBTECH 14:150-152). In addition IGF-1R is downstream of many other growth factor receptors, which makes it an even more generalised target. The implication of these findings is that if you can decrease the number of IGF-1 receptors on cells or antagonise their function then tumours cease to grow and can be removed immunologically. These studies establish that IGF-1R antagonists will be extremely important therapeutically.

Many cancer cells have constitutively active EGFR (Sandgreen, E. P., et al., 1990, Cell, 61:1121-135; Karnes, W. E. J., et al., 1992, Gastroenterology, 102:474-485) or other EGFR family members (Hines, N. E.,1993, Semin. Cancer Biol. 4:19-26). Elevated levels of activated EGFR occur in bladder, breast, lung and brain tumours (Harris, A. L., et al., 1989, In Furth & Greaves (eds) The Molecular Diagnostics of human cancer. Cold Spring Harbor Lab. Press, CSH, NY, pp353-357). Antibodies to EGFR can inhibit ligand activation of EGFR (Sato, J. D., et al., 1983 Mol. Biol. Med. 1:511-529) and the growth of many epithelial cell lines (Aboud-Pirak E., et al., 1988, J. Natl Cancer Inst. 85:1327-1331). Patients receiving repeated doses of a humanised chimeric anti-EGFR antibody showed signs of disease stabilization. The large doses required and the cost of production of humanised Mab is likely to limit the application of this type of therapy. These findings indicate that the development of EGF antagonists will be attractive anticancer agents.

Summary of the Invention

The present inventors have now obtained 3D structural information concerning the insulin-like growth factor receptor (IGF-1R) and the insulin receptor (IR) which provides a rational basis for the development of antagonists and agonists of the polypeptide ligands for specific therapeutic applications. This information can be used to predict the structure of related

members of the insulin receptor family and epidermal growth factor family and to develop agonists and antagonists of their respective polypeptide ligands.

Accordingly, in a first apsect the present invention provides a method of screening for, or designing, an agonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

(i) selecting or designing a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by

(a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or

(b) amino acids derived from an insulin receptor family member or EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a); and

(ii) testing the substance for the ability to act as an agonist of the ligand of an insulin receptor family member or EGF receptor family member.

In a second apsect the present invention provides a method of screening for, or designing, an antagonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

(i) selecting or designing a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by

(a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or

(b) amino acids derived from an insulin receptor family member or an EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a); and

(ii) testing the substance for the ability to act as an antagonist of the ligand of an insulin receptor family member or EGF receptor family member.

The phrase "insulin receptor family" encompasses, for example, IGF-1R. IR and IRR. The phrase "EGF receptor family" encompasses for example, EGFR, ErbB2, ErbB3 and ErbB4. In general, insulin receptor family members and EGF receptor family members show similar domain arrangements and share significant sequence identity (preferably at least 20% identity between the families and at least 40% identity within each family).

The receptor site defined in the first and second aspects of the present invention comprises the L1-cysteine rich-L2 region (residues 1-462) of the ectodomain of IGF-1R. At the centre of this structure is a groove, bounded by all three domains, of sufficient size to accommodate a ligand molecule. By "stereochemical complementarity" we mean that the biologically active substance or a portion thereof correlates, in the manner of the classic "lock-and-key" visualisation of ligand-receptor interaction, with the groove in the receptor site. Preferably, the stereochemical complementarity is such that the compound has a K_I for the receptor site of less than 10^{-6}M. More preferably, the K_I value is less than 10^{-8}M and more preferably less than 10^{-9}M.

In preferred embodiments of the first and second aspects of the present invention, the method further involves selecting or designing a substance which has portions that match residues positioned on the surface of the receptor site which faces the groove. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions which promote desolvation of the biologically active substance within the site, in such a way that retention of the biologically active substance within the groove is favoured energetically.

In a preferred embodiment of the first aspect of the present invention, the method includes screening for, or designing, a substance which possesses a stereochemistry and/or geometry which allows it to interact with both the L1 and L2 domains of the receptor site. As described above, the insulin receptor exists as homodimers held together by disulphide bonds. Electron miscroscopy studies described herein indicate that the insulin receptor monomers dimerise in nature in such a manner that the grooves of each monomer may face each other. Accordingly, the method of the first aspect of the present invention may involve screening for, or designing, a biologically active substance which interacts with the L1 domain of one monomer and the L2 domain of the other monomer.

In a third aspect the present invention provides a method of selecting or designing an agonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

(i) selecting or designing a substance which interacts with

(a) a fragment of IGF-1R characterised by amino acids 1-462 positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or

(b) a fragment derived from an insulin family receptor member or EGF receptor family member which is equivalent to the fragment defined in paragraph (a);

wherein the interaction of the substance with the fragment alters the position of at least one of the L1, L2 or cys-rich domains of the fragment relative to the position of at least one of the other domains; and

(ii) testing the substance for the ability to act as an agonist of the ligand of an insulin receptor family member or EGF receptor family member.

In a preferred embodiment of the third aspect of the present invention the substance interacts with the fragment in the region of the L1 domain-cys rich domain interface, causing the L1 and cys-rich domains to move away from each other. In a further preferred embodiment the substance interacts with the hinge region between the L2 domain and the cys-rich domain causing an alteration in the positions of the domains relative to each other. In a further preferred embodiment the substance interacts with the beta sheet of the L1 domain causing an alteration in the position of the L1 domain relative to the position of the cys-rich domain or L2 domain.

In a fourth aspect the present invention provides an agonist of a ligand of an insulin receptor family member or EGF receptor family member obtained by a method according to the first or third aspects of the present invention.

In a fifth aspect the present invention provides an antagonist of ligand of an insulin receptor family member or EGF receptor family member obtained by a method according to the second aspect of the present invention.

The agonists or antagonists of the fourth and fifth aspects of the present invention may be mutant insulin family member or EGF family member ligands where at least one mutation occurs in the region of the ligand which interacts with residues on the surface of the receptor site facing toward the groove. For example, the IGF-1 ligand has a predominance of basic residues in the C region which may interact with the acidic patch of the cys-rich region near L1. An acidic patch on the other side of the ligand may interact with the patch of basic residues (residues 307-310) on the N-terminal

end of L2. Accordingly, mutants of IGF-1 which exhibit altered activity may be generated by introducing modifications in the C region of IGF-1 or residues in the acidic patch on the other side of the hormone.

In a sixth aspect the present invention provides a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by

(a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or

(b) amino acids derived from an insulin receptor family member or an EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a);

with the proviso that the substance is not a naturally occurring ligand of an insulin receptor family member or EGF receptor family member or a mutant thereof.

By "mutant" we mean a ligand which has been modified by one or more point mutations, insertions of amino acids or deletions of amino acids.

In a preferred embodiment of the sixth aspect of the present invention, the stereochemical complementarity is such that the compound has a K_I for the receptor site of less than 10^{-6}M. More preferably, the K_I value is less than 10^{-8}M and more preferably less than 10^{-9}M.

In a seventh aspect the present invention provides a pharmaceutical composition for treatment of a disease associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member which includes an agonist obtained by a method according to the first or third aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In an eighth aspect the present invention provides a pharmaceutical composition for treatment of a disease associated with activity of a ligand of an insulin receptor family member or EGF receptor family member which includes an antagonist obtained by a method according to the second aspect of the present invention and a pharmaceutically acceptable carrier or diluent.

In a ninth aspect the present invention provides a method of preventing or treating a disease associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member which method includes administering to a subject in need thereof an agonist

obtained by a method according to the first or third aspects of the present invention.

Diseases associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member include diabetes, osteoporosis, nerve degeneration and a range of catabolic states.

In a tenth aspect the present invention provides a method of preventing or treating a disease associated with activity of a ligand of an insulin receptor family member or EGF receptor family member which method includes administering to a subject in need thereof an antagonist obtained by a method according to the second aspect of the present invention.

Diseases associated with activity of a ligand of an insulin receptor family member or EGF receptor family member include cancer, leukaemia and many types of tumour states including but not restricted to breast cancer, brain tumours, ovarian cancer, pancreatic tumours, lung cancer, melanoma, rhabdomyosarcoma, mesothelioma and glioblastoma.

Brief Description of the Drawings

Figure 1. IGF-1R residues 1-462, in terms of atomic coordinates refined to a resolution of 2.6 Å (average accuracy ≈ 0.3Å). The coordinates are in relation to a Cartesian system of orthogonal axes.

Figure 2. Depiction of the residues lining the groove of the IGF-1R receptor fragment 1-462.

Figure 3. Gel filtration chromatography of affinity-purified IGF-1R/462 protein. The protein was purified on a Superdex S200 column (Pharmacia) fitted to a BioLogic L.C. system (Biorad), equilibrated and eluted at 0.8 ml/min with 40 mM Tris/150 mM NaCl/0.02% NaN3 adjusted to pH 8.0. (a) Protein eluting in peak 1 contained aggregated IGF-1R/462 protein, peak 2 contained monomeric protein and peak 3 contained the c-myc undecapeptide used for elution from the Mab 9E10 immunoaffinity column. (b) Non-reduced SDS-PAGE of fraction 2 from IGF-1R/462 obtained following Superdex S200 (Fig.1a). Standard proteins are indicated.

Figure 4. Ion exchange chromatography of affinity-purified, truncated IGF-1R ectodomain. A mixture of gradient and isocratic elution chromatography was performed on a Resource Q column (Pharmacia) fitted to a BioLogic System (Biorad), using 20 mM Tris/pH 8.0 as buffer A and the same buffer containing 1M NaCl as buffer B. Protein solution in TBSA was diluted at least 1:2 with water and loaded onto the column at 2 ml/min. Elution was monitored by absorbance (280 nm) and conductivity (mS/cm). Target protein (peak 2) eluted isocratically with 20 mM Tris/0.14 M NaCl pH 8.0. Inset: Isoelectric focusing gel (pH 3 - 7; Novex Australia Pty Ltd)of fraction 2. The pI was estimated at 5.1 from standard proteins (not shown).

Figure 5. Gel filtration chromatography of affinity purified IR/485 protein. Affinity-purified material at 1 mg/ml produced a dominant peak at apparent mass ~ 140 kDa (interpreted as a dimer) (a); whereas affinity-purified material at 0.02 mg/ml produced a dominant peak at apparent mass ~ 85kDa (interpreted as a monomer) (b).

Figure 6. (a) SDS-PAGE of IR/485 following gel filtration chromatography. The protein migrated as a single broad band of apparent molecular mass ~ 78 kDa (reduced - lane A) or ~ 68kDa (non-reduced - lane B). (b) Isoelectric focussing of the IR/485 protein. The IR/485 fragment reacted positively in an ELISA with Mab 83-7, gave a single sequence corresponding to the N-terminal 10 residues of IR, showing several isoforms on isoelectric focussing from pI6.0-6.8. The fragment was further purified by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations (see Figure 7). Fractions A and D were each enriched in a component isoform from the ladder of isoforms present in the unfractionated mixture. Both these fractions produced crystals, whereas no crystals were obtained from fractions B and C.

Figure 7. Purification of the IR/485 protein by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations.

Figure 8. Polypeptide fold for residues 1-462 of IGF-1R. The L1 domain is at the top. viewed from the N-terminal end and L2 is at the bottom. The space

at the centre is of sufficient size to accommodate IGF-1. Helices are indicated by curled ribbon and b-strands by arrows. Cysteine side chains are drawn as ball-and-stick with lines showing disulfide bonds. The arrow points in the direction of view for Figure 9.

Figure 9. Amino acid sequences of IGF-1R and related proteins. a, L1 and L2 domains of human IGF-1R and IR are shown based on a sequence alignment for the two proteins and a structural alignment for the L1 and L2domains. Positions showing conservation physico-chemical properties of amino acids are boxed, residues used in the structural alignment are shaded yellow and residues which form the Trp 176 pocket are in red. Secondary structure elements for L1 (above the sequences) and L2 (below) are indicated as cylinders for helices and arrows for b-strands. Strands are colour coded according to the b-sheet to which they belong. Disulfide bonds are also indicated. b, Cys-rich domains of human IGF-1R, IR and EGFR (domains 2 and 4) are aligned based on sequence and structural considerations. Secondary structural elements and disulfide bonds are indicated above the sequences. The dashed bond is only present in IR. Different types of disulfide bonded modules are labelled below the sequences as open, filled or broken lines. Boxed residues show conservation of physico-chemical properties and structurally conserved residues for modules 4-7 are shaded yellow. Residues from EGFR which do not conform to the pattern are shaded grey and the conserved Trp 176 and the semi-conserved Gln 182 are shaded red. This figure was prepared using ALSCRIPT (Barton, G. J., 1993, Prot. Engineering, 6:37-40).

Figure 10. Stereo view of a superposition of the L1 (white) and L2 (black) domains. Residues numbers above are for L1 and below for L2. The side chain of Trp 176 which protrudes into the core of L1 is drawn as ball-and-stick.

Figure 11. Schematic diagram showing the association of three β-finger motifs. β-strands are drawn as arrows and disulfide bonds as zigzags.

Figure 12. GRASP [Nicolls, A. et al., 1993, Biophys. J. 64, 166-170] surface diagram of the L1 domain of IGF-1R shown in a similar view to Figure 8. The

N-terminal β-strand is at the top. The mutation L87A [Nakae, J. et al., 1995, J. Biol. Chem. 270, 22017-22022] and four regions (residues 12-15, 34-44, 64-67 and 89-91 of IR) shown to be important in insulin binding to IR [Williams, P. F. et al., 1995, J. Biol. Chem. 270, 3012-3016] correspond to a patch of residues on the large β-sheet. Residues numbers for IR/IGF-1R are given and residues are coloured according to the magnitude of Kd(mutant)/Kd(wild type), red, > 40; orange, 10-40; yellow, 2.5-10; green, < 2.5; non-secreting, white; untested, blue. All mutants on the opposite face of the domain do not affect insulin affinity.

Figure 13: Sequence Alignment of hIGF-1R, hIR and hIRR Ectodomains. Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA. For assignment of homologous 3D structures see Figure 9.

Figure 14: Sequence Alignment of EGFR, ErbB2, ErbB3 and ErbB4 Ectodomains. Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA. For alignment on the IGF-1R fragment and assignment of homologous 3D structures, see Figure 9.

Figure 15 Sequence Alignment and Classification of the Disulphide-bonded Modules in the Cys-rich domains of IGF-1R, IR, IRR, EGFR, ErbB2, ErbB3 and ErbB4.

Figure 16. Gel filtration chromatography of insulin receptor ectodomain and MFab complexes. hIR -11 ectodomain dimer (5 - 20 mg) was complexed with MFab derivatives (15-25 mg each) of the anti-hIR antibodies 18-44, 83-7 and 83-14 (Soos et al., 1986). Elution profiles were generated from samples loaded onto a Superdex S200 column (Pharmacia), connected to a BioLogic chromatography system (Biorad) and monitored at 280 nm. The column was eluted at 0.8 ml/min with 40 mM Tris/150 mM sodium chloride/0.02% sodium azide buffer adjusted to pH 8.0: Profile 0, hIR -11ectodomain. Profile 1, ectodomain mixed with MFab 18-44; Profile 2 , ectodomain mixed with MFab18-44 and MFab 83-14; Profile 3, ectodomain mixed with MFab 18-44, MFab 83-14 and MFab 83-7. The apparent mass of each complex was

determined from a plot of the following standard proteins: thyroglobulin (660 kDa), ferritin (440 kDa), bovine gammaglobulin (158 kDa), bovine serum albumin (67 kDa), chicken ovalbumin (44 kDa) and equine myoglobin (17 kDa).

Figure 17. Micrographs of hIR and hIGF-1R ectodomains.(a) Undecorated hIR ectodomain dimer stained with methylamine tungstate showing parallel bars. (b) Undecorated hIR ectodomain dimer stained with uranyl formate, showing well-spaced parallel bars corresponding to the cartoon below. (c) Undecorated hIGF-1R ectodomain dimer stained with uranyl formate. Magnification bars for (a), (b) and (c) 50nm.

Figure 18. Micrographs of hIR and hIGF-1R ectodomains. (a) Thinly stained region of undecorated hIR ectodomain dimers in uranyl formate, showing U-shaped particles (circled) as well as parallel bars as in the cartoon below. (b) Undecorated hIGF-1R ectodomain dimer under similar staining conditions. Magnification bars 50 nm.

Figure 19. hIR ectodomain dimer complexed with MFab 83-7 and stained with KPT. Three projections can be recognised: circled particles have the Fab arms displaced either clockwise as in the cartoon below left,or anticlockwise as in the cartoon below middle; arrowed particles have the Fab arms in a central position, cartoon below right. Magnification bar 50 nm.

Figure 20. hIR ectodomain dimer complexed with MFab 83-7 and stained with uranyl formate showing the parallel bar structure in particles having the Fab arms displaced (circled). Magnification bar 50 nm.

Figure 21. (a) hIR ectodomain dimer complexed with MFab 83-14 stained with potassium phosphotungstate, showing Fab arms attached near the bottom of U-shaped particles (circled). The corresponding cartoon is shown below left. (b) hIR ectodomain dimer complexed with MFab 83-14 stained with uranyl acetate, showing both the view described above (circled) and the parallel-bar view with diagonally projecting Fab arms (arrowed), as in the cartoon below right. Magnification bars 50 nm.

Figure 22 . Double complex of hIR ectodomain dimer with MFabs 83-7 and 18-44 showing particles of complex shape (circled) with four Fab arms attached, consistent with the cartoon below. Magnification bar 50 nm.

Figure 23. Images of hIR ectodomain dimer co-complexed with MFabs 83-7, 83-14 and 18-44 showing examples of complex particles (circled) where it is possible to identify that there are more than four MFabs bound to the dimeric central region. Magnification bar 50 nm.

Figure 24. Schematic illustrating the proposed model of the hIR ectodomain dimer. The dimensions of the molecular envelope are as shown in the diagram, as is the position of the two-fold axis.

Detailed Description of the Invention

We describe herein the expression, purification, and crystallization of a recombinant IGF-1R fragment (residues 1-462) containing the L1-cysteine-rich-L2 region of the ectodomain. The selected truncation position is just downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992. J Biol Chem., 267:10759-10763) and occurs at a position where the sequences of the IR and EGFR families diverge markedly (Ward, C. W., et al.,1995, Proteins: Struct., Funct., Genet. 22:141-153; Lax, I., et al., 1988, Molec. Cellul. Biol. 8:1970-1978) suggesting it represents a domain boundary. To limit the effects of glycosylation, the IGF-1R fragment was expressed in Lec8 cells, a glycosylation mutant of Chinese hamster ovary (CHO) cells, whose defined glycosylation defect produces N-linked oligosaccharides truncated at N-acetyl glucosamine residues distal to mannose residues (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383). Such an approach has facilitated glycoprotein crystallization (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, J., et al., 1996, J. Biol. Chem. 271:33639-33646).

The IGF-1R construct described herein included a c-myc peptide tag (Hoogenboom, H. R., et al.,1991, Nucleic Acids Res. 19:4133-4137) that is recognised by the Mab 9E10 (Evan, G. I., et al., 1985, Mol. Cell. Biol. 5:3610-3616) enabling the expressed product to be purified by peptide elution from an antibody affinity column followed by gel filtration over Superdex S200. The purified proteins crystallized under a sparse matrix screen (Jancarik, J. & Kim, S.-H., 1991, J. Appl. Cryst. 24:409-411) but the crystals were of variable

quality, with the best diffracting to 3.0-3.5Å. Isocratic gradient elution by anion-exchange chromatography yielded protein that was less heterogenous and gave crystals of sufficient quality to determine the structure of the first three domains of the human IGF-1R.

The IGF-1R fragment consisted of residues 1-462 of IGF-1R linked via an enterokinase-cleavable pentapeptide sequence to an eleven residue c-myc peptide tag at the C-terminal end. The fragment was expressed in Lec8 cells by continuous media perfusion in a bioreactor using porous carrier disks. It was secreted into the culture medium and purified by peptide elution from an anti-c-myc antibody column followed by Superdex S200 gel filtration. The receptor fragment bound two anti-IGF-1R monoclonal antibodies, 24-31 and 24-60, which recognize conformational epitopes, but could not be shown to bind IGF-1 or IGF-2. Crystals of variable quality were grown as rhombic prisms in 1.7 M ammonium sulfate at pH 7.5 with the best diffracting to 3.0-3.5 Å. Further purification by isocratic elution on an anion-exchange column gave protein which produced better quality crystals, diffracting to 2.6 Å, that were suitable for X-ray structure determination.

The structure of this fragment (IGF-1R residues 1-462; L1-cys rich-L2domains) has been determined to 2.6 Å resolution by X-ray diffraction. The L domains each adopt a compact shape consisting of a single stranded right-handed β-helix. The cys-rich region is composed of eight disulphide-bonded modules, seven of which form a rod-shaped domain with modules associated in a novel manner. At the centre of this reasonably extended structure is a space, bounded by all three domains, and of sufficient size to accommodate a ligand molecule. Functional studies on IGF-1R and other members of the insulin receptor family show that the regions primarily responsible for hormone-binding map to this central site. Thus this structure gives a first view of how members of the insulin receptor family might interact with their ligands.

Another group has reported the crystallization of a related receptor, the EGFR in a complex with its ligand EGF (Weber, W., et al., 1994, J Chromat. 679:181-189). However difficulties were encountered with these crystals which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure of this complex (Weber, W., et al., 1994, J Chromat 679:181-189) or the generation of accurate models of structurally related receptor domains such as IGF-1R and IR by homology modelling.

The present inventors have applied the same process to the IR and generated a fragment (residues 1-485) that covers the first three domains of the IR. This fragment has been expressed in transformed Lec8 cells, purified, and crystallized by similar methodologies to yield crystals suitable for X-ray diffraction.

The present inventors have therefore developed 3D structural information about cytokine receptors to enable a more accurate understanding of how the binding of ligand leads to signal transduction. Such information provides a rational basis for the development of antagonists or agonists for specific therapeutic applications, something that heretofore could not have been predicted *de novo* from available sequence data.

The precise mechanisms underlying the binding of agonists and antagonists to the IGF-1 receptor site are not fully clarified. However, the binding of the agonists or antagonists to the receptor site, preferably with an affinity in the order of 10^{-8}M or higher, is understood to arise from enhanced stereochemical complementarity, relative to naturally occurring IGF-1 ligands.

Such stereochemical complementarity, pursuant to the present invention, is characteristic of a molecule that matches intra-site surface residues lining the groove of the receptor site as eneumerated by the coordinates set out in Figure 1. The residues lining the groove are depicted in Figure 2. Substances which are complemetary to the shape of the receptor site characterised by amino acids positioned at atomic coordinates set out in Figure 1 may be able to bind to the receptor site and, when the binding is sufficiently strong, substantially prohibit binding of the naturally occurring ligands to the site.

It will be appreciated that it is not necessary that the complementarity between agonists or antagonists and the receptor site extend over all residues lining the groove in order to inhibit binding of the natural ligand. Accordingly, agonists or antagonists which bind to a portion of the residues lining the groove are encompassed by the present invention.

In general, the design of a molecule possessing stereochemical complementarity can be accomplished by means of techniques that optimize, either chemically or geometrically, the "fit" between a molecule and a target receptor. Known techniques of this sort are reviewed by Sheridan and Venkataraghavan, Acc. Chem Res. 1987 20 322; Goodford, J. Med. Chem.

1984 27 557; Beddell, Chem. Soc. Reviews 1985, 279; Hol, Angew. Chem. 1986 25 767 and Verlinde C.L.M.J & Hol, W.G.J. Structure 1994, 2, 577, the respective contents of which are hereby incorporated by reference. See also Blundell et al., Nature 1987 326 347 (drug development based on information regarding receptor structure).

Thus, there are two preferred approaches to designing a molecule, according to the present invention, that complements the shape of IGF-1R or a related receptor molecule. By the geometric approach, the number of internal degrees of freedom (and the corresponding local minima in the molecular conformation space) is reduced by considering only the geometric (hard-sphere) interactions of two rigid bodies, where one body (the active site) contains "pockets" or "grooves" that form binding sites for the second body (the complementing molecule, as ligand). The second preferred approach entails an assessment of the interaction of respective chemical groups ("probes") with the active site at sample positions within and around the site, resulting in an array of energy values from which three-dimensional contour surfaces at selected energy levels can be generated.

The geometric approach is illustrated by Kuntz et al., J. Mol. Biol. 1982 161 269, the contents of which are hereby incorporated by reference, whose algorithm for ligand design is implemented in a commercial software package distributed by the Regents of the University of California and further described in a document, provided by the distributor, which is entitled "Overview of the DOCK Package, Version 1.0,", the contents of which are hereby incorporated by reference. Pursuant to the Kuntz algorithm, the shape of the cavity represented by the IGF-R1 site is defined as a series of overlapping spheres of different radii. One or more extant data bases of crystallographic data, such as the Cambridge Structural Database System maintained by Cambridge University (University Chemical Laboratory, Lensfield Road, Cambridge CB2 1EW, U.K.) and the Protein Data Bank maintained by Brookhaven National Laboratory (Chemistry Dept. Upton, NY 11973, U.S.A.), is then searched for molecules which approximate the shape thus defined.

Molecules identified in this way, on the basis of geometric parameters, can then be modified to satisfy criteria associated with chemical complementarity, such as hydrogen bonding, ionic interactions and Van der Waals interactions.

The chemical-probe approach to ligand design is described, for example, by Goodford, J. Med. Chem. 1985 28 849, the contents of which are hereby incorporated by reference, and is implemented in several commercial software packages, such as GRID (product of Molecular Discovery Ltd., West Way House, Elms Parade, Oxford OX2 9LL, U.K.). pursuant to this approach, the chemical prerequisites for a site-complementing molecule are identified at the outset, by probing the active site (as represented via the atomic coordinates shown in Fig. 1) with different chemical probes, e.g., water, a methyl group, an amine nitrogen, a carboxyl oxygen, and a hydroxyl. Favored sites for interaction between the active site and each probe are thus determined, and from the resulting three-dimensional pattern of such sites a putative complementary molecule can be generated.

The chemical-probe approach is especially useful in defining variants of a molecule known to bind the target receptor. Accordingly, crystallographic analysis of IGF-1 bound to the receptor site may provide useful information regarding the interaction between the archetype ligand and the active site of interest.

A further use of the structure of IGF-1R fragment described here is in facilitating structure determination of a related protein such as a larger fragment of this receptor, another member of the insulin receptor family or a member of the EGF receptor family. This new structure could be either alone or in complex with its ligand. For crystallographic analysis this is achieved using the method of molecular replacement (Brunger, Meth. Enzym. 1997 276 558-580, Navaza and Saludjian, *ibid.* 581-594, Tong and Rossmann, *ibid.* 594-611, Bentley, *ibid.* 611-619) in a program such as XPLOR. In this procedure diffraction data is collected from a crystalline protein of unknown structure. A transform of these data (Patterson function) is compared with a Patterson function calculated from a known structure. Firstly, the one Patterson function is rotated on the other to determine the correct orientation of the unknown molecule in the crystal. The translation function is then calculated to determine the location of the molecule with respect to the crystal axes. Once the molecule has been correctly positioned in the unit cell initial phases for the experimental data may be calculated. These phases are necessary for calculation of an electron density map from which structural differences may be observed and for refinement of the structure. Due to limitations in the method the search molecule must be structurally related to

that which is to be determined. However it is sufficient for only part of the unknown structure (e.g. < 50%) to be similar to the search molecule. Thus the three dimensional structure of IGF-1R residues 1-462 may be used to solve structures consisting of related receptors, enabling a program of drug design as outlined above.

In summary, the general principles of receptor-based drug design can be applied by persons skilled in the art, using the crystallographic results presented above, to produce agonists or antagonists of IGF-1R or other related receptors, having sufficient stereochemical complementarity to exhibit high affinity binding to the receptor site.

The present invention is further described below with reference to the following, non-limiting examples.

EXAMPLE 1

Expression, Purification and Crystalization of the IGF-1R Fragment.

Several factors hamper macromolecular crystallization including sample selection, purity, stability, solubility (McPherson, A., et al., 1995, Structure 3:759-768); Gilliland, G. L., & Ladner, J. E., 1996, Curr. Opin. Struct. Biol. 6:595-603), and the nature and extent of glycosylation (Davis, S. J., et al., 1993, Protein Eng. 6:229-232). Initial attempts to obtain structural data from soluble IGF-1R ectodomain (residues 1-906) protein, expressed in Lec8 cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) and purified by affinity chromatography, produced large, well-formed crystals (1.0 mm x 0.2 mm x 0.2 mm) which gave no discernable X-ray diffraction pattern (unpublished data). Similar difficulties have been encountered with crystals of the structurally related epidermal growth factor receptor (EGFR) ectodomain which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure (Weber, W. et al., 1994, J Chromat 679:181-189). This prompted us to search for a fragment of IGF-1R that was more amenable to X-ray crystallographic studies.

The fragment expressed (residues 1-462) comprises the L1-cysteine-rich-L2 region of the ectodomain. The selected truncation position at Val462 is four residues downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992, J Biol Chem. 267:10759-10763) and occurs at a position where the sequences of the IR and the structurally related EGFR families diverge markedly (Lax, I., et al., 1988, Molec Cell Biol. 8:1970-1978; Ward, C. W., et

al., 1995, Proteins: Struct., Funct., Genet. 22:141-153), suggesting it represents a domain boundary. The expression strategy included use of the pEE14 vector (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163) in glycosidase-defective Lec8 cells (Stanley, P., 1989, Molec. Cellul. Biol. 9:377-383), which produce N-linked oligosaccharides lacking the terminal galactose and N-acetylneuraminic acid residues (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, T., et al., 1996, J Biol Chem 271:33639-33646.). The construct contained a C-terminal c-myc affinity tag (Hoogenboom, H. R., et al., 1991, Nucl Acids Res. 19:4133-4137), which facilitated immunoaffinity purification by specific peptide elution and avoided aggressive purification conditions. These procedures yielded protein which readily crystallized after a gel filtration polish. This provided a general protocol to enhance crystallisation prospects for labile, multidomain glycoproteins.

The structure of this fragment is of considerable interest since it contains the major determinants governing insulin and IGF-1 binding specificity (Gustafson, T. A. & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Andersen, A. S., et al., 1990, Biochemistry, 29:7363-7366; Schumacher, R., et al., 1991, J. Biol. Chem. 266:19288-19295; Schumacher, R., et al., 1993, J. Biol. Chem. 268:1087-1094; Schäffer, L., et al., 1993, J. Biol. Chem. 268:3044-3047; Williams, P. F., et al., 1995, , J. Biol. Chem. 270:3012-3016) and is very similar to an IGF-1R fragment (residues 1-486) reported to act as a strong dominant negative for several growth functions and which induces apoptosis of tumour cells in vivo (D'Ambrosio, C., et al., 1996, Cancer Res. 56:4013-4020).

The expression plasmid pEE14/IGF-1R/462 was constructed by inserting the oligonucleotide cassette:

AatII

5' GACGTC GACGATGACGATAAG GAACAAAAACTCATC

D V D D D D K E Q K L I

(EK cleavage) (c-myc tail)

S E E D L N (Stop)

TCAGAAGAGGATCTGAAT TAGAATTC GACGTC 3'

EcoRI *AatII*

encoding an enterokinase cleavage site, c-myc epitope tag (Hoogenboom, H. R., et al., 1991, Nucleic acids Res. 19:4133-4137) and stop codon into the AatII site (within codon 462) of IGF-1 receptor cDNA in the mammalian expression vector pECE (Ebina, Y., et al., 1985, Cell, 40:747-758; kindly supplied by W. J. Rutter, UCSF, USA), and introducing the DNA comprising the 5' 1521 bp of the cDNA (Ullrich, A., et al., 1986, EMBO J. 5:2503-2512) ligated to the oligonucleotide cassette into the EcoRI site of the mammalian plasmid expression vector pEE14 (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163; Celltech Ltd., UK). Plasmid pEE14/IGF-1R/462 was transfected into Lec8 mutant CHO cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) obtained from the American Tissue Culture Collection (CRL:1737) using Lipofectin (Gibco-BRL). Cell lines were maintained after transfection in glutamine-free medium (Glascow modification of Eagle's medium (GMEM; ICN Biomedicals, Australia) and 10% dialysed FCS (Sigma, Australia) containing 25 μM methionine sulphoximine (MSX; Sigma, Australia) as described (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163). Transfectants were screened for protein expression by Western blotting and sandwich enzyme-linked immunosorbant assay (ELISA) (Cosgrove, L., et al., 1995,) using monoclonal antibody (Mab) 9E10 (Evan et al., 1985) as the capture antibody and either biotinylated anti-IGF-1R Mab 24-60 or 24-31 for detection(Soos et al., 1992; gifts from Ken Siddle, University of Cambridge, UK). Large-scale cultivation of selected clones expressing IGF-1R/462 was carried out in a Celligen Plus bioreactor (New Brunswick Scientific, USA) containing 70 g Fibra-Cel Disks (Sterilin, UK) as carriers in a 1.25 L working volume. Continuous perfusion culture using GMEM medium supplemented with non-essential amino acids, nucleosides, 25 μM MSX and 10% FCS was maintained for 1 to 2 weeks followed by the more enriched DMEM/F12 without glutamine, with the same supplemention for the next 4-5 weeks. The fermentation production run was carried out three times under similar conditions and resulted in an estimated overall yield of 50 mg of receptor protein from 430 L of harvested medium. Cell growth was poor during the initial stages of the fermentation when GMEM medium was employed. but improved dramatically following the switch to the more enriched medium. Target protein productivity was essentially constant during the period from

~100 to 700 h of the 760 h fermentation, as measured by ELISA using Mab 9E10 as the capture antibody and biotinylated Mab 24-31 as the developing antibody.

Soluble IGF-1R/462 protein was recovered from harvested fermentation medium by affinity chromatography on columns prepared by coupling Mab 9E10 to divinyl sulphone-activated agarose beads (Mini Leak; Kem En Tec, Denmark) as recommended by the manufacturer. Mini-Leak Low and Medium affinity columns with antibody loadings of 1.5-4.5 mg/ml of hydrated matrix were obtained, with the loading range of 2.5-3 mg/ml giving optimal performance (data not shown). Mab 9E10 was produced by growing hybridoma cells (American Tissue Culture Collection) in serum-free medium in the Celligen Plus bioreactor and recovering the secreted antibody (4 g) using protein A glass beads (Prosep-A, Bioprocessing Limited, USA). Harvested culture medium containing IGF-1R/462 protein was adjusted to pH 8.0 with Tris-HCl (Sigma), made 0.02% (w/v) in sodium azide and passed at 3-5 ml/min over 50 ml Mab 9E10 antibody columns at 4° C. Bound protein was recovered by recycling a solution of 2-10 mg of the undecamer c-myc peptide EQKLISEEDLN (Hoogenboom et al., 1991) in 20 ml of Tris-buffered saline containing 0.02% sodium azide (TBSA). Between 65% and 75% of the product was recovered from the medium as estimated by ELISA, with a further 15-25% being recovered by a second pass over the columns. Peptide recirculation (~10 times) through the column eluted bound protein more efficiently than a single, slower elution. Residual bound protein was eluted with sodium citrate buffer at pH 3.0 into 1 M Tris HCl pH 8.0 to neutralize the eluant, and columns were re-equilibrated with TBSA.

Gel filtration over Superdex S200 (Pharmacia, Sweden), of affinity-purified material showed a dominant protein peak at ~63 kDa, together with a smaller quantity of aggregated protein (Figure 3a). The peak protein migrated primarily as two closely spaced bands on reduced , sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Figure 3b), reacted positively in the ELISA with both Mab 24-60 and Mab 24-31, and gave a single sequence corresponding to the N-terminal 14 residues of IGF-1R. No binding of IGF-1 or IGF-2 could be detected in the solid plate binding assay (Cosgrove et al., 1995, Protein Express Purif. 6:789-798). The IGF-1R/462 fragment was further purified by ion-exchange chromatography on Resource Q (Pharmacia, Sweden). Using shallow salt gradients, protein enriched in the

slowest migrating SDS-PAGE band was obtained (data not shown), which formed relatively large, well-formed crystals (see below). Isoelectric focusing showed the presence of one major and two minor isoforms. Protein purified on Resource Q with an isocratic elution step of 0.14 M NaCl in 20 mM TrisCl at pH 8.0 (fraction 2, Figure 4) showed less heterogeneity on isoelectric focusing (Figure 4 inset) and SDS-PAGE (data not shown) and produced crystals of sufficient quality for structure determination (see below).

Crystals were grown by the hanging drop vapour diffusion method using purified protein concentrated in Centricon 10 concentrators (Amicon Inc, USA) to 5-10 mg/ml in 10-20 mM Tris-HCl pH 8.0 and 0.02% (w/v) azide, or 100 mM ammonium sulfate and 0.02% (w/v) azide. A search for crystallization conditions was performed initially using the factorial screen (Jancarik, J. & Kim, S.-H.,1991, J Appl Cryst 24:409-411) and subsequently optimised. Crystals were examined on an M18XHF rotating anode generator (Siemens, Germany) equipped with Franks mirrors (MSC, USA) and RAXIS IIC and IV image plate detectors (Rigaku, Japan).

From the initial crystallization screen of this protein, crystals of about 0.1 mm in size grew in one week. Upon refining conditions, crystals of up to 0.6 x 0.4 x 0.4 mm could be grown from a solution of 1.7-2.0 M ammonium sulfate, 0.1 M HEPES pH 7.5. The crystals varied considerably in shape and diffraction quality, growing predominantly as rhombic prisms with a length to width ratio of up to 5:1, but sometimes as rhombic bipyramids, the latter form being favoured when using material which had been eluted from the Mab 9E10 column at pH 3.0. Each crystal showed a minor imperfection in the form of very faint lines from the centre to the vertices. Protein from dissolved crystals did not appear to be different from the protein stock solution when run on an isoelectric focusing gel. Upon X-ray examination, the crystals diffracted to 3.0-4.0 Å and were found to belong to the space group $P2_12_12_1$ with a = 76.8 Å, b = 99.0 Å, c = 119.6 Å. In the diffraction pattern, the crystal variability noted above was manifest as a large (1-2°) and anisotropic mosaic spread, with concomitant variation in resolution. To improve the quality of the crystals, they were grown in the presence of various additives or were recrystallized. These methods failed to substantially improve the crystal quality although bigger crystals were obtained by recrystallization. The variability in crystal quality appeared to be due to protein heterogeneity, as demonstrated by the observation that more

highly purified protein, eluted isocratically from the Resource Q column and showing one major band on isoelectric focusing (Figure 4 inset), produced crystals of sufficient quality for structure determination. These crystals diffracted to 2.6 Å resolution with cell dimensions, a = 77.0 Å, b = 99.5 Å, c = 120.1 Å and mosaic spread of 0.5°. Heavy metal derivatives of the IGF-1R/462 crystals have been obtained and are leading to the determination of an atomic resolution structure of this fragment, which contains the L1, cysteine-rich and L2 domains of human IGF-1R.

EXAMPLE 2

Expression, Purification and Crystalization of the IR Fragment

A similar strategy was adopted for the human insulin receptor. The fragment expressed (residues 1-485) comprises the L1-cysteine-rich-L2 region of the IR ectodomain but extends 13 residues further before the attachment of the 17 residue EK cleavage site linker and c-myc tail. The selected truncation position corresponds to a unique and convenient Bgl II restriction site. The expression strategy was also based on the pEE14 expression vector in glycosidase-defective Lec8 cells and use of a C-terminal c-myc affinity tag for immunoaffinity purification by specific peptide elution. These procedures yielded IR protein which readily crystallized after a gel filtration polish.

The expression plasmid pHIR485 was constructed by ligating the double-stranded oligonucleotide cassette:

```
   Bgl II                                                          Xba I
5' AGATC TCCGACGATGACGATAAG GAACAAAAACTCATCTCAGAAGAGGATCTGAAT TAG TCTAGA 3'
   K  I   S  D  D  D  D  K   E  Q  K  L  I  S  E  E  D  L  N
                EK cleavage          c-myc tail              Stop
```

encoding an enterokinase cleavage site, c-myc epitope tag (Hoogenboom, H. R., et al., 1991, Nucleic acids Res. 19:4133-4137) and stop codon , to the larger 11.1 kilobasepair Bgl II / Xba I fragment isolated from digestion of the mammalian expression plasmid pEH3 (a derivative of the mammalian plasmid expression vector pEE14 [Bebbington, C. R. & Hentschel, C. C. G., 1987. In: Glover, D. M., ed. DNA Cloning. Academic Press. San Diego. Vol 3, p163: Celltech Ltd., UK] which holds the entire coding sequence of human insulin receptor within a Hind III /Xba I fragment). Lec8 mutant CHO cells

(Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) obtained from the American Tissue Culture Collection (CRL:1737) were transfected with pHIR485 using Lipofectamine (Gibco-BRL). Cell lines were maintained after transfection in glutamine-free medium (Glascow modification of Eagle's medium - GMEM; ICN Biomedicals, Australia) and 10% dialysed FCS (Sigma, Australia) containing 25 μM methionine sulphoximine (MSX; Sigma, Australia) as described (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163). Transfectants were screened for protein expression by Western blotting and sandwich enzyme-linked immunosorbant assay (ELISA) (Cosgrove, L., et al., 1995,) using anti-hIR (Mab) 83.7 as the primary antibody and biotinylated monoclonal antibody (Mab) 9E10 (Evan et al., 1985) for detection (Soos et al., 1986; gifts from Ken Siddle, University of Cambridge, UK).

Large-scale cultivation of selected clones expressing IR/485 was carried out in a Celligen Plus bioreactor (New Brunswick Scientific, USA) containing 70 g Fibra-Cel Disks (Sterilin, UK) as carriers in a 1.25 L working volume. Continuous perfusion culture was carried out using DMEM/F12 without glutamine medium (ICN), supplemented with non-essential amino acids, nucleosides, 25 μM MSX and 5 - 10% FCS and resulted in an estimated overall yield of 115 mg of receptor protein from 165 L of harvested medium. Target protein productivity was essentially constant during the fermentation, as measured by ELISA.

Soluble IR/485 protein was recovered from harvested fermentation medium by affinity chromatography on columns of Mab 9E10 essentially as described in Example 1. Between 92 -98% of the product was recovered from the medium by this affinity-chromatography step, as estimated by ELISA.

Gel filtration over Superdex 200 (Pharmacia, Sweden), of the affinity-purified material at 1mg/ml produced a dominant protein peak at apparent mass ~140 kDa (Figure 5a - interpreted as dimer), whereas a peak at apparent mass ~85 kDa was obtained (Figure 5b - interpreted as monomer) at 0.02 mg/ml. The protein migrated as a single broad band of apparent molecular mass ~78 kDa (reduced- lane A) or ~68 kDa (non-reduced - lane B) on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Figure 6a) The IR/485 fragment reacted positively in the ELISA with Mab 83-7, gave a single sequence corresponding to the N-terminal 10 residues of IR, showing several isoforms on isoelectric focussing from pI 6.0 - 6.8 (Figure

6b). Crystallisation screening trials of the fragment produced crystals too small for X-ray diffraction studies. The fragment was further purified by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations (Figure 7). Fractions A and D were each enriched in a component isoform from the ladder of isoforms present in the unfractionated mixture (Figure 6b). Both these fractions produced crystals, whereas no crystals were obtained from fractions B and C.

Crystals were grown by the hanging drop vapour diffusion method using purified protein concentrated in Centricon 10 concentrators (Amicon Inc, USA) to 5-10 mg/ml in 10mM Tris-HCl pH 8.0 and 0.02% (w/v) azide. A search for crystallization conditions was performed initially using the factorial screen (Jancarik, J. & Kim, S.-H.,1991, J Appl Cryst 24:409-411) and subsequently optimised. Crystals were examined on an M18XHF rotating anode generator (Siemens, Germany) equipped with Franks mirrors (MSC, USA) and an RAXIS IIC image plate detector (Rigaku, Japan).

From the initial crystallization screen of this protein fraction D fine needles grew in about one week. In further experiments, crystals of up to 0.04 x 0.04 x 0.2 mm could be grown from a solution of 1.9-2.0 M ammonium sulfate, 2% PEG 400, 0.1 M HEPES pH 7.5. Upon X-ray examination, the crystals diffracted to 4 Å and were found to belong to the space group $P2_12_12_1$ with a = 103.2 Å, b = 130.0 Å, c = 161.6 Å. Despite their small size these crystals diffracted sufficiently well to allow collection of a low resolution data set. Further purification of the protein and refinement of crystallisation conditions should yield larger crystals, providing data to determine the structure of this fragment at medium resolution or better.

EXAMPLE 3

Structure of the IGF-1R/1-462

Crystals were cryo-cooled to-170°C in a mother liquor containing 20% glycerol, 2.2 M ammonium sulfate and 100 mM Tris at pH 8.0. Native and derivative diffraction data were recorded on Rigaku RAXIS IIc or IV area detectors using copper Kα radiation from a Siemens rotating anode generator with Yale/MSC mirroroptics. The space group was $P2_12_12_1$ with a = 77.39 Å, b = 99.72 Å. and c = 120.29 Å. Data were reduced using DENZO and SCALEPACK (Otwinowski, Z. & Minor, W., 1996, Mode.Meth. Enzym. 276:307-326). Diffraction was notably anisotropic for all crystals examined.

Phasing by multiple isomorphous replacement(MIR) was performed with PROTEIN (Steigeman, W. Dissertation (Technical Univ. Munich, 1974) using anomalous scattering for both UO2 and PIP derivatives. Statistics for data collection and phasing are given in Table 1. In the initial MIR map regions of protein and solvent could clearly be seen but the path of the polypeptide was by no means obvious. That map was subject to solvent flattening and histogram matching in DM (Cowtan, K.,1994, Joint CCP4 and ESF-EACBM newslett. Protein Crystallogr. 31:34-38). The structure was traced and rebuilt using O (Jones, T. A., et al., 1991, Acta Crystallogr. A47:110-119) and refined with X-PLOR 3.851 (Brunger, A. T., 1996, X-PLOR ReferenceManual 3.851, Yale Univ., New Haven, CT). After 5 rounds of rebuilding and energy minimisation the R-factor dropped to 0.279 and Rfree = 0.359 for data 7-2.6 Å resolution. The current model contains 458 amino acids and 3 N-linked carbohydrates but no solvent molecules. For residues with B(Ca) > 70 Å2atomic positions are less reliable (37-42, 155-159, 305, 336-341, 404-406,453-458). There is weak electron density for residues 459-461 but the c-myc tail appears completely disordered.

The 1-462 fragment consists of the N-terminal three domains of IGF-1R (L1, cys-rich, L2) and contains regions of the molecule which dictate ligand specificity (17-23). The molecule adopts a reasonably extended structure (approximately 40 x 48 x 105 Å) with domain 2 (cys-rich region) making contact along the length of domain 1 (L1) but very little contact with the third domain (L2) (see Figure 8). This leaves a space at the centre of the molecule of approximately 24 Å x 24 Å x 24 Å which is bounded on three sides by the three domains of the molecule. The space is of sufficient size to accommodate the ligand, IGF-1.

The L domains

Each of the L domains (residues 1-150 and300-460) adopt a compact shape (24 x 32 x 37 Å) consisting of a single-stranded right handed β-helix and capped on the ends by short a-helices and disulfide bonds. The body of the domain looks like a loaf of bread with the base formed from a flat six-stranded β-sheet, 5 residues long and the sides being β-sheets three residues long (Figures 8 & 9). The top is irregular but in places is similar for the two domains. The two domains are superposable with an rms deviation in Ca positions of1.6 Å for 109 atoms (Figure 10). Although this fold is reminiscent of other β-helix proteins it is much simpler and smaller with very few

elaborations and thus it represents a new superfamily of domains. One notable difference between the two domains is that the indole ring of Trp 176 from the cys-rich region (Figure 9b) is inserted into the hydrophobic core of L1 and the C-terminal helix is only vestigial (Figure 8). For the insulin receptor family the sequence motif of residues which form the Trp pocket in L1 does not occur in L2 (Figure 9a). However in the EGF receptor, which has an additional cys-rich region after the L2 domain (14, 15), the pocket motif can be found in both L domains and the Trp is conserved in both cys-rich regions (Figure 9b).

The repetitive nature of the β-helix is reflected in the sequence and the first five turns were correctly identified by Bajaj, M., et al. (1987, Biochim.Biophys. Acta 916:220-226), the conserved Gly residues being found in turns making one bottom edge of the domain. However, their conclusions about the fold were incorrect. The"helix-like" repeat is actually a pair of bends at the top edge of the domain. In their Motif V, the Gly is not in a bend but is followed by the insertion of a conserved loop of 7-8 residues (see Figure 9a). Glycine is structurally important in the Gly bends as mutation of these residues compromises folding of the receptor [van der Vorm, E.R., et al., 1992, J. Biol. Chem. 267, 66-71; Wertheimer, E. et al., 1994, J. Biol. Chem. 269, 7587-7592].

Upon comparing the L domains with other right-handed β-helix structures such as pectate lyase (Yoder, M. D., et al., 1993,.Structure, 1:241-251-1507) and the p22 tailspike protein (Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880) there are some striking similarities as well as differences. In all cases the ends of the domain are capped by α-helices but the L domains also have a disulphide bond at each end to hold the termini. The other β-helix domains are considerably longer and have significant twist to their sheets while the L domains have flat sheets. Although the sizes of the helix repeats are similar (here 24-25 residues vs 22-23 for pectate lyase) the cross-sections are quite different. The L domains have a rectangular cross-section while pectate lyase and p22 tailspike protein are V-shaped and have many, and sometimes quite large, insertions (Yoder, M. D., et al., 1993,.Structure, 1:241-251-1507; Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880). In the hydrophobic core a common feature is the stacking of aliphatic residues from successive turns of the β-helix and near the C-terminus of each L domain there is also a short Asn ladder, reminiscent of the long Asn ladder

observed in pectate lyase (Yoder, M. D., et al., 1993,.Structure 1:241-251-1507). On the opposite side of the L domains the Gly bend as well as the two bends and sheet preceding it have no counterpart in the other β-helix domains. Thus although the L domains are built on similar principles to the other β-helix domains they constitute a separate superfamily.

The cys-rich domain

The cys-rich domain is composed of eight disulfide-bonded modules (Figure 9b), the first of which sits at the end of L1 while the remainder make a curved rod running diagonally across L1 and reaching to L2 (Figure 8). The strands in modules 2-7 run roughly perpendicular to the axis of the rod in a manner more akin to laminin (Stetefeld, J., et al.,1996, J.Mol.Biol. 257:644-657) than to TNF receptor (Banner, D. W., et al., 1993, Cell, 73:431-445) but the modular arrangement of the cys-rich domain is different to other cys-rich proteins for which structures are known. The first 3 modules of IGF-1R have a common core, containing a pair of disulfide bonds, but show considerable variation in the loops (Figure 9b). The connectivity of these modules is the same as the first half of EGF (Cys 1-3and 2-4) but their structures do not appear to be closely related to any member of the EGF family. Modules 4 to 7 have a different motif, β-finger, and best match residues 2152-2168 of fibrillin (Dowling, A. K., et al., 1996, Cell, 85:597-605). Each is composed of three polypeptide strands, the first and third being disulfide bonded and the latter two forming a β-ribbon. The β-ribbon of each β- finger module lines up antiparallel to form a tightly twisted 8-stranded β-sheet (Figures 8 and 11). Module 6 deviates from the common pattern with the first segment being replaced by an α-helix followed by a large loop that is likely to have a role in ligand binding (see below). As module 5 is most similar to module 7 it is possible that the four modules arose from serial gene duplications. The final module is a disulfide linked bend of five residues.

The fact that the two major types of cys-rich modules occur separately implies that these are the minimal building blocks of cys-rich domains found in many proteins. Although it can be as short as 16 residues, the motif of modules 4-7 is clearly distinct and capable of forming a regular extended structure. Thus cys-rich domains such as these can be considered as made of repeat units each composed of a small number of modules.

Hormone binding

Attempts have been made to locate the IGF-1 (and insulin) binding site by examining natural (Taylor, S. I., 1992, Diabetes, 41:1473-1490) and site-directed mutants (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016; Mynarcik, D. C et al., 1996, J. Biol. Chem. 271:2439-2442; Mynarcik, D. C., et al., 1997, J. Biol. Chem. 272:2077-2081), chimeric receptors (Andersen, A. S., et al., 1990, Biochemistry 29:7363-7366; Gustafson, T. A., & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Schäffer, L., et al.,1993, J. Biol. Chem. 268:3044-3047; Schumacher, R., 1993, J. Biol. Chem. 268:1087-1094; Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408) and by crosslinking studies (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258; Fabry, M., 1992, J. Biol. Chem. 267:8950-8956; Waugh, S. M., et al., 1989, Biochemistry, 28:3448-3458; Kurose, T., et al., 1994),.J. Biol. Chem.269:29190-29197-34). IGF-1R/IR chimeras not only show which regions of the receptors account for ligand specificity but also provide an efficient means of identifying some parts of the hormone binding site. Paradoxically regions controlling specificity are not the same for insulin and IGF-1. Replacing the first 68 residues of IGF-1R with those of IR confers insulin binding ability on the chimeric IGF-1R (Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408) and replacing residues 198-300 in the cys-rich region of IR with the corresponding residues 191-290 of IGF-1R allows the chimeric receptor to bind IGF-1 (Schäffer, L., et al.,1993, J. Biol. Chem. 268:3044-3047). Thus a receptor can be constructed which binds both IGF-1 and insulin with near native affinity. From the structure it is clear that if the hormone bound in the central space it could contact both these regions.

From analysis a series of chimeras examined by Gustafson, T. A., & Rutter, W. J. (J. Biol. Chem. 265:18663-18667, 1990) the specificity determinant in the cys-rich region can be limited further to residues 223-274. This region corresponds to modules 4-6 and includes a large and somewhat mobile loop (residues 255-263, mean B[Ca atoms] = 57 Å2) which extends into the central space (see Figure 8). In IR this loop is four residues bigger and is stabilised by an additional disulfide bond (Schäffer, L. & Hansen, P.H..1996, Exp. Clin. Endocrinol. Diabetes, 104: Suppl. 2, 89). The larger loop of IR may serve to exclude IGF-1 from the hormone binding site but allow the smaller insulin molecule to bind. It is interesting to note that mosquito IR homologue, which has a loop two residues larger than the

mammalian IRs, also appears to bind insulin but not IGF-1 (Graf, R., et al., 1997, Insect Molec.Biol. 6:151-163). Analysis of the structure indicates that the insulin/IGF-1 specificity is controlled by residues in this loop (amino acids 253-272 in IGF-1R; amino acids 260-283 in IR)

As chimeras only address residues which differ between the two receptors a more precise analysis of the site can be obtained from single site mutants. In particular, from an alanine-replacement study, four regions of L1 important for insulin binding were identified (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016). The first three are at similar positions on successive turns of the b-helix and the fourth lies on the conserved bulge on the large b-sheet (Figure 12). Thus there is a footprint for insulin binding to the L1 domain which lies on the first half of large b-sheet facing into the central space. Residues further along the sheet which are conserved in IGF-1R and could also be important. The conservative substitution of leucine for methionine at residue 119 of IR (113 of IGF-1R) causes a mild form of leprechaunism [Hone, J. et al., 1994, J. Med. Genet. 31, 715-716]. This residue is buried and the mutation could perturb neighbouring residues to affect insulin binding.

The axis of the L2 domain is perpendicular to that of the L1 domain and N-terminal end of its β-helix is presented to the hormone-binding site. On this face of the L2 domain the only mutation studied so far is the naturally occurring IR mutant, S323L, which gives rise to Rabson-Mendehall syndrome and severe insulin resistance (Roach, P.,1994, Diabetes 43:1096-1102). As this mutant only affects insulin binding and not cell-surface expression, residue 323 of IR (residue 313 of IGF-1R) is probably at or near the binding site. Structurally this residue lies in the middle of a region (residues 309-318 of IGF-1R) which is conserved in both IR and IGF-1R and the surrounding region, 332-345 (of IGF-1R), is also quite well conserved in the these receptors (Figure 9a). Therefore this region is quite likely to form part of the hormone-binding site but would not have been detected by chimeras. It is interesting to note that in this region IRR is not as well conserved as the other two receptors (Shier, P. & Watt, V.M., 1989, J.Biol.Chem. 264:4605-14608).

The distance from this putative hormone-binding region on L2 to that found on L1 is about 30 Å (Figure 8). Thus L1 and L2 appear too far apart to bind IGF-1 or insulin. However, in the crystal structure there is a deep cleft

between part of the cys-rich domain (residue 262)and L2 (residue 305) and this cleft is occupied by a loop from a neighbouring molecule. Thus it seems probable that the position of the L2 domain in the receptor structure or the hormone-receptor complex adopts a different position with respect to the cys-rich domain than that found in the crystal. The movement required to bring L2 sufficiently close to L1 is small, namely a rotation of approximately 25° about residue 298.

A number of IR mutants have been identified which constitutively activate the receptor and the majority of these are found in the α chain. Curiously all α chain mutants involve changes to or from proline or the deletion of an amino acid, implying that they cause local structural rearrangements. The mutation R86N is similar to wild type but R86P reduces cell-surface expression and insulin binding while constitutively activating autophosphorylation [Grønskov, K. et al., 1993, Biochem. Biophys. Res. Commun. 192, 905-911]. The proline mutation probably disturbs residues preceding 87 which lie in the interface between the L1 and cys-rich domains but it could also affect insulin binding. In the cys-rich domain residues 233, 281, 244 and 247 of IR are not conserved in IGF-1R (Figure 9b) yet L233P [Klinkhamer, M.P. et al., 1989, EMBO J. 8, 2503-2507], deletion of N281 [Debois-Mouthon, C. et al., 1996, J. Clin. Endochronol. Metab. 81, 719-727] or the triple mutant P243R, P244R and H247D [Rafaeloff, R. et al., 1989, J. Biol. Chem. 264, 15900-15904] cause constitutive kinase activation. Due to their locations each of these three mutants appears likely to compromise the folding of a β-finger domain and, in turn, the structural integrity of the rod-like cys-rich domain. The structural ramifications of these mutations could be significant for the whole receptor ectodomain as disturbing the L1/cys-rich interface or distorting the rod-like domain could affect the relative position of L1 and the cys-rich domain in this context.

L1 has been further implicated as deletion of K121 on the opposite side of L1 from the cys-rich domain was also found to cause autophosphorylation [Jospe, N. et al., 1994, J. Clin. Endochronol. Metab. 79, 1294-1302]. By contrast this mutation does not affect insulin binding. Thus a possible mechanism emerges for insulin binding and signal transduction. When insulin binds between L1 and L2 it modifies the relative position of L1 and the cys-rich domain in the receptor, perhaps by hinge motion between L2 and the cys-rich domain like that suggested above, and the structural

rearrangement is transmitted across the plasma membrane. In the absence of insulin the same signal can be initiated by mutations in the cys-rich region or at the L1/cys-rich interface but at the expense on insulin binding. The signal can also be initiated more directly by mutations on the opposite side of L1 which affect the interaction of L1 with other parts of the ectodomain, possibly the other half of the receptor dimer.

Ligand Studies

Although there is no structural information about an IGF-1/IGF-1R complex a number of studies have probed the nature of this interaction. Results from cross-linking experiments with IGF-1 and insulin and their cognate receptors are consistent with the hormone binding site proposed above. For example B29 of insulin can be cross-linked to the cys-rich region (residues 205-316((Yip, C. C., et al., 1988, Biochim. Biophys. Res. Commun. 157:321-329) or the L1 domain (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258). However these two regions are reasonably well separated and those studies may indicate that B29 is mobile. Other studies unfortunately do not map the site any more precisely.

Analogues and site-directed mutants of IGF-1 and -2 have been more fruitful. Relative to insulin IGF-1 and -2 contain two extra regions, the C region between B and A and a D peptide at the C-terminus. For IGF-1 replacement of the C region by a four Gly linker reduced affinity for IGF-1R by a factor of 40 but increased affinity for IR 5-fold (Bayne, M.L.,et al., 1988, J. Biol.Chem. 264:11004-11008). Changes in affinity are consistent with the deletion in IGF-1 complementing differences in the cys-rich regions of IGF-1R and IR noted above. Mutation of residues either side of the C region (residue 24 for IGF-1 [Cascieri, M.A., et al., 1988, Biochemistry 27:3229-3233], residues 27,43 for IGF-2, [Sakano, K., et al., 1991, J. Biol. Chem. 266:20626-20635]) also have deleterious effects on the affinity of the hormone forIGF-1R as has truncation of the nearby D peptide in IGF-2 (Roth, B.V., et al., 1991, Biochem. Biophys. Res. Commun. 181:907-914). Insulin has been extensively mutated. Binding studies [summarised in Kristensen, C. et al., 1997, J. Biol. Chem. 272, 12978-12983] indicate that insulin may bind its receptor via a hydrophobic patch (residues A2, A3, A19, B8, B11, B12, B15 and possibly B23 & B24). However this patch is normally buried and requires the removal of the B chain's C-terminus from the observed position. Assuming IGF-1, -2 and insulin bind their receptors in the same

orientation, these data suggest an approximate orientation for the hormone when bound to the receptor.

One notable feature of IGF-1 and -2 is the large number of charged residues and their uneven distribution over the surface. Basic residues are predominantly found in the C region and, in solution, this region is not well ordered in either IGF-1 or -2 (Sato, A., et al., 1993, Int J Peptide Protein Res. 41:433-440; Torres, A. M., et al., 1995,J. Mol. Biol. 248:385-401). In contrast the binding site of the receptor has a sizable patch of acidic residues in the corner where the cys-rich domain departs from L1. Other acidic residues which are specific to this receptor are found along the inside face of the cys-rich domain and the loop (residues 255-263) extending from module 6. Thus it is possible that electrostatics play an important part in IGF-1 binding with the C region binding to the acidic patch of the cys-rich region near L1 and the acidic patch on the other side of the hormone directed towards a small patch of basic residues (residues 307-310) on the N-terminal end of L2.

Although the structure of this fragment gives significant information about the nature of the hormone binding site, residues outside this region have also been shown to affect binding of ligand. A number of studies have implicated residues 704-715 of IR (Mynarcik, D. C et al., 1996, J. Biol. Chem. 271, 2439-2442; Kurose, T., et al., 1994, J. Biol. Chem.269:29190-29197). These residues could contact insulin on one of the sides left open in the current structure. Using insulin labelled at the B1 residue, Fabry, M., et al.,(1992, J. Biol. Chem. 267:8950-8956) cross linked insulin to the fragment 390-488, part of which is not near the site as described. The explanation for this could be either 488 reaches back to the hormone binding site, or this region could contact another hormone bound to the other half of the receptor. Further structural information is needed to establish how these other regions contact the hormone and to elucidate how binding of the hormone is communicated to the kinase inside the cell.

The structure of the L1-cys-rich-L2 domains of IGF-1R presented here represents the first structural information for the extracellular portion of a member of the insulin receptor family. The L domains display a novel fold which is common to the EGF receptor family and the modular architecture of the cys-rich domain implies that smaller building blocks should be used to describe the composition of cysteine-rich domains. This fragment contains the major specificity determinants of receptors of this class for their ligands.

It has an elongated structure with a space in the middle which could accommodate the ligand. The three sides of this site correspond to regions which have been implicated in hormone binding. Although other sites are present in the receptor ectodomain which interact with the ligand this structure gives us an initial view of how the insulin, IGF-1 and -2 might interact with their cell surface receptors to control their metabolic and mitogenic effects

Such information will provide valuable insight into the structure of the corresponding domains of the IR and insulin receptor-related receptor as well as members of the related EGFR family (Bajaj, M., et al., 1987, Biochim Biophys Acta 916:220-226; Ward, C. W. et al., 1995, Proteins: Struct Funct Genet 22:141-153).

EXAMPLE 4

Prediction of 3D Structure of the Corresponding Domains of IRR and IR Based on Structure of IGF-1R Frgament.

The sequence identities between the different members of the insulin receptor family are sufficient to allow accurate sequence alignments to facilitate 3D structure predictions by homology modelling. The alignments of the ectodomains of human IGF-1R, IR, and IRR are shown in Figure 13.

EXAMPLE 5

Prediction of 3D Structure of EGFR and its Family Members ERB2, ERB3 and ERB4.

The sequence identities between the different members of the EGFR receptor family and the insulin receptor family are sufficient to allow accurate sequence alignments to facilitate 3D structure predictions by homology modelling. The alignments of the ectodomains of human EGFR, ERB2, ERB3 and ERB4 are shown in Figure 14. The ectodomains of the EGFR family members are composed of four domains : L1 domain. cys-rich domain, L2 domain and a second cys-rich domain all of which can be modelled from the structure of the IGF-1R fragment residues 1-462.

The sequence alignment analysis and characterization of the repeat modules in the cys-rich region of IGF-1R and the homologous regions of the

IR, IRR and the first and second cys-rich regions of EGFR, ErbB2, ErbB3 and ErbB4 are shown in Figure 15. A representative of each subtype of cys repeat is found in the IGF-1R fragment 1-462 and is used to model each of these modules in the other receptors. Note the nature and order of modules in the second cys-rich repeat of the EGFR family is different to that seen in the first cys-rich region.

EXAMPLE 6

Single-Molecule Imaging of Human Insulin Receptor Ectodomain and its Fab Complexes

Cloning and expression of hIR -11 ectodomain protein

A full length clone of the human IR exon -11 form (hIR -11) was prepared by exchanging an Aat II fragment, nucleotides 1195 to 2987 , of the exon +11 clone (plasmid pET; Ellis et al., 1986; gift from Dr W. J. Rutter, UCSF) of hIR (Ebina et al., 1985, *Cell* **40**, 747-758) with the equivalent Aat II fragment from a plasmid (pHIR/P12-1, ATCC 57493) encoding part of the extracellular domain and the entire cytoplasmic domain of hIR -11 (Ullrich et al., 1985, *Nature* **313** , 756-761). The ectodomain fragment of hIR -11 (2901 bp, coding for the 27 residue signal sequence and residues His1-Asn914) was produced by SalI and SspI digestion and inserted into the mammalian expression vector pEE6.HCMV-GS (Celltech Limited, Slough, Berkshire, UK) into which a stop codon linker had been inserted, as described previously (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798) for the hIR exon +11 ectodomain.

The resulting recombinant plasmid pHIR II (2 μg) was transfected into glycosylation deficient Chinese hamster ovary (Lec 8) cells (Stanley, 1989, *Molec. Cellul. Biol.* **9**, 377-383) with Lipofectin (Gibco-BRL). After transfection, the cells were maintained in glutamine-free medium GMEM (ICN Biomedicals, Australia) as described previously (Bebbington & Hentschel, 1987, In *DNA Cloning* (Glover, D., ectodomain.), Vol III, Academic Press, san Diego; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798). Expressing cell lines were selected for growth in GMEM with 25 μM methionine sulphoximine (MSX, Sigma). Transfectants were screened for protein expression using sandwich ELISA with anti-IR monoclonal antibodies 83-7 and 83-14. Metabolic labelling of cells, immunoprecipitations, insulin binding assays and Scatchard analyses were performed as described

previously for the exon +11 form of hIR ectodomain (Cosgrove et al., 1995, , *Protein Expression and Purification* **6**, 789-798).

hIR -11 ectodomain production and purification

The selected clone (inoculum of 1.28 x 108 cells) was grown in a spinner flask packed with 10 g of Fibra-cel disc carriers (Sterilin, U.K.) in 500 ml of GMEM medium containing 10% fetal calf serum (FCS) and 25 μM MSX. Selection pressure was maintained for the duration of the culture.

Ectodomain was recovered from harvested media by affinity chromatography on immobilized insulin and further purified by gel filtration chromatography on Superdex S200 (Pharmacia; 1 x 40 cm) in Tris-buffered saline containing 0.02% sodium azide (TBSA) as described previously (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798). Solutions of purified hIR -11 ectodomain were stored at 4° C prior to use.

Production of Fab fragments and their complexes with ectodomain

Purification of Mabs 83-7, 83-14 and 18-44 from ascites fluid by affinity chromatography using Protein A-Sepharose, and the production of Fabs, were based on the methodologies described in Coligan et al.,1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons. Fab was produced from monoclonal antibody by mercuripapain digestion for 1-4 h, followed by gel filtration on Superdex S200. Products were monitored by reducing and non-reducing SDS-PAGE. For 83-7 Mab, an IgG Type 1 monoclonal antibody, the bivalent (Fab)2' isolated by this method was reduced to monovalent Fab 83-7 by mild reduction with mM L-cysteine.HCl in 100 mM Tris pH 8.0 (Coligan et al., 1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons).

Complexes of Fab with hIR -11 ectodomain were produced by mixing ~ 2.5 to 3.5 molar excess of Fab with hIR -11 ectodomain at ambient temperature in TBSA at pH 8.0. After 1-3 h, the complex was separated from unbound Fab by gel filtration over a Superdex S200 column in the same buffer.

Electron microscopy

Uncomplexed hIR -11 ectodomain and the Fab complexes described above were diluted in phosphate-buffered saline (PBS) to concentrations of the order of 0.01-0.03 mg/ml. Prior to dilution, 10% glutaraldehyde (Fluka) was added to the PBS to achieve a final concentration of 1% glutaraldehyde.

Droplets of ~ 3ml of this solution were applied to thin carbon film on 700-mesh gold grids after glow-discharging in nitrogen for 30 s. After 1 min. the excess protein solution was drawn off and followed by application and withdrawal of 4-5 droplets of negative stain [2% uranyl acetate (Agar), 2% uranyl formate (K and K), 2% potassium phosphotungstate (Probing and Structure) adjusted to pH 6.0 with KOH, or 2% methylamine tungstate (Agar) adjusted to pH 6.8 with NH4OH]. In the case of both uranyl acetate and uranyl formate staining, an intermediate wash with 2 or 3 droplets of PBS was included prior to application of the stain. The grids were air-dried and then examined at 60kV accelerating voltage in a JEOL 100B transmission electron microscope at a magnification of 100,000x. It was found that there was a typical thickness of negative stain in which Fabs were most easily seen, hence areas for photography had to be chosen from particular zones of the grid. Electron micrographs were recorded on Kodak SO-163 film and developed in undiluted Kodak D19 developer. The electron-optical magnification was calibrated under identical imaging conditions by recording single-molecule images of the antigen-antibody complex of influenza virus neuraminidase heads and NC10 MFab (Tulloch et al., 1986, *J.Mol. Biol.* **190**, 215-225; Malby et al., 1994, *Structure*, **2**, 733-746).

Image processing

Electron micrographs showing particles in a limited number of identifiable projections were chosen for digitisation. Micrographs were digitised on a Perkin-Elmer model 1010 GMS PDS flatbed scanning microdensitometer with a scanning aperture (square) size of 20 mm and stepping increment of 20 mm corresponding to a distance of 0.2 nm on the specimen. Particles were selected from the digitised micrograph using the interactive windowing facility of the SPIDER image processing system (Frank et al., 1996, *J. Struct. Biol.* **116**, 190-199). Particles were scaled to an optical density range of 0.0 - 2.0 and aligned by the PSPC reference-free alignment algorithm (Marco et al., 1996, *Ultramicroscopy*, **66**, 5-10). Averages were then calculated over a subset of correctly aligned particles chosen interactively as being representative of a single view of the particle. The final average image presented here is derived from a library of 94 images.

Biochemical characterization of expressed hIR -11 ectodomain

The recombinant protein examined corresponded to the the first 914 residues of the 917 residue ectodomain of the exon -11 form of the human

insulin receptor (Ullrich et al., 1986, *Nature* **313** , 756-761). Expressed protein was shown, by SDS-PAGE and autoradiography of immunoprecipitated product from metabolically labelled cells, to exist as a homodimeric complex of ~270 - 320 kDa apparent mass, which dissociated under reducing conditions into monomeric α and β' subunits of respective apparent mass ~120 kDa and ~35 kDa (data not shown).

Purified hIR -11 ectodomain, expressed in Lec8 cells and purified by affinity chromatography on an insulin affinity column, ran as a symmetrical peak on a Superdex S200 gel filtration column (Figure 16). The protein eluted with an apparent mass of ~400 kDa, calculated from a standard curve generated by the elution positions of standard proteins (not shown). As expected for protein expressed in Lec 8 cells, whose glycosylation defect produces truncated oligosaccharides (Stanley, 1989, . *Molec. Cellul. Biol.* **9**, 377-383), this value is less than the apparent mass (450 - 500 kDa) reported for hIR +11 ectodomain expressed in wild-type CHO-K1 cells (Johnson et al., 1988, *Proc. Natl Acad. Sci USA* **85**, 7516-7520; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798).

Radioassay of insulin binding to purified ectodomain gave linear Scatchard plots and Kd values of 1.5 - 1.8 x 10-9 M, similar to the values of 2.4 - 5.0 x 10-9 M reported for the hIR -11 ectodomain (Andersen et al., 1990, *Biochemistry* **29**, 7363-7366; Markussen et al., 1991, *J. Biol. Chem.* **266**, 18814-18818; Schaffer, 1994, *Eur. J. Biochem.* **221**, 1127-1132) and the values of ~1.0 - 5.0 x 10-9 M reported for the hIR +11 ectodomain (Schaefer et al., 1992, *J. Biol. Chem.* **267**, 23393-23402; Whittaker et al., 1994, *Molec. Endocrinol.* **8**, 1521-1527; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798).

Expression of hIGF-1R ectodomain

Cloning, expression and purification of this protein used elements common to those described for hIR -11 ectodomain (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798) and resulted in purified product that was recognised by receptor-specific Mabs 17-69, 24-31 and 24-60 (Soos et al., 1992, *J. Biol. Chem.* **267**, 12955-63) and was composed of α and β' subunits of mass similar to those of hIR ectodomain (unpublished data).

Preparation of hIR -11 ectodomain/MFab complexes

A complex of hIR -11 ectodomain and Fab from antibody 83-14 eluted as a symmetrical peak of 460 -500 kDa (Figure 16), as did complexes

generated from a mixture of hIR -11 ectodomain with Fab from antibody 18-44 and a mixture of hIR -11 ectodomain with Fab 83-7 (not shown). A co-complex of ectodomain with Fabs from antibodies 18-44 and 83-14 eluted at ~ 620 kDa (Figure 12), as did a co-complex with MFabs 83-14/83-7 and another with MFabs 83-7/18-44 (not shown). A complex of hIR -11 ectodomain with all three MFab derivatives, 18-44, 83-7 and 83-14, eluted at an apparent mass of ~ 710 kDa (Figure 16).

Electron microscopy

Imaging of hIR -11 and hIGF-1R ectodomains

Single-molecule imaging of undecorated dimeric hIR -11 ectodomain was carried out under a variety of negative staining conditions, which emphasised different aspects of the structure of the molecular envelope. The least aggressive or penetrative stain was potassium phosphotungstate (KPT) , which revealed consistent globular particles with very little internal structure other than a suggestion of a division into two parallel bars. Staining with methylamine tungstate also revealed the parallel bar images, as shown in Figure 17a.

Further investigation using progressively more penetrative, but also potentially more disruptive, stains confirmed the observations above. Staining with uranyl acetate and uranyl formate showed the separation of the parallel bars most clearly (Figure 17b), but uranyl acetate showed evidence of disrupting the structure of the particles, i.e. a decrease in the consistency of the particle shape and a tendency for particles to look unravelled or denatured despite having been subjected to chemical cross-linking prior to staining. In areas of thicker stain, parallel bars predominated (Figure 17b), whereas in more thinly stained regions, U-shaped particles could be identified, sometimes outnumbering the parallel-bar structures (Figure 18a). An averaged image of the parallel bars seen by staining hIR -11 ectodomain with uranyl formate is shown as an insert in Figure 17b.

In Figures 17c and 18b, images of hIGF-1R ectodomain are shown for comparison with Figure 17b and 18a, respectively, under similar staining conditions.

Imaging of hIR -11 ectodomain complexed with 83-7 MFab

This complex was particularly noteworthy for the consistency of the form of the particles, especially under the gentler staining conditions afforded by stains such as KPT and methylamine tungstate. The particles

were interpreted as having been restricted in the views they presented, after air-drying on the carbon support film, by the almost diametrically opposite binding of the two Fab arms to the antigen to form a highly elongated complex structure. Under these conditions three distinct views could be recognised as shown in Figure 19. Two views (interpreted as top-down/bottom-up) show the Fab arms displaced clockwise or anti-clockwise as extensions of the parallel plates with two-fold symmetry. The third view shows an image with the two Fab arms in line roughly through the centre of the receptor on its opposite sides, interpreted as a side projection of binding half-way up the plates (Figure 19).

Figure 20 shows a field of particles of hIR -11 ectodomain complexed with 83-7 MFab, stained with uranyl formate.The use of the more aggressive uranyl stains operating at lower pHs revealed internal structure of the molecular envelope at the expense of consistency of the particle morphology. For example, staining with uranyl acetate or uranyl formate showed that parallel bars can be seen in particles in which the Fab arms are displaced either clockwise or anticlockwise but not where the intermediate central or axial position of the two Fab arms is presented in projection. These observations show 83-7 MFab binding roughly half-way up the side-edge of each hIR -11 ectodomain plate. The epitope recognised by Mab 83-7 has been mapped to the cys-rich region, residues 191-297, by analysis of chimeric receptors (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* **88**, 9858-9862).

Imaging of hIR -11 ectodomain complexed with either 83-14 MFab or 18-44 MFab

Figure 21a shows the complexes formed with Fabs from the most insulin-mimetic antibody Mab 83-14. Projections showing the Fab arms bound to and extending out from near the base of the U-shaped particles can be identified. A second field of particles (Figure 21b) shows objects composed of two parallel bars as observed for the undecorated ectodomain, with Fab arms projecting obliquely from diametrically opposite extremities. Similar but less definitive images were also seen when MFab 18-44 was bound to hIR -11 ectodomain (not shown). The epitope for Mab 83-14 is between residues 469-592 (Prigent et al., 1990) in the connecting domain. This domain contains one of the disulphide bonds (Cys524-Cys524) between

the two monomers in the IR dimer (Schaffer and Ljungqvist, 1992, *Biochem. Biophys. Res. Commun.* **189,** 650-653). The epitope for Mab 18-44 is a linear epitope, residues 765-770 (Prigent et al., 1990, . *J. Biol. Chem.* **265,** 9970-9977) in the β-chain, near the end of the insert domain (O'Bryan et al., 1991, *Mol. Cell. Biol.* **11,** 5016-5031). The insert domain contains the second disulphide bond connecting the two monomers in the IR dimer (Sparrow et al., 1997, *J. Biol. Chem.*, 272, 29460-29467).

Imaging of hIR -11 ectodomain co-complexed with two different MFabs per monomer

The double complex of hIR -11 ectodomain with MFabs 83-7 and 18-44 was stained with 2% KPT at pH 6.0, and revealed the molecular envelopes shown in Figure 22. The particle appears complex in shape and can assume a number of different orientations on the carbon support film, giving rise to a number of different projections in the micrograph. The predominant view is of an asymmetric X-shape (some examples circled). It shows the 83-7 MFab arms bound at opposite ends of the parallel bars with the two 18-44 MFabs appearing as shorter projections extending out from either side of each ectodomain.

Images of the double complex of hIR -11 ectodomain with 83-7 and 83-14 MFabs gave X-shaped images similar to those seen with the 83-7/18-44 double complex (not shown). In contrast the double complex of hIR -11 ectodomain with 18-44 and 83-14 MFabs did not present the characteristic asymmetric X-shapes described above (images not shown). Instead, the molecular envelope appeared to be elongated in many views, with only an occasional X-shaped projection. While a detailed interpretation of these images would be premature, it is clear that MFabs 18-44 and 83-14, two of the more potent insulin mimetic antibodies (Prigent et al., 1990, *J. Biol. Chem.* 265, 9970-9977), can bind simultaneously to the receptor.

Imaging of hIR -11 ectodomain co-complexed with three different MFabs per monomer

Figure 23 shows a field of particles from a micrograph of hIR -11 ectodomain complexed simultaneously with MFabs 83-7, 83-14 and 18-44. In the thicker stain regions the molecular envelope is X-shaped. and looks very similar to that of the double complexes of hIR -11 ectodomain with either 83-7 and 18-44 or 83-7 and 83-14. However, in the more thinly stained regions, particles of greater complexity are visible and it is possible occasionally to

identify that there are in fact more than four MFabs bound to the ectodomain dimer.

The single-molecule imaging of hIR -11 ectodomain presented here suggests a molecular envelope for this dimeric species significantly different from that of any previously published study. However, an unequivocal determination of the molecular envelope even from the present study is not entirely straightforward. A major complicating factor here has been the relative fragility of the expressed ectodomain when exposed to the rigors of electron microscope preparation by negative staining. For example, staining with potassium phosphotungstate (KPT, pH 6.0-7.0) frequently suggested a denaturation of the dimeric molecules, but when appropriate conditions were satisfied, good seemingly interpretable molecular envelope images were achieved; staining with methylamine tungstate (pH ~7.0) supported the best KPT molecular envelope images, but had the suggestion of a swelling of the molecular structure at neutral pH; and the acid-pH stains of uranyl acetate (pH ~4.2) and uranyl formate (pH~3.0), with their ability to penetrate the ectodomain structure, appeared to illuminate not so much the molecular envelope as the zones of high projected protein density within the dimer.

An amalgam of impressions from these various staining regimens has led to the following interpretation of single-molecule images of these undecorated, or naked, dimers: the predominant dimeric molecular image encountered here has been that of 'parallel bars'of projected protein density. This view is so predominant, indeed, that it suggests there is either a single preferred orientation of the molecules on the glow-discharged carbon support film, or that this impression of parallel bars of density may represent a mixture of superficially similar structure projections, with the subtleties of these different projections being masked by the relatively coarse resolution of this single-molecule direct imaging. The impression of parallel bars of projected protein density is particularly predominant in regions of thicker negative stain. A second view of the molecular envelope, appreciably less well represented in regions of thicker stain but predominant in regions of thin staining, is that of 'open' U's, or V's. These two views of hIR -11 ectodomain were supported by the single-molecule imaging of hIGF-1R ectodomain under comparable conditions of negative staining.

If the assumption is made that these two recognisable projected views, that of parallel bars and of open U's/V's, are different views of the

same dimeric molecule, an assumption strongly supported by the MFab complex imaging, a coarse model of the molecular envelope can be rationalized as in the schematic Figure 24. The model structure is roughly that of a cube, composed of two almost-parallel plates of high protein density, separated by a deep cleft of low protein main-chain and side-chain density able to be penetrated by stain, and connected by intermediate stain-excluding density near what is assumed here to be their base (that is, nearest the membrane-anchoring region). The width of the low-density cleft appears to be of the order of 30-35Å, sufficient to accommodate the binding of the insulin molecule of diameter ca. 30Å, although we have no electron microscopical evidence to support insulin-binding in this cleft at this stage.

It has been established through imaging of bound 83-7 MFab that there is a dimeric two-fold axis normal to the membrane surface between these plates of density. Occasionally, dimer images display a relative displacement of the bars of density, interpreted here as a limited capacity for a shearing of the interconnecting zone between the two plates along their horizontal axis parallel to the membrane; other images show bars skewed from parallel, implying a limited capacity for the plates to rotate independently around the two-fold axis, again via this interconnecting zone. These two observations each suggest a relatively flexible connectivity between the dimer plates in the membrane-proximal region of intermediate protein density, which could possibly contribute to the transmembrane signalling process.

The approximate overall measured dimensions of the ectodomain dimer depicted in Figure 24 are 110 x 90 x 120Å, calibrated against the dimensions of imaged influenza neuraminidase heads, known from the solved X-ray structure (Varghese et al., 1983, *Nature* **303**, 35-40). It can be noted that there is a compatibility here between the molecular weights and molecular dimensions of these two molecular species: the compact tetrameric influenza neuraminidase heads of Mr ~200 kDa occupy a volume almost 100 x 100 x 60 Å; the more open dimeric insulin receptor ectodomains of similar Mr ~240 kDa imaged here occupy a volume approximately 110 x 90 x 120 Å , roughly twice that of the neuraminidase heads, accommodating the slightly higher molecular weight and substantial central low-density cleft.

The low-resolution roughly cubic compact structure proposed here differs substantially from the T-shaped model proposed by Christiansen et al.

(1991, *Proc. Natl. Acad. Sci. U. S. A.* **88**, 249-252) and Tranum-Jensen et al., (1994, *J. Membrane Biol.* **140**, 215-223) for the whole receptor and the elongated model proposed by Schaefer et al. (1992, *J. Biol. Chem.* **267**, 23393-23402) for soluble ectodomain. Significantly, those previous studies did not provide any convincing independent electron microscopical evidence that their imaged objects were in fact insulin receptor.

In the present study, the identity of the imaged molecules as hIR -11 ectodomain has been confirmed by imaging complexes of the dimer with Fabs of the three well-established conformational Mabs against native hIR, 83-7, 83-14 and 18-44 (Soos et al.,1986, *Biochem. J.* **235**, 199-208; 1989, *Proc. Natl Acad. Sci. USA* **86**, 5217-5221), bound singly and in combination. In all these instances, virtually every particle in the field of view exhibited MFab decoration through binding to conformational epitopes, establishing not only the identity of the imaged particles but also the conformational integrity of the expressed ectodomains. Furthermore, the cleanliness and uniformity of these hIR -11 ectodomain preparations, both naked and decorated, visualised here by electron microscopy demonstrate their high suitability for X-ray crystallization trials.

The known flexibility of the Fab arms exacerbates image-to-image variability beyond the limited extent already described for the undecorated dimeric ectodomains, complicating any precise interpretation of these antigen-antibody complexes. Such molecular flexibility also renders largely impractical any single-molecule computer image averaging to facilitate image interpretation, progressively more so with the higher order antigen-antibody complexes studied here.

The most readily interpretable of these images, showing least image-to-image variability, are those of 83-7 MFab bound to dimers where, fortuitously, the antigen-antibody complex is constrained in its degrees of rotational freedom on the carbon support film. Many projected images show the two Fab arms in line roughly through the centre of the antigen on its opposite sides (Figure 19, arrowed examples), interpreted as a side projection of binding half-way up the plates from their membrane-proximal base. Other sub-sets of images (Figure 19, circled examples) show the two Fab arms still parallel but displaced clockwise or anticlockwise with 2-fold symmetry, each Fab approximating an extension of one of the parallel bars of antigen density, interpreted here as representing top or bottom projections

along the 2-fold axis. The third projection, along the axis of the Fab arms, could not be sampled here because of the constraining geometry of this molecular complex. These observations suggest binding of 83-7 MFab roughly half-way up the side-edge of the hIR -11 ectodomain plate. This then allows an initial attempt at spatially mapping the 83-7 MFab epitope, which has been sequence-mapped to residues 191-297 in the cys-rich region of the insulin receptor (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* **88**, 9858-9862). The spatial separation and relative orientations of the two binding epitopes of Mab 83-7 on the hIR -11 ectodomain dimer as indicated here appear inconsistent with the proposal that Mab 83-7 could bind intramolecularly to hIR (O'Brien et al., 1987, *Biochem J.* **6**, 4003-4010).

Decoration of the ectodomain dimer with 83-7 MFab established that the two plates of high protein-density are arranged with 2-fold symmetry. Decoration with either 83-14 or 18-44 MFab , on the other hand, allowed sampling of the third projection of the ectodomain dimer precluded by 83-7 MFab binding. Significantly, this third view established unequivocally the U-shaped projection of the hIR -11 ectodomain dimer, something which was only able to be assumed with the undecorated ectodomain images. Further, this projection has allowed a rough spatial mapping close to the base of the U-shaped dimer for the epitopes recognised by 83-14 MFab (residues 469-592, connecting domain) and 18-44 MFab (residues 765-770, b-chain insert domain; exon 11 plus numbering, Prigent et al., 1990, *J. Biol. Chem.* **265**, 9970-9977).

Inherent in the model structure presented in Figure 20 is the implication that, with the two-fold axis aligned normal to the membrane surface, the mouth of the low-density cleft where insulin binding may occur would lie most distant from the transmembrane anchor, whilst the zone of intermediate density connecting the two high-density plates would be in close proximity to the membrane. It follows, in this model, that the L1/cys-rich/L2 domains(Bajaj et al., 1997, *Biochim. Biophys. Acta* **916**, 220-226; Ward et al.,1995, *Proteins: Struct., Funct., Genet.* **22**, 141-153), which comprise much of the insulin-binding region (see Mynarcik et al., 1997, . *J. Biol. Chem.* **272**, 2077-2081). most probably lie in the membrane-distal upper halves of the two plates, whilst the membrane-proximal lower halves contain the connecting domains, the fibronectin-type domains, the insert domains and the interchain disulphide bonds (Schaffer and Ljungqvist, 1992, *Biochem.*

Biophys. Res. Commun. **189**, 650-653; Sparrow et al., 1997, *J. Biol. Chem.*, 272, 29460-29467). Such a disposition of domains is supported by the images seen with the single MFab decoration, the 83-7 MFab epitope in the cys-rich region being spatially mapped roughly half-way up the side-edge of the ectodomain plates, and the 83-14 and 18-44 MFab epitopes (connecting domain and β-chain insert domain, respectively) being mapped near the base of the plates. Our preference is for a single a-b¢ monomer to occupy a single plate, although the possibility of a single monomer straddling the two plates of protein density cannot be discounted.

The more complex images involving co-binding of two, and even more so of all three, MFabs to each monomer of the ectodomain dimer (Figures 22 and 23) are not easily interpretable with respect to relative domain arrangements within the monomer at present, not least of all because of the difficulty of finding conditions of negative staining that will simultaneously maintain the integrity of the Fab binding while highlighting recognisable and reproducible details of the internal structure of the dimeric IR ectodomain.

The data presented here demonstrate the ability of single-molecule imaging to give an initial insight into the topology of multidomain structures such as the ectodomain of hIR, and the value of combining this technique with that of either single or multiple monoclonal Fab attachment per monomer as a potential means of epitope (and domain) mapping of the structure. By imaging Fab complexes of other members of the family (such as hIGF-1R ectodomain) and combining available sequence-mapped epitope information with that presented here, a more comprehensive understanding of domain arrangements within the IR family ectodomains should be forthcoming.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive

Dated this twenty-fourth day of March 1998

COMMONWEALTH SCIENTIFIC
AND INDUSTRIAL RESEARCH
ORGANISATION
Patent Attorneys for the Applicant:

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Figure 1

```
ATOM      1  CB  GLU     1      55.907  11.986  66.300  1.00 59.11      AAAA C
ATOM      2  CG  GLU     1      56.138  11.019  65.162  1.00 78.17      AAAA C
ATOM      3  CD  GLU     1      57.382  11.319  64.321  1.00 85.10      AAAA C
ATOM      4  OE1 GLU     1      58.404  10.754  64.796  1.00 86.18      AAAA O
ATOM      5  OE2 GLU     1      57.424  12.013  63.270  1.00 78.70      AAAA O
ATOM      6  C   GLU     1      53.508  12.557  66.350  1.00 48.46      AAAA C
ATOM      7  O   GLU     1      52.685  11.863  65.784  1.00 51.27      AAAA O
ATOM     10  N   GLU     1      54.256  10.338  67.159  1.00 61.64      AAAA N
ATOM     12  CA  GLU     1      54.602  11.778  67.081  1.00 54.77      AAAA C
ATOM     13  N   ILE     2      53.608  13.860  66.375  1.00 37.66      AAAA N
ATOM     15  CA  ILE     2      52.768  14.699  65.604  1.00 40.87      AAAA C
ATOM     16  CB  ILE     2      52.925  16.122  66.160  1.00 41.97      AAAA C
ATOM     17  CG2 ILE     2      52.036  17.122  65.484  1.00 38.50      AAAA C
ATOM     18  CG1 ILE     2      52.560  16.006  67.663  1.00 46.58      AAAA C
ATOM     19  CD1 ILE     2      53.150  17.176  68.498  1.00 32.29      AAAA C
ATOM     20  C   ILE     2      53.122  14.711  64.139  1.00 46.47      AAAA C
ATOM     21  O   ILE     2      54.258  15.029  63.852  1.00 51.66      AAAA O
ATOM     22  N   CYS     3      52.235  14.409  63.196  1.00 49.61      AAAA N
ATOM     24  CA  CYS     3      52.435  14.677  61.773  1.00 38.93      AAAA C
ATOM     25  C   CYS     3      51.429  15.708  61.302  1.00 42.06      AAAA C
ATOM     26  O   CYS     3      50.290  15.521  61.690  1.00 42.37      AAAA O
ATOM     27  CB  CYS     3      52.159  13.415  60.999  1.00 35.66      AAAA C
ATOM     28  SG  CYS     3      53.019  12.004  61.674  1.00 36.98      AAAA S
ATOM     29  N   GLY     4      51.851  16.709  60.580  1.00 42.39      AAAA N
ATOM     31  CA  GLY     4      50.973  17.718  60.003  1.00 47.71      AAAA C
ATOM     32  C   GLY     4      51.703  18.407  58.869  1.00 48.23      AAAA C
ATOM     33  O   GLY     4      52.916  18.345  58.884  1.00 55.36      AAAA O
ATOM     34  N   PRO     5      51.056  19.212  58.048  1.00 49.63      AAAA N
ATOM     35  CD  PRO     5      51.637  19.947  56.860  1.00 45.28      AAAA C
ATOM     36  CA  PRO     5      49.605  19.341  58.083  1.00 41.57      AAAA C
ATOM     37  CB  PRO     5      49.397  20.703  57.474  1.00 44.30      AAAA C
ATOM     38  CG  PRO     5      50.630  21.036  56.683  1.00 46.43      AAAA C
ATOM     39  C   PRO     5      48.932  19.217  57.354  1.00 36.40      AAAA C
ATOM     40  O   PRO     5      49.403  17.094  57.396  1.00 43.35      AAAA O
ATOM     41  N   GLY     6      47.787  18.439  56.795  1.00 39.15      AAAA N
ATOM     43  CA  GLY     6      46.896  17.336  56.350  1.00 39.24      AAAA C
ATOM     44  C   GLY     6      47.710  16.365  55.509  1.00 33.68      AAAA C
ATOM     45  O   GLY     6      48.510  16.863  54.753  1.00 36.00      AAAA O
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ATOM     49  CB  ILE     7      48.556  12.797  55.933  1.00 36.31      AAAA C
ATOM     50  CG2 ILE     7      49.043  11.700  54.988  1.00 34.67      AAAA C
ATOM     51  CG1 ILE     7      49.561  12.857  57.067  1.00 39.34      AAAA C
ATOM     52  CD1 ILE     7      49.678  14.249  57.669  1.00 40.22      AAAA C
ATOM     53  C   ILE     7      47.339  13.762  53.977  1.00 45.00      AAAA C
ATOM     54  O   ILE     7      46.150  13.643  54.195  1.00 51.52      AAAA O
ATOM     55  N   ASP     8      47.767  13.631  52.751  1.00 45.60      AAAA N
ATOM     57  CA  ASP     8      46.938  13.293  51.631  1.00 44.05      AAAA C
ATOM     58  CB  ASP     8      47.003  14.469  50.651  1.00 44.21      AAAA C
ATOM     59  CG  ASP     8      45.909  14.379  49.600  1.00 43.48      AAAA C
ATOM     60  OD1 ASP     8      45.660  13.262  49.096  1.00 51.77      AAAA O
ATOM     61  OD2 ASP     8      45.253  15.374  49.251  1.00 46.84      AAAA O
ATOM     62  C   ASP     8      47.428  12.000  50.992  1.00 42.16      AAAA C
ATOM     63  O   ASP     8      48.423  12.143  50.330  1.00 48.50      AAAA O
ATOM     64  N   ILE     9      47.096  10.817  51.321  1.00 42.76      AAAA N
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ATOM     67  CB  ILE     9      47.212   8.483  52.077  1.00 40.82      AAAA C
ATOM     68  CG2 ILE     9      47.669   7.085  51.653  1.00 36.35      AAAA C
ATOM     69  CG1 ILE     9      47.888   8.917  53.364  1.00 41.17      AAAA C
ATOM     70  CD1 ILE     9      49.376   8.947  53.286  1.00 43.78      AAAA C
ATOM     71  C   ILE     9      46.530   9.137  49.794  1.00 51.48      AAAA C
ATOM     72  O   ILE     9      45.338   9.420  49.832  1.00 63.05      AAAA O
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ATOM     75  CA  ARG    10      46.283   8.089  47.600  1.00 54.17      AAAA C
ATOM     76  CB  ARG    10      45.703   9.358  47.023  1.00 48.54      AAAA C
ATOM     77  CG  ARG    10      46.361  10.169  45.952  1.00 46.55      AAAA C
ATOM     78  CD  ARG    10      46.002  11.635  46.264  1.00 52.63      AAAA C
ATOM     79  NE  ARG    10      45.082  12.226  45.284  1.00 59.27      AAAA N
ATOM     81  CZ  ARG    10      44.269  13.262  45.498  1.00 56.22      AAAA C
ATOM     82  NH1 ARG    10      44.153  13.891  46.666  1.00 55.14      AAAA N
ATOM     85  NH2 ARG    10      43.455  13.803  44.602  1.00 52.29      AAAA N
ATOM     88  C   ARG    10      47.019   7.373  46.492  1.00 57.23      AAAA C
ATOM     89  O   ARG    10      48.240   7.288  46.281  1.00 56.32      AAAA O
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ATOM     92  CA  ASN    11      46.800   5.917  44.494  1.00 50.73      AAAA C
ATOM     93  CB  ASN    11      47.704   6.798  43.671  1.00 44.65      AAAA C
ATOM     94  CG  ASN    11      46.878   7.732  42.829  1.00 50.72      AAAA C
ATOM     95  OD1 ASN    11      45.749   7.451  42.403  1.00 72.59      AAAA O
ATOM     96  ND2 ASN    11      47.499   8.869  42.587  1.00 54.38      AAAA N
ATOM     99  C   ASN    11      47.635   4.736  44.915  1.00 53.07      AAAA C
ATOM    100  O   ASN    11      47.303   3.701  44.347  1.00 51.95      AAAA O
ATOM    101  N   ASP    12      48.566   4.822  45.878  1.00 50.96      AAAA N
ATOM    103  CA  ASP    12      49.204   3.570  46.263  1.00 55.44      AAAA C
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ATOM    105  CG  ASP   12      50.879   4.026  44.314  1.00 68.25      AAAA C
ATOM    106  OD1 ASP   12      50.441   3.185  43.457  1.00 58.31      AAAA O
ATOM    107  OD2 ASP   12      51.391   5.120  43.989  1.00 70.56      AAAA O
ATOM    108  C   ASP   12      49.061   3.322  47.758  1.00 59.23      AAAA C
ATOM    109  O   ASP   12      49.687   3.849  48.711  1.00 59.65      AAAA O
ATOM    110  N   TYR   13      48.411   2.187  48.036  1.00 59.64      AAAA N
ATOM    112  CA  TYR   13      48.328   1.672  49.397  1.00 64.06      AAAA C
ATOM    113  CB  TYR   13      47.968   0.196  49.409  1.00 64.56      AAAA C
ATOM    114  CG  TYR   13      47.467  -0.357  50.721  1.00 69.18      AAAA C
ATOM    115  CD1 TYR   13      46.216  -0.024  51.248  1.00 72.71      AAAA C
ATOM    116  CE1 TYR   13      45.746  -0.541  52.450  1.00 71.51      AAAA C
ATOM    117  CD2 TYR   13      48.233  -1.247  51.457  1.00 70.36      AAAA C
ATOM    118  CE2 TYR   13      47.788  -1.778  52.661  1.00 71.64      AAAA C
ATOM    119  CZ  TYR   13      46.542  -1.420  53.160  1.00 71.31      AAAA C
ATOM    120  OH  TYR   13      46.144  -1.977  54.358  1.00 63.25      AAAA O
ATOM    122  C   TYR   13      49.622   1.839  50.198  1.00 65.99      AAAA C
ATOM    123  O   TYR   13      49.621   2.321  51.354  1.00 65.01      AAAA O
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ATOM    127  CB  GLN   14      53.174   1.318  49.219  1.00 68.37      AAAA C
ATOM    128  CG  GLN   14      52.863  -0.078  48.686  1.00 84.62      AAAA C
ATOM    129  CD  GLN   14      53.990  -0.515  47.754  1.00 92.28      AAAA C
ATOM    130  OE1 GLN   14      53.945  -0.161  46.573  1.00 94.82      AAAA O
ATOM    131  NE2 GLN   14      54.920  -1.254  48.361  1.00 98.03      AAAA N
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ATOM    135  O   GLN   14      53.266   3.292  51.644  1.00 62.09      AAAA O
ATOM    136  N   GLN   15      51.628   4.038  50.349  1.00 57.02      AAAA N
ATOM    138  CA  GLN   15      51.724   5.399  50.834  1.00 51.71      AAAA C
ATOM    139  CB  GLN   15      50.861   6.220  49.911  1.00 43.75      AAAA C
ATOM    140  CG  GLN   15      51.566   6.605  48.648  1.00 59.65      AAAA C
ATOM    141  CD  GLN   15      51.554   8.105  48.428  1.00 72.96      AAAA C
ATOM    142  OE1 GLN   15      51.168   9.005  49.184  1.00 80.58      AAAA O
ATOM    143  NE2 GLN   15      52.016   8.378  47.211  1.00 74.17      AAAA N
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ATOM    151  CB  LEU   16      48.950   3.295  54.159  1.00 37.73      AAAA C
ATOM    152  CG  LEU   16      47.502   3.425  53.707  1.00 41.40      AAAA C
ATOM    153  CD1 LEU   16      46.837   2.063  53.790  1.00 42.43      AAAA C
ATOM    154  CD2 LEU   16      46.687   4.424  54.545  1.00 35.93      AAAA C
ATOM    155  C   LEU   16      51.042   4.280  55.039  1.00 51.52      AAAA C
ATOM    156  O   LEU   16      50.913   4.601  56.235  1.00 52.53      AAAA O
ATOM    157  N   LYS   17      52.252   3.936  54.560  1.00 51.01      AAAA N
ATOM    159  CA  LYS   17      53.420   3.914  55.404  1.00 50.73      AAAA C
ATOM    160  CB  LYS   17      54.609   3.252  54.737  1.00 56.10      AAAA C
ATOM    161  CG  LYS   17      54.539   1.733  54.931  1.00 62.40      AAAA C
ATOM    162  CD  LYS   17      54.768   1.278  56.387  1.00 63.95      AAAA C
ATOM    163  CE  LYS   17      55.316  -0.141  56.426  1.00 68.40      AAAA C
ATOM    164  NZ  LYS   17      56.537  -0.225  57.554  1.00 73.83      AAAA N
ATOM    169  C   LYS   17      53.944   5.270  55.852  1.00 44.78      AAAA C
ATOM    169  O   LYS   17      54.492   5.262  56.933  1.00 39.39      AAAA O
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ATOM    178  CZ  ARG   18      51.628  11.444  52.021  1.00 48.86      AAAA C
ATOM    179  NH1 ARG   18      51.068  10.941  50.943  1.00 47.96      AAAA N
ATOM    182  NH2 ARG   18      51.377  12.656  52.555  1.00 43.72      AAAA N
ATOM    185  C   ARG   18      53.268   7.924  57.077  1.00 44.03      AAAA C
ATOM    186  O   ARG   18      53.402   9.010  57.644  1.00 45.53      AAAA O
ATOM    187  N   LEU   19      52.445   7.069  57.632  1.00 46.36      AAAA N
ATOM    189  CA  LEU   19      51.653   7.282  58.794  1.00 50.25      AAAA C
ATOM    190  CB  LEU   19      50.186   6.924  58.674  1.00 50.83      AAAA C
ATOM    191  CG  LEU   19      49.202   7.371  57.608  1.00 46.43      AAAA C
ATOM    192  CD1 LEU   19      47.846   6.743  57.852  1.00 22.57      AAAA C
ATOM    193  CD2 LEU   19      49.018   8.866  57.495  1.00 45.88      AAAA C
ATOM    194  C   LEU   19      52.210   6.428  59.912  1.00 49.87      AAAA C
ATOM    195  O   LEU   19      51.870   6.810  61.030  1.00 51.54      AAAA O
ATOM    196  N   GLU   20      53.270   5.708  59.652  1.00 49.35      AAAA N
ATOM    198  CA  GLU   20      53.819   4.933  60.679  1.00 49.60      AAAA C
ATOM    199  CB  GLU   20      54.876   3.960  59.982  1.00 57.91      AAAA C
ATOM    200  CG  GLU   20      55.893   4.940  59.272  1.00 70.16      AAAA C
ATOM    201  CD  GLU   20      57.095   4.077  58.757  1.00 69.35      AAAA C
ATOM    202  OE1 GLU   20      58.123   4.795  58.722  1.00 71.38      AAAA O
ATOM    203  OE2 GLU   20      56.993   2.885  58.420  1.00 72.84      AAAA O
ATOM    204  C   GLU   20      54.310   5.417  61.989  1.00 43.55      AAAA C
ATOM    205  O   GLU   20      54.301   4.652  62.937  1.00 40.01      AAAA O
ATOM    206  H   ASN   21      54.633   6.659  62.207  1.00 41.06      AAAA N
ATOM    208  CA  ASN   21      55.054   7.204  63.454  1.00 47.17      AAAA C
ATOM    209  C   ASN   21      54.066   8.141  64.108  1.00 49.76      AAAA C
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ATOM	212	CG	ASN	21	57.413	7.051	62.796	1.00	68.38	AAAA C
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ATOM	214	ND2	ASN	21	58.348	7.469	61.890	1.00	77.90	AAAA N
ATOM	216	N	CYS	22	53.129	8.711	63.351	1.00	47.44	AAAA N
ATOM	218	CA	CYS	22	52.107	9.614	63.879	1.00	42.99	AAAA C
ATOM	219	C	CYS	22	51.215	9.089	65.021	1.00	40.43	AAAA C
ATOM	220	O	CYS	22	50.750	7.923	65.069	1.00	36.07	AAAA O
ATOM	221	CB	CYS	22	51.182	9.921	62.690	1.00	44.82	AAAA C
ATOM	222	SG	CYS	22	52.076	10.328	61.148	1.00	39.51	AAAA S
ATOM	223	N	THR	23	51.287	9.801	66.137	1.00	36.24	AAAA N
ATOM	225	CA	THR	23	50.339	9.482	67.204	1.00	43.51	AAAA C
ATOM	226	CB	THR	23	50.944	9.481	68.593	1.00	41.38	AAAA C
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ATOM	230	C	THR	23	49.250	10.599	67.116	1.00	44.55	AAAA C
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ATOM	234	CA	VAL	24	48.732	12.855	66.442	1.00	35.29	AAAA C
ATOM	235	CB	VAL	24	48.925	13.979	67.456	1.00	30.60	AAAA C
ATOM	236	CG1	VAL	24	48.056	15.157	67.082	1.00	27.21	AAAA C
ATOM	237	CG2	VAL	24	48.656	13.566	68.886	1.00	25.37	AAAA C
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ATOM	239	O	VAL	24	49.987	13.963	64.791	1.00	44.40	AAAA O
ATOM	240	N	ILE	25	47.855	13.450	64.203	1.00	40.13	AAAA N
ATOM	242	CA	ILE	25	47.908	14.094	62.882	1.00	32.05	AAAA C
ATOM	243	CB	ILE	25	47.113	13.299	61.853	1.00	25.85	AAAA C
ATOM	244	CG2	ILE	25	47.027	14.039	60.542	1.00	18.73	AAAA C
ATOM	245	CG1	ILE	25	47.677	11.896	61.705	1.00	29.80	AAAA C
ATOM	246	CD1	ILE	25	47.169	11.155	60.471	1.00	27.41	AAAA C
ATOM	247	C	ILE	25	47.397	15.490	62.941	1.00	32.92	AAAA C
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ATOM	249	N	GLU	26	48.264	16.472	63.042	1.00	36.60	AAAA N
ATOM	251	CA	GLU	26	47.832	17.847	63.226	1.00	29.24	AAAA C
ATOM	252	CB	GLU	26	48.875	18.703	63.856	1.00	29.92	AAAA C
ATOM	253	CG	GLU	26	49.490	20.144	64.116	1.00	38.06	AAAA C
ATOM	254	CD	GLU	26	49.561	20.762	65.013	1.00	37.39	AAAA C
ATOM	255	OE1	GLU	26	50.654	20.937	64.489	1.00	41.56	AAAA O
ATOM	256	OE2	GLU	26	49.571	21.175	66.182	1.00	49.16	AAAA O
ATOM	257	C	GLU	26	47.413	18.376	61.869	1.00	37.79	AAAA C
ATOM	259	O	GLU	26	48.161	19.069	61.181	1.00	39.69	AAAA O
ATOM	260	N	GLY	27	46.117	19.104	61.582	1.00	37.28	AAAA N
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ATOM	262	C	GLY	27	44.531	17.400	59.893	1.00	33.72	AAAA C
ATOM	263	O	GLY	27	43.988	16.715	60.775	1.00	33.29	AAAA O
ATOM	264	N	TYR	28	44.304	17.209	58.604	1.00	29.24	AAAA N
ATOM	266	CA	TYR	28	43.318	16.189	58.253	1.00	28.93	AAAA C
ATOM	267	CB	TYR	28	42.403	16.794	57.217	1.00	31.53	AAAA C
ATOM	268	CG	TYR	28	43.058	17.256	55.962	1.00	31.78	AAAA C
ATOM	269	CD1	TYR	28	43.704	16.355	55.116	1.00	36.07	AAAA C
ATOM	270	CE1	TYR	28	44.361	16.706	53.967	1.00	29.91	AAAA C
ATOM	271	CD2	TYR	28	43.130	19.572	55.606	1.00	30.99	AAAA C
ATOM	272	CE2	TYR	28	43.769	18.972	54.428	1.00	28.77	AAAA C
ATOM	273	CZ	TYR	28	44.367	19.021	53.652	1.00	31.53	AAAA C
ATOM	274	OH	TYR	28	44.971	18.425	52.464	1.00	44.74	AAAA O
ATOM	276	C	TYR	28	43.953	14.946	57.697	1.00	29.23	AAAA C
ATOM	277	O	TYR	28	45.119	15.147	57.383	1.00	35.58	AAAA O
ATOM	278	N	LEU	29	43.250	13.900	57.445	1.00	26.63	AAAA N
ATOM	280	CA	LEU	29	43.764	12.730	56.803	1.00	29.83	AAAA C
ATOM	281	CB	LEU	29	43.830	11.611	57.856	1.00	27.09	AAAA C
ATOM	282	CG	LEU	29	44.212	10.258	57.242	1.00	31.90	AAAA C
ATOM	283	CD1	LEU	29	45.538	10.396	56.469	1.00	35.03	AAAA C
ATOM	284	CD2	LEU	29	44.551	9.203	58.290	1.00	25.05	AAAA C
ATOM	285	C	LEU	29	42.897	12.342	55.616	1.00	33.84	AAAA C
ATOM	286	O	LEU	29	41.689	12.165	55.806	1.00	43.29	AAAA O
ATOM	287	N	HIS	30	43.389	12.285	54.395	1.00	35.95	AAAA N
ATOM	289	CA	HIS	30	42.681	11.891	53.197	1.00	34.92	AAAA C
ATOM	290	CB	HIS	30	42.893	12.801	52.027	1.00	32.85	AAAA C
ATOM	291	CG	HIS	30	42.372	14.155	52.046	1.00	25.09	AAAA C
ATOM	292	CD2	HIS	30	41.519	14.753	52.907	1.00	40.88	AAAA C
ATOM	293	ND1	HIS	30	42.717	15.120	51.128	1.00	33.66	AAAA N
ATOM	295	CE1	HIS	30	42.080	16.281	51.444	1.00	31.33	AAAA C
ATOM	296	NE2	HIS	30	41.329	16.093	52.539	1.00	37.27	AAAA N
ATOM	298	C	HIS	30	43.173	10.538	52.714	1.00	37.68	AAAA C
ATOM	299	O	HIS	30	44.357	10.388	52.541	1.00	38.70	AAAA O
ATOM	300	N	ILE	31	42.308	9.542	52.584	1.00	40.02	AAAA N
ATOM	302	CA	ILE	31	42.750	8.271	51.992	1.00	39.47	AAAA C
ATOM	303	CB	ILE	31	42.668	7.204	53.063	1.00	37.95	AAAA C
ATOM	304	CG2	ILE	31	43.161	5.830	52.651	1.00	23.86	AAAA C
ATOM	305	CG1	ILE	31	43.481	7.555	54.335	1.00	41.66	AAAA C
ATOM	306	CD1	ILE	31	43.170	6.575	55.473	1.00	28.22	AAAA C
ATOM	307	C	ILE	31	41.884	8.044	50.755	1.00	46.52	AAAA C
ATOM	308	O	ILE	31	40.753	7.589	50.827	1.00	43.56	AAAA O
ATOM	309	N	LEU	32	42.314	8.489	49.556	1.00	49.89	AAAA N
ATOM	311	CA	LEU	32	41.484	8.235	48.380	1.00	49.77	AAAA C

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ATOM    312  CB  LEU    32      41.127   9.515  47.603  1.00 47.48      AAAA C
ATOM    313  CG  LEU    32      42.091  10.688  47.562  1.00 45.33      AAAA C
ATOM    314  CD1 LEU    32      41.517  11.812  46.673  1.00 35.77      AAAA C
ATOM    315  CD2 LEU    32      42.371  11.229  48.960  1.00 49.18      AAAA C
ATOM    316  C   LEU    32      42.136   7.296  47.353  1.00 51.00      AAAA C
ATOM    317  O   LEU    32      43.338   7.370  47.186  1.00 41.36      AAAA O
ATOM    318  N   LEU    33      41.270   6.722  46.497  1.00 50.74      AAAA N
ATOM    320  CA  LEU    33      41.602   6.175  45.197  1.00 49.92      AAAA C
ATOM    321  CB  LEU    33      42.091   7.262  44.182  1.00 34.83      AAAA C
ATOM    322  CG  LEU    33      41.233   8.537  44.164  1.00 33.92      AAAA C
ATOM    323  CD1 LEU    33      41.892   9.587  43.298  1.00 37.49      AAAA C
ATOM    324  CD2 LEU    33      39.823   8.313  43.644  1.00 33.01      AAAA C
ATOM    325  C   LEU    33      42.618   5.073  45.287  1.00 48.35      AAAA C
ATOM    326  O   LEU    33      43.580   5.077  44.538  1.00 54.14      AAAA O
ATOM    327  N   ILE    34      42.543   4.213  46.254  1.00 47.61      AAAA N
ATOM    329  CA  ILE    34      43.523   3.184  46.540  1.00 51.70      AAAA C
ATOM    330  CB  ILE    34      44.101   3.346  47.963  1.00 57.98      AAAA C
ATOM    331  CG2 ILE    34      44.538   2.043  48.600  1.00 48.98      AAAA C
ATOM    332  CG1 ILE    34      45.267   4.371  47.967  1.00 46.70      AAAA C
ATOM    333  CD1 ILE    34      45.561   4.704  49.439  1.00 66.47      AAAA C
ATOM    334  C   ILE    34      42.829   1.844  46.408  1.00 59.85      AAAA C
ATOM    335  O   ILE    34      41.726   1.531  46.856  1.00 60.11      AAAA O
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ATOM    339  CB  SER    35      42.767  -0.882  44.469  1.00 64.16      AAAA C
ATOM    340  OG  SER    35      41.731  -1.846  44.498  1.00 75.76      AAAA O
ATOM    342  C   SER    35      43.928  -1.564  46.537  1.00 70.73      AAAA C
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ATOM    347  CB  LYS    36      44.046  -3.131  49.885  1.00 81.22      AAAA C
ATOM    348  CG  LYS    36      45.147  -3.654  50.775  1.00 78.87      AAAA C
ATOM    349  CD  LYS    36      44.693  -4.575  51.887  1.00 81.39      AAAA C
ATOM    350  CE  LYS    36      44.890  -6.025  51.492  1.00 89.38      AAAA C
ATOM    351  NZ  LYS    36      44.371  -6.989  52.506  1.00 91.63      AAAA N
ATOM    353  C   LYS    36      44.252  -4.362  47.753  1.00 81.41      AAAA C
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ATOM    359  CA  ALA    37      45.361  -6.396  46.986  1.00 90.10      AAAA C
ATOM    360  CB  ALA    37      46.700  -6.655  46.327  1.00 95.49      AAAA C
ATOM    361  C   ALA    37      45.111  -7.473  47.995  1.00 92.36      AAAA C
ATOM    362  O   ALA    37      45.668  -7.627  49.012  1.00 92.35      AAAA O
ATOM    363  N   SER    38      44.031  -9.301  47.622  1.00 94.31      AAAA N
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ATOM    366  CB  SER    38      42.405 -10.164  47.858  1.00 97.44      AAAA C
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ATOM    369  C   SER    38      44.702 -10.263  48.821  1.00 96.87      AAAA C
ATOM    370  O   SER    38      44.761 -10.778  49.924  1.00 98.06      AAAA O
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ATOM    373  CA  ASP    39      46.921 -11.148  47.990  1.00 99.19      AAAA C
ATOM    374  CB  ASP    39      47.579 -11.050  46.652  1.00102.13      AAAA C
ATOM    376  CG  ASP    39      47.696 -12.397  45.948  0.01101.22      AAAA C
ATOM    376  OD1 ASP    39      46.644 -12.978  45.623  0.01101.42      AAAA O
ATOM    377  OD2 ASP    39      48.833 -12.848  45.718  0.01101.41      AAAA O
ATOM    378  C   ASP    39      47.660 -10.564  49.105  1.00 99.40      AAAA C
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ATOM    383  CB  TYR    40      49.511  -7.393  49.130  1.00103.67      AAAA C
ATOM    384  CG  TYR    40      50.159  -6.281  49.887  1.00107.81      AAAA C
ATOM    385  CD1 TYR    40      50.931  -5.325  49.228  1.00109.56      AAAA C
ATOM    386  CE1 TYR    40      51.540  -4.280  49.910  1.00109.67      AAAA C
ATOM    387  CD2 TYR    40      50.044  -6.115  51.254  1.00109.28      AAAA C
ATOM    388  CE2 TYR    40      50.618  -5.102  51.976  1.00109.83      AAAA C
ATOM    389  CZ  TYR    40      51.372  -4.181  51.276  1.00110.16      AAAA C
ATOM    390  OH  TYR    40      51.999  -3.127  51.893  1.00109.84      AAAA O
ATOM    392  C   TYR    40      48.343  -8.529  51.100  1.00 99.10      AAAA C
ATOM    393  O   TYR    40      47.168  -8.182  51.183  1.00 99.05      AAAA O
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ATOM    396  CA  LYS    41      48.443  -8.549  53.546  1.00100.30      AAAA C
ATOM    397  CB  LYS    41      49.385  -9.160  54.599  1.00104.42      AAAA C
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ATOM    399  CD  LYS    41      47.776 -11.107  54.919  0.01100.66      AAAA C
ATOM    400  CE  LYS    41      47.205 -10.880  56.308  0.01 99.86      AAAA C
ATOM    401  NZ  LYS    41      47.882 -11.728  57.328  0.01 99.62      AAAA N
ATOM    405  C   LYS    41      48.035  -7.136  53.947  1.00 98.99      AAAA C
ATOM    406  O   LYS    41      47.615  -6.371  53.057  1.00103.33      AAAA O
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ATOM    410  CB  SER    42      46.385  -5.520  56.147  1.00 95.33      AAAA C
ATOM    411  OG  SER    42      45.547  -6.140  57.426  1.00104.63      AAAA O
ATOM    413  C   SER    42      48.628  -4.715  56.687  1.00 80.78      AAAA C
ATOM    414  O   SER    42      49.326  -5.259  57.538  1.00 81.03      AAAA O
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ATOM    417  CA  TYR    43      49.069  -2.498  57.635  1.00 67.25      AAAA C
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ATOM   419  CB  TYR  43      49.086  -1.119  56.965  1.00 65.37      AAAA C
ATOM   419  CG  TYR  43      49.953  -1.021  55.727  1.00 63.92      AAAA C
ATOM   420  CD1 TYR  43      50.931  -1.935  55.406  1.00 63.87      AAAA C
ATOM   421  CE1 TYR  43      51.698  -1.781  54.274  1.00 66.09      AAAA C
ATOM   422  CD2 TYR  43      49.770   0.050  54.870  1.00 63.30      AAAA C
ATOM   423  CE2 TYR  43      50.536   0.214  53.728  1.00 67.62      AAAA C
ATOM   424  CZ  TYR  43      51.508  -0.712  53.432  1.00 66.94      AAAA C
ATOM   425  OH  TYR  43      52.262  -0.563  52.305  1.00 65.23      AAAA O
ATOM   427  C   TYR  43      48.248  -2.381  58.925  1.00 64.88      AAAA C
ATOM   428  O   TYR  43      47.088  -2.851  59.030  1.00 62.90      AAAA O
ATOM   429  N   ARG  44      48.782  -1.567  59.825  1.00 57.88      AAAA N
ATOM   431  CA  ARG  44      48.019  -1.285  61.039  1.00 56.45      AAAA C
ATOM   432  CB  ARG  44      47.842  -2.611  61.760  1.00 46.51      AAAA C
ATOM   433  CG  ARG  44      47.815  -2.375  63.244  1.00 54.66      AAAA C
ATOM   434  CD  ARG  44      46.885  -3.327  63.986  1.00 58.54      AAAA C
ATOM   435  NE  ARG  44      47.090  -2.927  65.403  1.00 68.56      AAAA N
ATOM   437  CZ  ARG  44      46.464  -3.536  66.395  1.00 64.82      AAAA C
ATOM   438  NH1 ARG  44      45.644  -4.529  66.132  1.00 61.63      AAAA N
ATOM   441  NH2 ARG  44      46.674  -3.139  67.628  1.00 66.03      AAAA N
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ATOM   451  CD1 PHE  45      50.373   3.051  59.998  1.00 45.72      AAAA C
ATOM   452  CD2 PHE  45      48.127   2.428  59.728  1.00 35.95      AAAA C
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ATOM   454  CE2 PHE  45      48.358   2.096  58.406  1.00 39.92      AAAA C
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ATOM   456  C   PHE  45      48.181   2.123  64.203  1.00 41.65      AAAA C
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ATOM   463  C   PRO  46      49.558   2.768  67.233  1.00 41.30      AAAA C
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ATOM   469  CG  LYS  47      52.032   3.995  65.902  1.00 67.95      AAAA C
ATOM   470  CD  LYS  47      53.563   3.976  65.891  1.00 61.33      AAAA C
ATOM   471  CE  LYS  47      54.115   4.649  67.147  1.00 72.19      AAAA C
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ATOM   483  CD1 LEU  48      46.637   9.310  63.878  1.00 36.96      AAAA C
ATOM   484  CD2 LEU  48      45.591   7.738  62.294  1.00 34.49      AAAA C
ATOM   485  C   LEU  48      46.186   7.022  66.807  1.00 42.21      AAAA C
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ATOM	527	CD	GLU	53	42.517	20.396	59.697	1.00	40.82	AAAA C
ATOM	528	OE1	GLU	53	42.638	19.908	58.556	1.00	57.56	AAAA O
ATOM	529	OE2	GLU	53	42.799	21.559	59.931	1.00	35.74	AAAA O
ATOM	530	C	GLU	53	39.506	16.789	61.388	1.00	39.19	AAAA C
ATOM	531	O	GLU	53	38.922	16.311	62.386	1.00	38.95	AAAA O
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ATOM	535	CB	TYR	54	37.654	15.602	58.636	1.00	30.71	AAAA C
ATOM	536	CG	TYR	54	38.247	16.476	57.388	1.00	21.18	AAAA C
ATOM	537	CD1	TYR	54	38.487	15.733	56.305	1.00	20.22	AAAA C
ATOM	538	CE1	TYR	54	38.980	16.243	55.086	1.00	21.04	AAAA C
ATOM	539	CD2	TYR	54	38.577	17.944	57.307	1.00	23.97	AAAA C
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ATOM	549	CB	LEU	55	39.011	10.663	59.510	1.00	14.78	AAAA C
ATOM	550	CG	LEU	55	39.349	9.314	58.818	1.00	26.98	AAAA C
ATOM	551	CD1	LEU	55	40.668	9.477	58.040	1.00	26.66	AAAA C
ATOM	552	CD2	LEU	55	39.496	8.093	59.705	1.00	14.45	AAAA C
ATOM	553	C	LEU	55	38.201	11.548	57.238	1.00	37.43	AAAA C
ATOM	554	O	LEU	55	36.995	11.632	57.427	1.00	39.55	AAAA O
ATOM	555	N	LEU	56	38.700	11.348	56.035	1.00	41.83	AAAA N
ATOM	557	CA	LEU	56	37.955	11.201	54.799	1.00	36.98	AAAA C
ATOM	558	CB	LEU	56	37.998	12.446	53.949	1.00	33.29	AAAA C
ATOM	559	CG	LEU	56	37.984	12.514	52.416	1.00	30.35	AAAA C
ATOM	560	CD1	LEU	56	37.076	11.460	51.821	1.00	47.95	AAAA C
ATOM	561	CD2	LEU	56	37.286	13.807	51.985	1.00	33.47	AAAA C
ATOM	562	C	LEU	56	38.595	10.047	54.008	1.00	39.75	AAAA C
ATOM	563	O	LEU	56	39.714	10.208	53.547	1.00	44.38	AAAA O
ATOM	564	N	LEU	57	37.846	8.968	53.800	1.00	36.68	AAAA N
ATOM	566	CA	LEU	57	38.133	7.832	53.034	1.00	41.53	AAAA C
ATOM	567	CB	LEU	57	37.944	6.588	53.916	1.00	37.00	AAAA C
ATOM	568	CG	LEU	57	39.064	6.554	55.026	1.00	36.13	AAAA C
ATOM	569	CD1	LEU	57	38.513	6.980	56.417	1.00	33.26	AAAA C
ATOM	570	CD2	LEU	57	39.630	5.162	55.039	1.00	24.11	AAAA C
ATOM	571	C	LEU	57	37.203	7.825	51.838	1.00	46.03	AAAA C
ATOM	572	O	LEU	57	35.985	7.993	51.969	1.00	44.78	AAAA O
ATOM	573	N	PHE	58	37.792	7.899	50.642	1.00	47.07	AAAA N
ATOM	575	CA	PHE	58	36.995	8.002	49.467	1.00	48.75	AAAA C
ATOM	576	CB	PHE	58	36.704	9.448	49.102	1.00	46.67	AAAA C
ATOM	577	CG	PHE	58	36.447	9.615	47.692	1.00	54.66	AAAA C
ATOM	578	CD1	PHE	58	37.413	9.706	46.697	1.00	55.19	AAAA C
ATOM	579	CD2	PHE	58	35.200	10.301	47.326	1.00	53.96	AAAA C
ATOM	580	CE1	PHE	58	37.124	10.063	45.396	1.00	50.36	AAAA C
ATOM	581	CE2	PHE	58	34.885	10.655	46.011	1.00	41.84	AAAA C
ATOM	582	CZ	PHE	58	35.877	10.521	45.037	1.00	46.50	AAAA C
ATOM	583	C	PHE	58	37.351	7.052	48.379	1.00	49.71	AAAA C
ATOM	584	O	PHE	58	38.487	7.073	47.934	1.00	52.16	AAAA O
ATOM	585	N	ARG	59	36.471	6.118	47.944	1.00	44.26	AAAA N
ATOM	587	CA	ARG	59	36.753	5.281	46.815	1.00	40.80	AAAA C
ATOM	588	CB	ARG	59	36.911	5.993	45.427	1.00	23.79	AAAA C
ATOM	589	CG	ARG	59	35.869	7.020	45.121	1.00	46.53	AAAA C
ATOM	590	CD	ARG	59	35.921	7.562	43.706	1.00	37.64	AAAA C
ATOM	591	NE	ARG	59	35.822	6.422	42.806	1.00	49.23	AAAA N
ATOM	593	CZ	ARG	59	34.950	5.932	42.036	1.00	41.36	AAAA C
ATOM	594	NH1	ARG	59	33.702	6.277	41.931	1.00	47.00	AAAA N
ATOM	597	NH2	ARG	59	35.237	4.729	41.327	1.00	42.58	AAAA N
ATOM	600	C	ARG	59	38.037	4.494	47.049	1.00	42.25	AAAA C
ATOM	601	O	ARG	59	38.981	4.513	46.232	1.00	44.11	AAAA O
ATOM	602	N	VAL	60	38.001	3.625	48.023	1.00	40.94	AAAA N
ATOM	604	CA	VAL	60	39.101	2.743	48.341	1.00	39.14	AAAA C
ATOM	605	CB	VAL	60	39.624	3.066	49.751	1.00	40.12	AAAA C
ATOM	606	CG1	VAL	60	40.407	1.872	50.296	1.00	35.05	AAAA C
ATOM	607	CG2	VAL	60	40.425	4.352	49.893	1.00	28.86	AAAA C
ATOM	608	C	VAL	60	38.539	1.337	48.368	1.00	43.56	AAAA C
ATOM	609	O	VAL	60	37.535	1.224	49.072	1.00	47.66	AAAA O
ATOM	610	N	ALA	61	39.094	0.371	47.659	1.00	41.92	AAAA N
ATOM	612	CA	ALA	61	38.617	-0.992	47.749	1.00	42.05	AAAA C
ATOM	613	CB	ALA	61	38.302	-1.483	46.364	1.00	52.40	AAAA C
ATOM	614	C	ALA	61	39.613	-1.934	48.386	1.00	43.08	AAAA C
ATOM	615	O	ALA	61	40.757	-1.602	48.670	1.00	50.59	AAAA O
ATOM	616	N	GLY	62	39.200	-3.105	48.849	1.00	45.71	AAAA N
ATOM	618	CA	GLY	62	40.136	-4.079	49.385	1.00	45.39	AAAA C
ATOM	619	C	GLY	62	40.262	-3.902	50.872	1.00	48.04	AAAA C
ATOM	620	O	GLY	62	40.587	-4.835	51.604	1.00	52.34	AAAA O
ATOM	621	N	LEU	63	39.985	-2.734	51.383	1.00	46.90	AAAA N
ATOM	623	CA	LEU	63	40.003	-2.443	52.805	1.00	49.11	AAAA C

ATOM	624	CB	LEU	63	40.274	-0.953	53.027	1.00	41.41	AAAA C
ATOM	625	CG	LEU	63	40.265	-0.423	54.443	1.00	53.41	AAAA C
ATOM	626	CD1	LEU	63	41.172	-1.164	55.416	1.00	48.27	AAAA C
ATOM	627	CD2	LEU	63	40.637	1.047	54.246	1.00	50.51	AAAA C
ATOM	628	C	LEU	63	38.643	-2.881	53.323	1.00	54.20	AAAA C
ATOM	629	O	LEU	63	37.587	-2.430	52.837	1.00	57.73	AAAA O
ATOM	630	N	GLU	64	38.658	-3.862	54.190	1.00	53.97	AAAA N
ATOM	631	CA	GLU	64	37.462	-4.448	54.749	1.00	56.96	AAAA C
ATOM	633	CB	GLU	64	37.689	-5.956	54.734	1.00	65.33	AAAA C
ATOM	634	CG	GLU	64	37.832	-6.484	53.293	1.00	75.14	AAAA C
ATOM	635	CD	GLU	64	37.404	-7.940	53.128	1.00	78.10	AAAA C
ATOM	636	OE1	GLU	64	37.424	-8.698	54.132	1.00	63.93	AAAA O
ATOM	637	OE2	GLU	64	37.036	-8.320	51.978	1.00	88.77	AAAA O
ATOM	638	C	GLU	64	37.096	-4.007	56.163	1.00	57.12	AAAA C
ATOM	639	O	GLU	64	35.986	-4.332	56.600	1.00	59.82	AAAA O
ATOM	640	N	SER	65	37.766	-3.042	56.761	1.00	50.64	AAAA N
ATOM	642	CA	SER	65	37.539	-2.523	58.060	1.00	47.19	AAAA C
ATOM	643	CB	SER	65	37.743	-3.596	59.139	1.00	49.24	AAAA C
ATOM	644	OG	SER	65	37.501	-2.971	60.429	1.00	50.90	AAAA O
ATOM	646	C	SER	65	38.516	-1.405	58.432	1.00	48.35	AAAA C
ATOM	647	O	SER	65	39.716	-1.692	58.374	1.00	52.75	AAAA O
ATOM	649	N	LEU	66	38.054	-0.289	58.984	1.00	41.03	AAAA N
ATOM	650	CA	LEU	66	38.956	0.758	59.405	1.00	41.94	AAAA C
ATOM	651	CB	LEU	66	38.247	2.083	59.498	1.00	25.25	AAAA C
ATOM	652	CG	LEU	66	37.283	2.476	58.402	1.00	34.49	AAAA C
ATOM	653	CD1	LEU	66	36.974	3.951	58.512	1.00	30.81	AAAA C
ATOM	654	CD2	LEU	66	37.767	2.200	56.994	1.00	34.34	AAAA C
ATOM	655	C	LEU	66	39.646	0.462	60.734	1.00	45.39	AAAA C
ATOM	656	O	LEU	66	40.762	0.947	60.927	1.00	41.05	AAAA O
ATOM	657	N	GLY	67	39.000	-0.346	61.583	1.00	45.21	AAAA N
ATOM	659	CA	GLY	67	39.773	-0.672	62.799	1.00	48.14	AAAA C
ATOM	660	C	GLY	67	40.998	-1.508	62.445	1.00	44.51	AAAA C
ATOM	661	O	GLY	67	41.855	-1.724	63.287	1.00	45.42	AAAA O
ATOM	662	N	ASP	68	41.013	-2.189	61.309	1.00	47.60	AAAA N
ATOM	664	CA	ASP	68	42.194	-2.834	60.738	1.00	50.99	AAAA C
ATOM	665	CB	ASP	68	42.012	-3.417	59.361	1.00	39.43	AAAA C
ATOM	666	CG	ASP	68	41.205	-4.679	59.311	1.00	45.82	AAAA C
ATOM	667	OD1	ASP	68	40.912	-5.341	60.320	1.00	44.69	AAAA O
ATOM	668	OD2	ASP	68	40.819	-5.065	58.187	1.00	47.23	AAAA O
ATOM	669	C	ASP	68	43.363	-1.837	60.596	1.00	45.89	AAAA C
ATOM	670	O	ASP	68	44.436	-2.269	60.903	1.00	44.84	AAAA O
ATOM	671	N	LEU	69	43.145	-0.609	60.247	1.00	42.49	AAAA N
ATOM	673	CA	LEU	69	44.175	0.352	60.048	1.00	45.80	AAAA C
ATOM	674	CB	LEU	69	43.920	1.393	58.945	1.00	45.25	AAAA C
ATOM	675	CG	LEU	69	43.902	0.882	57.494	1.00	54.25	AAAA C
ATOM	676	CD1	LEU	69	43.541	2.037	56.565	1.00	47.26	AAAA C
ATOM	677	CD2	LEU	69	45.211	0.200	57.113	1.00	50.76	AAAA C
ATOM	678	C	LEU	69	44.347	1.107	61.350	1.00	49.50	AAAA C
ATOM	679	O	LEU	69	45.470	1.210	61.851	1.00	54.51	AAAA O
ATOM	680	N	PHE	70	43.296	1.737	61.869	1.00	44.60	AAAA N
ATOM	682	CA	PHE	70	43.423	2.564	63.046	1.00	39.67	AAAA C
ATOM	683	CB	PHE	70	42.997	3.973	62.700	1.00	26.08	AAAA C
ATOM	684	CG	PHE	70	43.465	4.501	61.390	1.00	45.32	AAAA C
ATOM	685	CD1	PHE	70	42.532	4.749	60.384	1.00	47.41	AAAA C
ATOM	686	CD2	PHE	70	44.815	4.767	61.130	1.00	48.77	AAAA C
ATOM	687	CE1	PHE	70	42.945	5.263	59.159	1.00	56.16	AAAA C
ATOM	688	CE2	PHE	70	45.229	5.256	59.895	1.00	47.24	AAAA C
ATOM	689	CZ	PHE	70	44.293	5.506	58.896	1.00	49.54	AAAA C
ATOM	690	C	PHE	70	42.655	1.999	64.219	1.00	40.09	AAAA C
ATOM	691	O	PHE	70	41.874	2.734	64.838	1.00	35.74	AAAA O
ATOM	692	N	PRO	71	43.053	0.852	64.768	1.00	39.19	AAAA N
ATOM	693	CD	PRO	71	44.269	0.058	64.411	1.00	39.94	AAAA C
ATOM	694	CA	PRO	71	42.444	0.237	65.899	1.00	35.30	AAAA C
ATOM	695	CB	PRO	71	43.308	-0.983	66.246	1.00	38.03	AAAA C
ATOM	696	CG	PRO	71	44.669	-0.564	65.717	1.00	38.36	AAAA C
ATOM	697	C	PRO	71	42.453	1.089	67.126	1.00	33.72	AAAA C
ATOM	698	O	PRO	71	42.005	0.630	68.159	1.00	39.32	AAAA O
ATOM	699	N	ASN	72	43.058	2.220	67.231	1.00	36.55	AAAA N
ATOM	701	CA	ASN	72	43.204	3.032	68.401	1.00	32.60	AAAA C
ATOM	702	CB	ASN	72	44.637	2.916	68.962	1.00	36.89	AAAA C
ATOM	703	CG	ASN	72	44.735	1.638	69.761	1.00	47.03	AAAA C
ATOM	704	OD1	ASN	72	44.644	1.619	70.979	1.00	64.42	AAAA O
ATOM	705	ND2	ASN	72	44.880	0.475	69.169	1.00	63.17	AAAA N
ATOM	708	C	ASN	72	42.875	4.477	68.135	1.00	30.11	AAAA C
ATOM	709	O	ASN	72	43.099	5.201	69.104	1.00	36.53	AAAA O
ATOM	710	N	LEU	73	42.309	4.809	66.978	1.00	27.62	AAAA N
ATOM	712	CA	LEU	73	41.940	6.207	66.730	1.00	34.07	AAAA C
ATOM	713	CB	LEU	73	41.476	6.373	65.292	1.00	28.37	AAAA C
ATOM	714	CG	LEU	73	40.819	7.713	64.882	1.00	29.33	AAAA C
ATOM	715	CD1	LEU	73	41.918	8.721	64.963	1.00	31.86	AAAA C
ATOM	716	CD2	LEU	73	40.202	7.518	63.478	1.00	32.07	AAAA C
ATOM	717	C	LEU	73	40.929	6.569	67.817	1.00	32.14	AAAA C
ATOM	718	O	LEU	73	40.073	5.737	68.081	1.00	35.02	AAAA O
ATOM	719	N	THR	74	41.081	7.585	68.582	1.00	29.47	AAAA N
ATOM	721	CA	THR	74	40.150	7.826	69.683	1.00	34.80	AAAA C

ATOM	722	CB	THR	74	41.028	7.744	70.952	1.00	46.09	AAAA C
ATOM	723	OG1	THR	74	41.729	6.485	70.880	1.00	46.30	AAAA O
ATOM	725	OG2	THR	74	40.262	7.831	72.253	1.00	39.45	AAAA C
ATOM	726	C	THR	74	39.424	9.155	69.602	1.00	35.48	AAAA C
ATOM	727	O	THR	74	38.270	9.322	70.077	1.00	35.32	AAAA O
ATOM	728	N	VAL	75	40.047	10.198	69.073	1.00	29.80	AAAA N
ATOM	730	CA	VAL	75	39.351	11.474	68.892	1.00	34.91	AAAA C
ATOM	731	CB	VAL	75	39.856	12.445	69.955	1.00	26.03	AAAA C
ATOM	732	CG1	VAL	75	39.173	13.801	69.934	1.00	24.51	AAAA C
ATOM	733	CG2	VAL	75	39.675	11.910	71.366	1.00	19.87	AAAA C
ATOM	734	C	VAL	75	39.613	12.045	67.494	1.00	37.57	AAAA C
ATOM	735	O	VAL	75	40.724	11.808	67.022	1.00	35.99	AAAA O
ATOM	736	N	ILE	76	38.600	12.555	66.796	1.00	35.91	AAAA N
ATOM	738	CA	ILE	76	38.696	13.340	65.592	1.00	31.48	AAAA C
ATOM	739	CB	ILE	76	37.831	12.769	64.492	1.00	29.60	AAAA C
ATOM	740	CG2	ILE	76	37.856	13.630	63.208	1.00	19.54	AAAA C
ATOM	741	CG1	ILE	76	38.222	11.314	64.277	1.00	28.52	AAAA C
ATOM	742	CD1	ILE	76	37.149	10.556	63.478	1.00	28.85	AAAA C
ATOM	743	C	ILE	76	38.157	14.718	66.000	1.00	33.84	AAAA C
ATOM	744	O	ILE	76	36.987	14.777	66.274	1.00	38.84	AAAA O
ATOM	745	N	ARG	77	38.906	15.733	66.230	1.00	30.32	AAAA N
ATOM	747	CA	ARG	77	38.605	16.901	67.021	1.00	30.82	AAAA C
ATOM	748	CB	ARG	77	39.961	17.475	67.461	1.00	26.62	AAAA C
ATOM	749	CG	ARG	77	39.993	18.836	68.058	1.00	52.42	AAAA C
ATOM	750	CD	ARG	77	41.290	18.957	68.908	1.00	49.10	AAAA C
ATOM	751	NE	ARG	77	41.411	17.817	69.773	1.00	39.23	AAAA N
ATOM	753	CZ	ARG	77	40.977	18.016	71.064	1.00	48.79	AAAA C
ATOM	754	NH1	ARG	77	40.440	19.104	71.610	1.00	30.34	AAAA N
ATOM	757	NH2	ARG	77	41.061	17.012	71.941	1.00	40.38	AAAA N
ATOM	760	C	ARG	77	37.643	17.733	66.225	1.00	31.75	AAAA C
ATOM	761	O	ARG	77	36.944	18.637	66.664	1.00	31.40	AAAA O
ATOM	762	N	GLY	78	37.688	17.661	64.884	1.00	32.87	AAAA N
ATOM	764	CA	GLY	78	36.982	18.409	63.950	1.00	16.23	AAAA C
ATOM	765	C	GLY	78	37.199	19.880	64.063	1.00	31.58	AAAA C
ATOM	766	O	GLY	78	36.363	20.775	63.674	1.00	34.03	AAAA O
ATOM	767	N	TRP	79	38.439	20.321	64.304	1.00	31.21	AAAA N
ATOM	769	CA	TRP	79	38.757	21.740	64.337	1.00	30.80	AAAA C
ATOM	770	CB	TRP	79	40.177	21.943	64.845	1.00	39.07	AAAA C
ATOM	771	CG	TRP	79	40.626	23.343	65.164	1.00	36.64	AAAA C
ATOM	772	CD2	TRP	79	41.691	24.001	64.433	1.00	28.52	AAAA C
ATOM	773	CE2	TRP	79	41.826	25.288	65.002	1.00	36.49	AAAA C
ATOM	774	CE3	TRP	79	42.473	23.625	63.370	1.00	37.96	AAAA C
ATOM	775	CD1	TRP	79	40.199	24.235	66.113	1.00	29.59	AAAA C
ATOM	776	NE1	TRP	79	40.917	25.413	66.054	1.00	27.67	AAAA N
ATOM	778	CZ2	TRP	79	42.770	26.213	64.543	1.00	31.83	AAAA C
ATOM	779	CZ3	TRP	79	43.389	24.548	62.876	1.00	46.14	AAAA C
ATOM	780	CH2	TRP	79	43.525	25.794	63.470	1.00	35.31	AAAA C
ATOM	781	C	TRP	79	38.606	22.418	62.986	1.00	28.75	AAAA C
ATOM	782	O	TRP	79	38.585	23.624	62.961	1.00	23.61	AAAA O
ATOM	783	N	LYS	80	38.659	21.684	61.895	1.00	31.84	AAAA N
ATOM	785	CA	LYS	80	38.305	22.153	60.573	1.00	32.78	AAAA C
ATOM	786	CB	LYS	80	39.453	22.498	59.689	1.00	41.17	AAAA C
ATOM	787	CG	LYS	80	39.838	23.911	59.470	1.00	34.69	AAAA C
ATOM	788	CD	LYS	80	41.025	24.350	60.306	1.00	44.77	AAAA C
ATOM	789	CE	LYS	80	41.276	25.811	59.898	1.00	50.41	AAAA C
ATOM	790	NZ	LYS	80	42.530	25.752	59.092	1.00	67.26	AAAA N
ATOM	791	C	LYS	80	37.585	20.960	59.917	1.00	34.52	AAAA C
ATOM	792	O	LYS	80	37.950	19.843	60.237	1.00	37.62	AAAA O
ATOM	793	N	LEU	81	36.477	21.267	59.207	1.00	31.77	AAAA N
ATOM	795	CA	LEU	81	35.742	20.157	58.600	1.00	31.02	AAAA C
ATOM	796	CB	LEU	81	34.290	20.315	59.092	1.00	31.20	AAAA C
ATOM	797	CG	LEU	81	34.115	20.319	60.632	1.00	36.97	AAAA C
ATOM	798	CD1	LEU	81	32.832	21.080	60.954	1.00	27.98	AAAA C
ATOM	799	CD2	LEU	81	34.089	18.955	61.297	1.00	28.77	AAAA C
ATOM	800	C	LEU	81	35.733	20.023	57.104	1.00	29.86	AAAA C
ATOM	801	O	LEU	81	36.082	20.947	56.368	1.00	29.34	AAAA O
ATOM	802	N	PHE	82	35.430	18.813	56.594	1.00	27.78	AAAA N
ATOM	804	CA	PHE	82	35.176	18.653	55.182	1.00	28.68	AAAA C
ATOM	805	CB	PHE	82	35.513	17.226	54.795	1.00	32.78	AAAA C
ATOM	806	CG	PHE	82	35.348	16.901	53.357	1.00	30.48	AAAA C
ATOM	807	CD1	PHE	82	36.378	17.130	52.447	1.00	32.86	AAAA C
ATOM	808	CD2	PHE	82	34.142	16.361	52.914	1.00	30.93	AAAA C
ATOM	809	CE1	PHE	82	36.217	16.769	51.104	1.00	43.27	AAAA C
ATOM	810	CE2	PHE	82	33.963	16.061	51.538	1.00	26.30	AAAA C
ATOM	811	CZ	PHE	82	35.005	16.238	50.672	1.00	37.73	AAAA C
ATOM	812	C	PHE	82	33.670	18.911	54.993	1.00	30.06	AAAA C
ATOM	813	O	PHE	82	32.830	18.045	55.278	1.00	27.36	AAAA O
ATOM	814	N	TYR	83	33.301	20.148	54.770	1.00	31.68	AAAA N
ATOM	815	CA	TYR	83	31.911	20.605	54.633	1.00	40.76	AAAA C
ATOM	816	C	TYR	83	31.043	19.977	55.726	1.00	44.00	AAAA C
ATOM	817	O	TYR	83	30.075	19.210	55.487	1.00	50.47	AAAA O
ATOM	818	CB	TYR	83	31.359	20.199	53.269	1.00	31.55	AAAA C
ATOM	819	CG	TYR	83	32.196	20.742	52.117	0.01	20.00	AAAA C
ATOM	820	CD1	TYR	83	33.254	19.982	51.609	0.01	20.00	AAAA C
ATOM	821	CD2	TYR	83	31.906	21.998	51.575	0.01	20.00	AAAA C

ATOM	822	CE1	TYR	83	34.027	20.480	50.556	0.01	20.00	AAAA C
ATOM	823	CE2	TYR	83	32.679	22.496	50.521	0.01	20.00	AAAA C
ATOM	824	CZ	TYR	83	33.740	21.737	50.012	0.01	20.00	AAAA C
ATOM	825	OH	TYR	83	34.492	22.222	48.989	0.01	20.00	AAAA O
ATOM	826	N	ASN	84	31.043	20.461	56.924	1.00	40.91	AAAA N
ATOM	827	CA	ASN	84	30.250	20.057	58.056	1.00	36.54	AAAA C
ATOM	828	CB	ASN	84	28.763	20.046	57.700	1.00	47.84	AAAA C
ATOM	829	CG	ASN	84	28.274	21.164	56.797	1.00	60.75	AAAA C
ATOM	830	OD1	ASN	84	28.319	22.343	57.119	1.00	45.55	AAAA O
ATOM	831	ND2	ASN	84	27.839	20.876	55.552	1.00	65.98	AAAA N
ATOM	832	C	ASN	84	30.686	18.679	58.556	1.00	36.33	AAAA C
ATOM	833	O	ASN	84	30.137	18.206	59.580	1.00	38.24	AAAA O
ATOM	834	N	TYR	85	31.455	17.900	57.800	1.00	32.78	AAAA N
ATOM	836	CA	TYR	85	31.617	16.504	58.202	1.00	35.45	AAAA C
ATOM	837	CB	TYR	85	31.473	15.579	57.000	1.00	35.54	AAAA C
ATOM	838	CG	TYR	85	30.078	15.733	56.453	1.00	41.35	AAAA C
ATOM	839	CD1	TYR	85	29.868	16.291	55.199	1.00	38.22	AAAA C
ATOM	840	CE1	TYR	85	28.611	16.445	54.704	1.00	40.83	AAAA C
ATOM	841	CD2	TYR	85	28.954	15.371	57.200	1.00	47.42	AAAA C
ATOM	842	CE2	TYR	85	27.661	15.533	56.705	1.00	45.91	AAAA C
ATOM	843	CZ	TYR	85	27.497	16.072	55.445	1.00	46.06	AAAA C
ATOM	844	OH	TYR	85	26.258	16.315	54.886	1.00	46.05	AAAA O
ATOM	846	C	TYR	85	32.977	16.367	58.891	1.00	32.08	AAAA C
ATOM	847	O	TYR	85	33.943	16.977	58.495	1.00	37.44	AAAA O
ATOM	848	N	ALA	86	33.027	15.691	59.979	1.00	30.21	AAAA N
ATOM	850	CA	ALA	86	34.257	15.325	60.670	1.00	34.10	AAAA C
ATOM	851	CB	ALA	86	33.999	15.370	62.157	1.00	25.48	AAAA C
ATOM	852	C	ALA	86	34.729	13.962	60.216	1.00	32.67	AAAA C
ATOM	853	O	ALA	86	35.795	13.481	60.577	1.00	35.10	AAAA O
ATOM	854	N	LEU	87	33.832	13.173	59.597	1.00	28.56	AAAA N
ATOM	856	CA	LEU	87	34.188	11.805	59.323	1.00	29.26	AAAA C
ATOM	857	CB	LEU	87	33.798	10.860	60.471	1.00	13.64	AAAA C
ATOM	858	CG	LEU	87	33.801	9.363	60.188	1.00	25.77	AAAA C
ATOM	859	CD1	LEU	87	35.140	8.915	59.571	1.00	27.21	AAAA C
ATOM	860	CD2	LEU	87	33.637	8.432	61.393	1.00	23.52	AAAA C
ATOM	861	C	LEU	87	33.530	11.429	58.021	1.00	35.60	AAAA C
ATOM	862	O	LEU	87	32.320	11.421	58.091	1.00	38.97	AAAA O
ATOM	863	N	VAL	88	34.174	11.300	56.975	1.00	37.86	AAAA N
ATOM	865	CA	VAL	88	33.438	11.032	55.629	1.00	33.32	AAAA C
ATOM	866	CB	VAL	88	33.666	10.095	54.853	1.00	22.38	AAAA C
ATOM	867	CG1	VAL	88	32.974	11.675	53.261	1.00	19.24	AAAA C
ATOM	868	CG2	VAL	88	33.165	13.402	55.042	1.00	13.27	AAAA C
ATOM	869	C	VAL	88	33.898	9.684	55.114	1.00	31.79	AAAA C
ATOM	870	O	VAL	88	35.069	9.407	55.117	1.00	33.57	AAAA O
ATOM	871	N	ILE	89	33.078	8.728	54.822	1.00	31.08	AAAA N
ATOM	873	CA	ILE	89	33.361	7.433	54.280	1.00	30.45	AAAA C
ATOM	874	CB	ILE	89	32.941	6.384	55.296	1.00	30.17	AAAA C
ATOM	875	CG2	ILE	89	32.898	4.954	54.901	1.00	37.24	AAAA C
ATOM	876	CG1	ILE	89	33.893	6.420	56.500	1.00	24.92	AAAA C
ATOM	877	CD1	ILE	89	33.424	5.613	57.675	1.00	23.96	AAAA C
ATOM	878	C	ILE	89	32.509	7.206	53.027	1.00	40.64	AAAA C
ATOM	879	O	ILE	89	31.330	6.891	53.205	1.00	38.69	AAAA O
ATOM	880	N	PHE	90	33.082	7.464	51.845	1.00	41.45	AAAA N
ATOM	882	CA	PHE	90	32.346	7.371	50.591	1.00	37.67	AAAA C
ATOM	883	CB	PHE	90	32.347	8.776	50.110	1.00	32.17	AAAA C
ATOM	884	CG	PHE	90	31.581	9.081	48.865	1.00	39.77	AAAA C
ATOM	885	CD1	PHE	90	30.387	9.772	49.025	1.00	32.02	AAAA C
ATOM	886	CD2	PHE	90	32.052	9.721	47.620	1.00	29.28	AAAA C
ATOM	887	CE1	PHE	90	29.611	10.111	47.938	1.00	33.30	AAAA C
ATOM	888	CE2	PHE	90	31.290	9.086	46.534	1.00	43.09	AAAA C
ATOM	889	CZ	PHE	90	30.083	9.764	46.687	1.00	50.24	AAAA C
ATOM	890	C	PHE	90	32.856	6.384	49.557	1.00	40.72	AAAA C
ATOM	891	O	PHE	90	34.027	6.296	49.203	1.00	46.15	AAAA O
ATOM	892	N	GLU	91	32.024	5.519	49.001	1.00	39.16	AAAA N
ATOM	894	CA	GLU	91	32.248	4.601	47.954	1.00	42.45	AAAA C
ATOM	895	CB	GLU	91	32.479	5.231	46.583	1.00	38.08	AAAA C
ATOM	896	CG	GLU	91	31.136	5.865	46.250	1.00	58.86	AAAA C
ATOM	897	CD	GLU	91	30.855	5.776	44.757	1.00	63.55	AAAA C
ATOM	898	OE1	GLU	91	31.473	6.651	44.082	1.00	64.10	AAAA O
ATOM	899	OE2	GLU	91	30.058	4.813	44.573	1.00	63.64	AAAA O
ATOM	900	C	GLU	91	33.422	3.734	48.313	1.00	42.06	AAAA C
ATOM	901	O	GLU	91	34.298	3.411	47.587	1.00	44.71	AAAA O
ATOM	902	N	MET	92	33.352	3.209	49.482	1.00	46.52	AAAA N
ATOM	904	CA	MET	92	34.409	2.401	50.088	1.00	42.26	AAAA C
ATOM	905	CB	MET	92	34.299	2.659	51.584	1.00	38.37	AAAA C
ATOM	906	CG	MET	92	35.412	2.156	52.420	1.00	59.29	AAAA C
ATOM	907	SD	MET	92	36.802	3.306	52.401	1.00	57.67	AAAA S
ATOM	908	CE	MET	92	36.340	4.405	51.108	1.00	38.36	AAAA C
ATOM	909	C	MET	92	34.012	1.005	49.745	1.00	43.37	AAAA C
ATOM	910	O	MET	92	33.335	0.398	50.523	1.00	45.58	AAAA O
ATOM	911	N	THR	93	34.449	0.518	48.602	1.00	47.09	AAAA N
ATOM	913	CA	THR	93	34.175	-0.900	48.273	1.00	47.32	AAAA C
ATOM	914	CB	THR	93	34.666	-1.281	46.868	1.00	55.28	AAAA C
ATOM	915	OG1	THR	93	34.013	-0.488	45.892	1.00	57.81	AAAA O
ATOM	917	CG2	THR	93	34.332	-2.715	46.516	1.00	44.71	AAAA C

ATOM	918	C	THR	93	34.885	-1.874	49.186	1.00	51.83	AAAA C
ATOM	919	O	THR	93	36.115	-1.777	49.361	1.00	57.91	AAAA O
ATOM	920	N	ASN	94	34.237	-2.983	49.493	1.00	49.85	AAAA N
ATOM	922	CA	ASN	94	34.747	-4.069	50.285	1.00	45.64	AAAA C
ATOM	923	CB	ASN	94	36.241	-4.315	50.001	1.00	59.01	AAAA C
ATOM	924	CG	ASN	94	36.494	-4.849	48.599	1.00	75.44	AAAA C
ATOM	925	OD1	ASN	94	36.847	-4.081	47.688	1.00	77.49	AAAA O
ATOM	926	ND2	ASN	94	36.308	-6.153	48.408	1.00	79.63	AAAA N
ATOM	929	C	ASN	94	34.522	-3.838	51.763	1.00	42.58	AAAA C
ATOM	930	O	ASN	94	34.752	-4.814	52.501	1.00	46.36	AAAA O
ATOM	931	N	LEU	95	34.308	-2.609	52.182	1.00	37.28	AAAA N
ATOM	933	CA	LEU	95	34.324	-2.277	53.621	1.00	39.96	AAAA C
ATOM	934	CB	LEU	95	34.185	-0.786	53.851	1.00	34.05	AAAA C
ATOM	935	CG	LEU	95	34.323	-0.296	55.269	1.00	35.81	AAAA C
ATOM	936	CD1	LEU	95	35.785	-0.537	55.598	1.00	35.48	AAAA C
ATOM	937	CD2	LEU	95	33.847	1.177	55.344	1.00	25.46	AAAA C
ATOM	938	C	LEU	95	33.163	-2.986	54.275	1.00	43.75	AAAA C
ATOM	939	O	LEU	95	32.048	-2.936	53.772	1.00	44.04	AAAA O
ATOM	940	N	LYS	96	33.451	-3.863	55.213	1.00	46.50	AAAA N
ATOM	942	CA	LYS	96	32.364	-4.648	55.779	1.00	42.76	AAAA C
ATOM	943	CB	LYS	96	32.801	-6.075	55.995	1.00	41.41	AAAA C
ATOM	944	CG	LYS	96	32.760	-6.976	54.788	1.00	49.78	AAAA C
ATOM	945	CD	LYS	96	32.984	-8.446	55.127	1.00	58.09	AAAA C
ATOM	946	CE	LYS	96	33.772	-9.160	54.027	1.00	73.43	AAAA C
ATOM	947	NZ	LYS	96	34.098	-10.556	54.489	1.00	79.13	AAAA N
ATOM	951	C	LYS	96	31.970	-4.055	57.122	1.00	45.29	AAAA C
ATOM	952	O	LYS	96	30.978	-4.502	57.691	1.00	46.23	AAAA O
ATOM	953	N	ASP	97	32.685	-3.071	57.645	1.00	45.15	AAAA N
ATOM	955	CA	ASP	97	32.299	-2.384	58.861	1.00	42.15	AAAA C
ATOM	956	CB	ASP	97	32.294	-3.292	60.059	1.00	45.39	AAAA C
ATOM	957	CG	ASP	97	33.662	-3.562	60.624	1.00	56.95	AAAA C
ATOM	958	OD1	ASP	97	34.579	-2.825	61.012	1.00	59.88	AAAA O
ATOM	959	OD2	ASP	97	33.931	-4.782	60.714	1.00	56.01	AAAA O
ATOM	960	C	ASP	97	33.209	-1.224	59.201	1.00	41.25	AAAA C
ATOM	961	O	ASP	97	34.160	-1.074	58.437	1.00	47.03	AAAA O
ATOM	962	N	ILE	98	32.922	-0.366	60.129	1.00	40.41	AAAA N
ATOM	964	CA	ILE	98	33.675	0.920	60.340	1.00	37.83	AAAA C
ATOM	965	CB	ILE	98	32.983	2.006	61.006	1.00	38.99	AAAA C
ATOM	966	CG2	ILE	98	34.007	3.133	61.207	1.00	38.95	AAAA C
ATOM	967	CG1	ILE	98	31.835	2.499	60.092	1.00	34.84	AAAA C
ATOM	969	CD1	ILE	98	31.629	3.958	59.948	1.00	39.29	AAAA C
ATOM	970	C	ILE	98	34.954	0.532	61.114	1.00	35.11	AAAA C
ATOM	971	O	ILE	98	35.970	0.669	60.841	1.00	43.05	AAAA O
ATOM	972	N	GLY	99	34.619	-0.393	62.192	1.00	34.22	AAAA N
ATOM	973	CA	GLY	99	35.477	-0.972	63.121	1.00	33.74	AAAA C
ATOM	974	C	GLY	99	36.279	-0.084	64.024	1.00	35.90	AAAA C
ATOM	975	O	GLY	99	37.023	-0.572	64.899	1.00	38.21	AAAA O
ATOM	976	N	LEU	100	36.190	1.221	63.913	1.00	33.35	AAAA N
ATOM	978	CA	LEU	100	36.763	2.215	64.771	1.00	31.65	AAAA C
ATOM	979	CB	LEU	100	36.496	3.636	64.294	1.00	29.87	AAAA C
ATOM	980	CG	LEU	100	36.943	3.980	62.835	1.00	32.13	AAAA C
ATOM	981	CD1	LEU	100	36.710	5.479	62.610	1.00	21.38	AAAA C
ATOM	982	CD2	LEU	100	38.412	3.599	62.644	1.00	37.68	AAAA C
ATOM	983	C	LEU	100	36.312	1.976	66.194	1.00	31.94	AAAA C
ATOM	984	O	LEU	100	35.950	2.863	66.979	1.00	31.95	AAAA O
ATOM	985	N	TYR	101	36.704	0.851	66.779	1.00	31.87	AAAA N
ATOM	987	CA	TYR	101	36.329	0.395	68.071	1.00	33.33	AAAA C
ATOM	988	CB	TYR	101	36.491	-1.104	68.264	1.00	41.03	AAAA C
ATOM	989	CG	TYR	101	37.919	-1.559	68.369	1.00	46.66	AAAA C
ATOM	990	CD1	TYR	101	38.571	-1.380	69.587	1.00	51.20	AAAA C
ATOM	991	CE1	TYR	101	39.901	-1.743	69.749	1.00	49.44	AAAA C
ATOM	992	CD2	TYR	101	38.615	-2.112	67.322	1.00	45.15	AAAA C
ATOM	993	CE2	TYR	101	39.927	-2.505	67.479	1.00	47.08	AAAA C
ATOM	994	CZ	TYR	101	40.548	-2.321	68.688	1.00	49.43	AAAA C
ATOM	995	OH	TYR	101	41.834	-2.662	68.997	1.00	55.82	AAAA O
ATOM	997	C	TYR	101	36.989	1.059	69.214	1.00	33.46	AAAA C
ATOM	998	O	TYR	101	36.630	0.813	70.375	1.00	43.00	AAAA O
ATOM	999	N	ASN	102	37.752	2.091	69.068	1.00	38.12	AAAA N
ATOM	1001	CA	ASN	102	38.093	2.979	70.223	1.00	30.78	AAAA C
ATOM	1002	CB	ASN	102	39.603	2.911	70.363	1.00	48.63	AAAA C
ATOM	1003	CG	ASN	102	40.112	1.904	71.268	1.00	54.01	AAAA C
ATOM	1004	OD1	ASN	102	39.738	1.864	72.454	1.00	47.22	AAAA O
ATOM	1005	ND2	ASN	102	40.864	0.845	70.767	1.00	43.08	AAAA N
ATOM	1008	C	ASN	102	37.673	4.385	69.947	1.00	33.82	AAAA C
ATOM	1009	O	ASN	102	38.047	5.364	70.592	1.00	39.84	AAAA O
ATOM	1010	N	LEU	103	36.845	4.640	68.882	1.00	35.28	AAAA N
ATOM	1012	CA	LEU	103	36.473	6.040	68.621	1.00	36.57	AAAA C
ATOM	1013	CB	LEU	103	35.948	6.140	67.213	1.00	34.77	AAAA C
ATOM	1014	CG	LEU	103	35.525	7.492	66.612	1.00	30.32	AAAA C
ATOM	1015	CD1	LEU	103	36.606	8.513	66.646	1.00	23.20	AAAA C
ATOM	1016	CD2	LEU	103	35.198	7.169	65.146	1.00	37.10	AAAA C
ATOM	1017	C	LEU	103	35.484	6.508	69.691	1.00	37.31	AAAA C
ATOM	1018	O	LEU	103	34.449	5.874	69.837	1.00	34.24	AAAA O
ATOM	1019	N	ARG	104	35.810	7.456	70.563	1.00	33.31	AAAA N
ATOM	1021	CA	ARG	104	34.929	7.841	71.605	1.00	29.86	AAAA C

ATOM	1022	CB	ARG	104	35.569	7.657	73.018	1.00	39.17	AAAA C
ATOM	1023	CG	ARG	104	36.356	6.375	73.165	1.00	48.37	AAAA C
ATOM	1024	CD	ARG	104	35.425	5.183	73.248	1.00	50.71	AAAA C
ATOM	1025	NE	ARG	104	34.582	5.320	74.413	1.00	52.38	AAAA N
ATOM	1027	CZ	ARG	104	34.900	4.847	75.621	1.00	72.73	AAAA C
ATOM	1028	NH1	ARG	104	36.047	4.214	75.800	1.00	81.87	AAAA N
ATOM	1031	NH2	ARG	104	33.990	5.070	76.577	1.00	78.27	AAAA N
ATOM	1034	C	ARG	104	34.466	9.273	71.540	1.00	32.58	AAAA C
ATOM	1035	O	ARG	104	33.553	9.743	72.223	1.00	39.89	AAAA O
ATOM	1036	N	ASN	105	34.992	10.065	70.637	1.00	33.47	AAAA N
ATOM	1038	CA	ASN	105	34.549	11.450	70.590	1.00	30.97	AAAA C
ATOM	1044	C	ASN	105	34.907	12.149	69.310	1.00	31.00	AAAA C
ATOM	1045	O	ASN	105	36.086	12.067	69.050	1.00	37.79	AAAA O
ATOM	1039	CB	ASN	105	35.203	12.199	71.721	1.00	12.28	AAAA C
ATOM	1040	CG	ASN	105	34.786	13.568	71.756	1.00	24.93	AAAA C
ATOM	1041	OD1	ASN	105	35.125	14.549	71.127	1.00	38.14	AAAA O
ATOM	1042	ND2	ASN	105	33.828	13.985	72.649	1.00	35.96	AAAA N
ATOM	1046	N	ILE	106	33.969	12.669	68.576	1.00	31.90	AAAA N
ATOM	1048	CA	ILE	106	34.129	13.551	67.469	1.00	23.39	AAAA C
ATOM	1049	CB	ILE	106	33.239	13.185	66.307	1.00	16.54	AAAA C
ATOM	1050	CG2	ILE	106	33.132	14.408	65.374	1.00	20.38	AAAA C
ATOM	1051	CG1	ILE	106	33.928	12.034	65.558	1.00	18.30	AAAA C
ATOM	1052	CD1	ILE	106	33.055	11.293	64.643	1.00	25.48	AAAA C
ATOM	1053	C	ILE	106	33.803	14.909	68.009	1.00	27.40	AAAA C
ATOM	1054	O	ILE	106	32.628	15.106	68.243	1.00	32.86	AAAA O
ATOM	1055	N	THR	107	34.719	15.789	68.350	1.00	30.43	AAAA N
ATOM	1057	CA	THR	107	34.532	16.983	69.145	1.00	28.27	AAAA C
ATOM	1058	CB	THR	107	35.902	17.607	69.579	1.00	35.78	AAAA C
ATOM	1059	OG1	THR	107	36.819	16.503	69.738	1.00	40.26	AAAA O
ATOM	1061	CG2	THR	107	35.954	18.411	70.855	1.00	28.13	AAAA C
ATOM	1062	C	THR	107	33.728	17.950	68.332	1.00	27.95	AAAA C
ATOM	1063	O	THR	107	33.392	19.060	68.831	1.00	32.99	AAAA O
ATOM	1064	N	ARG	108	33.669	17.777	67.019	1.00	30.28	AAAA N
ATOM	1066	CA	ARG	108	33.046	18.809	66.180	1.00	31.25	AAAA C
ATOM	1067	CB	ARG	108	33.965	20.011	65.951	1.00	25.13	AAAA C
ATOM	1068	CG	ARG	108	33.105	21.174	65.543	1.00	30.68	AAAA C
ATOM	1069	CD	ARG	108	33.917	22.444	65.529	1.00	17.12	AAAA C
ATOM	1070	NE	ARG	108	33.511	23.376	64.451	1.00	33.40	AAAA N
ATOM	1072	CZ	ARG	108	34.048	23.608	63.266	1.00	46.41	AAAA C
ATOM	1073	NH1	ARG	108	35.160	22.929	62.868	1.00	40.30	AAAA N
ATOM	1076	NH2	ARG	108	33.454	24.543	62.494	1.00	39.82	AAAA N
ATOM	1079	C	ARG	108	32.701	19.328	64.784	1.00	31.50	AAAA C
ATOM	1080	O	ARG	108	33.379	17.391	64.430	1.00	32.67	AAAA O
ATOM	1081	N	GLY	109	31.567	19.909	64.284	1.00	32.60	AAAA N
ATOM	1083	CA	GLY	109	31.082	19.395	62.983	1.00	28.87	AAAA C
ATOM	1084	C	GLY	109	30.479	17.008	63.001	1.00	32.32	AAAA C
ATOM	1085	O	GLY	109	30.471	16.306	64.006	1.00	38.03	AAAA O
ATOM	1086	N	ALA	110	29.920	16.560	61.894	1.00	34.11	AAAA N
ATOM	1088	CA	ALA	110	29.086	15.371	61.833	1.00	36.77	AAAA C
ATOM	1089	CB	ALA	110	27.708	15.721	61.223	1.00	15.32	AAAA C
ATOM	1090	C	ALA	110	29.745	14.335	60.957	1.00	32.12	AAAA C
ATOM	1091	O	ALA	110	30.921	14.332	60.687	1.00	34.11	AAAA O
ATOM	1092	N	ILE	111	29.030	13.337	60.557	1.00	26.55	AAAA N
ATOM	1094	CA	ILE	111	29.569	12.273	59.771	1.00	32.90	AAAA C
ATOM	1095	CB	ILE	111	29.669	10.967	60.591	1.00	38.07	AAAA C
ATOM	1096	CG2	ILE	111	30.091	11.140	62.036	1.00	34.05	AAAA C
ATOM	1097	CG1	ILE	111	28.345	10.237	60.684	1.00	26.54	AAAA C
ATOM	1098	CD1	ILE	111	28.437	8.872	61.407	1.00	27.11	AAAA C
ATOM	1099	C	ILE	111	28.738	11.928	58.521	1.00	33.98	AAAA C
ATOM	1100	O	ILE	111	27.533	12.179	58.532	1.00	32.15	AAAA O
ATOM	1101	N	ARG	112	29.432	11.423	57.501	1.00	30.54	AAAA N
ATOM	1103	CA	ARG	112	28.773	11.107	56.247	1.00	27.48	AAAA C
ATOM	1104	CB	ARG	112	29.186	12.085	55.169	1.00	26.35	AAAA C
ATOM	1105	CG	ARG	112	28.548	11.653	53.816	1.00	25.93	AAAA C
ATOM	1106	CD	ARG	112	28.659	12.912	52.992	1.00	32.92	AAAA C
ATOM	1107	NE	ARG	112	27.950	12.726	51.770	1.00	50.34	AAAA N
ATOM	1109	CZ	ARG	112	27.778	13.503	50.720	1.00	47.61	AAAA C
ATOM	1110	NH1	ARG	112	28.334	14.695	50.696	1.00	44.92	AAAA N
ATOM	1113	NH2	ARG	112	27.012	12.925	49.789	1.00	46.00	AAAA N
ATOM	1116	C	ARG	112	29.200	9.738	55.791	1.00	29.74	AAAA C
ATOM	1117	O	ARG	112	30.343	9.611	55.406	1.00	36.52	AAAA O
ATOM	1118	N	ILE	113	28.326	8.754	55.886	1.00	33.99	AAAA N
ATOM	1120	CA	ILE	113	28.612	7.376	55.555	1.00	36.26	AAAA C
ATOM	1121	CB	ILE	113	28.457	6.461	56.760	1.00	33.27	AAAA C
ATOM	1122	CG2	ILE	113	28.850	5.021	56.449	1.00	15.95	AAAA C
ATOM	1123	CG1	ILE	113	29.374	7.012	57.874	1.00	31.92	AAAA C
ATOM	1124	CD1	ILE	113	29.324	6.250	59.176	1.00	42.34	AAAA C
ATOM	1125	C	ILE	113	27.729	6.959	54.398	1.00	39.26	AAAA C
ATOM	1126	O	ILE	113	26.637	6.482	54.664	1.00	50.72	AAAA O
ATOM	1127	N	GLU	114	28.175	7.199	53.190	1.00	35.86	AAAA N
ATOM	1129	CA	GLU	114	27.491	7.103	51.935	1.00	38.76	AAAA C
ATOM	1130	CB	GLU	114	27.471	8.443	51.216	1.00	25.58	AAAA C
ATOM	1131	CG	GLU	114	26.567	8.402	49.969	1.00	27.97	AAAA C
ATOM	1132	CD	GLU	114	26.349	9.840	49.578	1.00	36.85	AAAA C
ATOM	1133	OE1	GLU	114	26.763	10.662	50.414	1.00	45.57	AAAA O

ATOM	1134	OE2	GLU	114	25.787	10.106	48.488	1.00	35.53	AAAA O
ATOM	1135	C	GLU	114	29.039	6.072	50.944	1.00	44.17	AAAA C
ATOM	1136	O	GLU	114	29.120	5.538	51.090	1.00	49.97	AAAA O
ATOM	1137	N	LYS	115	27.191	5.556	50.096	1.00	40.55	AAAA N
ATOM	1139	CA	LYS	115	27.219	4.440	49.242	1.00	41.16	AAAA C
ATOM	1140	CB	LYS	115	27.275	4.764	47.718	1.00	23.62	AAAA C
ATOM	1141	CG	LYS	115	27.019	6.194	47.411	1.00	18.39	AAAA C
ATOM	1142	CD	LYS	115	26.537	6.355	45.982	1.00	24.74	AAAA C
ATOM	1143	CE	LYS	115	26.751	7.804	45.622	1.00	41.86	AAAA C
ATOM	1144	NZ	LYS	115	27.165	8.045	44.196	1.00	60.91	AAAA N
ATOM	1148	C	LYS	115	28.287	3.421	49.611	1.00	42.39	AAAA C
ATOM	1149	O	LYS	115	29.102	3.103	48.749	1.00	46.68	AAAA O
ATOM	1150	N	ASN	116	28.137	2.677	50.665	1.00	40.99	AAAA N
ATOM	1152	CA	ASN	116	29.022	1.570	50.976	1.00	37.33	AAAA C
ATOM	1153	CB	ASN	116	29.534	1.868	52.381	1.00	46.12	AAAA C
ATOM	1154	CG	ASN	116	30.372	3.153	52.345	1.00	48.92	AAAA C
ATOM	1155	OD1	ASN	116	31.337	3.016	51.583	1.00	38.59	AAAA O
ATOM	1156	ND2	ASN	116	29.927	4.174	53.056	1.00	37.35	AAAA N
ATOM	1159	C	ASN	116	28.275	0.277	50.974	1.00	42.52	AAAA C
ATOM	1160	O	ASN	116	28.067	-0.361	52.033	1.00	48.24	AAAA O
ATOM	1161	N	ALA	117	27.989	-0.188	49.772	1.00	40.94	AAAA N
ATOM	1163	CA	ALA	117	27.195	-1.376	49.542	1.00	43.35	AAAA C
ATOM	1164	CB	ALA	117	27.494	-1.884	48.156	1.00	47.63	AAAA C
ATOM	1165	C	ALA	117	27.294	-2.504	50.529	1.00	46.55	AAAA C
ATOM	1166	O	ALA	117	26.211	-2.998	50.890	1.00	51.24	AAAA O
ATOM	1167	N	ASP	118	28.484	-2.823	51.005	1.00	47.43	AAAA N
ATOM	1169	CA	ASP	118	28.559	-3.980	51.920	1.00	45.74	AAAA C
ATOM	1170	CB	ASP	118	29.659	-4.945	51.477	1.00	55.39	AAAA C
ATOM	1171	CG	ASP	118	29.684	-5.119	49.958	1.00	59.40	AAAA C
ATOM	1172	OD1	ASP	118	28.870	-5.976	49.608	1.00	64.40	AAAA O
ATOM	1173	OD2	ASP	118	30.448	-4.447	49.207	1.00	66.73	AAAA O
ATOM	1174	C	ASP	118	28.818	-3.586	53.353	1.00	37.29	AAAA C
ATOM	1175	O	ASP	118	29.127	-4.536	54.026	1.00	42.89	AAAA O
ATOM	1176	N	LEU	119	28.670	-2.327	53.685	1.00	36.46	AAAA N
ATOM	1178	CA	LEU	119	28.986	-1.895	55.047	1.00	40.58	AAAA C
ATOM	1179	CB	LEU	119	29.159	-0.389	55.145	1.00	34.31	AAAA C
ATOM	1180	CG	LEU	119	29.640	0.331	56.378	1.00	36.58	AAAA C
ATOM	1181	CD1	LEU	119	30.950	-0.101	56.948	1.00	35.77	AAAA C
ATOM	1182	CD2	LEU	119	29.791	1.830	56.104	1.00	29.68	AAAA C
ATOM	1183	C	LEU	119	27.937	-2.376	56.007	1.00	43.67	AAAA C
ATOM	1184	O	LEU	119	26.748	-2.248	55.743	1.00	45.32	AAAA O
ATOM	1185	N	CYS	120	28.361	-2.967	57.110	1.00	43.53	AAAA N
ATOM	1187	CA	CYS	120	27.378	-3.407	58.089	1.00	38.93	AAAA C
ATOM	1188	C	CYS	120	27.881	-3.921	59.426	1.00	41.91	AAAA C
ATOM	1189	O	CYS	120	28.660	-1.960	59.446	1.00	43.66	AAAA O
ATOM	1190	CB	CYS	120	27.285	-4.907	59.100	1.00	37.59	AAAA C
ATOM	1191	SG	CYS	120	26.568	-5.622	56.639	1.00	58.32	AAAA S
ATOM	1192	N	TYR	121	27.328	-3.456	60.509	1.00	38.05	AAAA N
ATOM	1194	CA	TYR	121	27.795	-3.010	61.927	1.00	38.68	AAAA C
ATOM	1195	CB	TYR	121	29.189	-3.572	62.130	1.00	34.61	AAAA C
ATOM	1196	CG	TYR	121	28.950	-5.032	62.519	1.00	36.52	AAAA C
ATOM	1197	CD1	TYR	121	29.087	-6.045	61.582	1.00	33.58	AAAA C
ATOM	1198	CE1	TYR	121	28.852	-7.350	61.980	1.00	41.21	AAAA C
ATOM	1199	CD2	TYR	121	28.560	-5.337	63.817	1.00	36.31	AAAA C
ATOM	1200	CE2	TYR	121	28.287	-6.630	64.201	1.00	39.48	AAAA C
ATOM	1201	CZ	TYR	121	28.432	-7.641	63.270	1.00	46.07	AAAA C
ATOM	1202	OH	TYR	121	28.161	-8.924	63.730	1.00	49.20	AAAA O
ATOM	1204	C	TYR	121	27.674	-1.523	61.789	1.00	38.83	AAAA C
ATOM	1205	O	TYR	121	28.445	-0.778	62.369	1.00	43.22	AAAA O
ATOM	1206	N	LEU	122	26.587	-1.045	61.180	1.00	39.58	AAAA N
ATOM	1208	CA	LEU	122	26.361	0.405	61.090	1.00	44.82	AAAA C
ATOM	1209	CB	LEU	122	25.990	0.715	59.634	1.00	46.48	AAAA C
ATOM	1210	CG	LEU	122	26.497	2.014	59.108	1.00	44.44	AAAA C
ATOM	1211	CD1	LEU	122	25.778	2.448	57.859	1.00	32.19	AAAA C
ATOM	1212	CD2	LEU	122	26.136	3.057	60.170	1.00	47.76	AAAA C
ATOM	1213	C	LEU	122	25.212	0.910	61.935	1.00	44.85	AAAA C
ATOM	1214	O	LEU	122	25.269	1.759	62.839	1.00	47.66	AAAA O
ATOM	1215	N	SER	123	24.104	0.137	61.843	1.00	40.12	AAAA N
ATOM	1217	CA	SER	123	22.949	0.435	62.703	1.00	33.98	AAAA C
ATOM	1218	CB	SER	123	21.754	-0.330	62.239	1.00	19.26	AAAA C
ATOM	1219	OG	SER	123	21.964	-1.762	62.402	1.00	34.35	AAAA O
ATOM	1221	C	SER	123	23.165	0.060	64.159	1.00	37.43	AAAA C
ATOM	1222	O	SER	123	22.326	0.280	65.025	1.00	35.33	AAAA O
ATOM	1223	N	THR	124	24.242	-0.698	64.432	1.00	39.03	AAAA N
ATOM	1225	CA	THR	124	24.554	-1.165	65.753	1.00	37.78	AAAA C
ATOM	1226	CB	THR	124	25.368	-2.461	65.719	1.00	42.39	AAAA C
ATOM	1227	OG1	THR	124	26.502	-2.020	64.924	1.00	47.70	AAAA O
ATOM	1229	CG2	THR	124	24.677	-3.622	65.006	1.00	40.93	AAAA C
ATOM	1230	C	THR	124	25.522	-0.206	66.445	1.00	39.29	AAAA C
ATOM	1231	O	THR	124	25.948	-0.642	67.499	1.00	41.41	AAAA O
ATOM	1232	N	VAL	125	25.737	1.001	65.985	1.00	37.80	AAAA N
ATOM	1234	CA	VAL	125	26.594	1.964	66.661	1.00	41.06	AAAA C
ATOM	1235	CB	VAL	125	27.683	2.542	65.714	1.00	39.50	AAAA C
ATOM	1236	CG1	VAL	125	28.570	3.599	66.352	1.00	28.36	AAAA C
ATOM	1237	CG2	VAL	125	28.693	1.565	65.110	1.00	33.07	AAAA C

ATOM	1238	C	VAL	125	25.759	3.107	67.179	1.00	41.17	AAAA C
ATOM	1239	O	VAL	125	24.941	3.750	66.531	1.00	41.22	AAAA O
ATOM	1240	N	ASP	126	26.972	3.636	68.367	1.00	44.54	AAAA N
ATOM	1242	CA	ASP	126	25.310	4.734	68.967	1.00	37.44	AAAA C
ATOM	1243	CB	ASP	126	24.862	4.335	70.342	1.00	34.73	AAAA C
ATOM	1244	CG	ASP	126	23.879	5.303	70.983	1.00	45.53	AAAA C
ATOM	1245	OD1	ASP	126	23.699	6.520	70.685	1.00	27.71	AAAA O
ATOM	1246	OD2	ASP	126	23.220	4.865	71.964	1.00	52.32	AAAA O
ATOM	1247	C	ASP	126	26.146	5.985	68.872	1.00	40.83	AAAA C
ATOM	1248	O	ASP	126	26.740	6.400	69.888	1.00	42.78	AAAA O
ATOM	1249	N	TRP	127	26.029	6.649	67.704	1.00	35.42	AAAA N
ATOM	1251	CA	TRP	127	26.777	7.856	67.410	1.00	33.02	AAAA C
ATOM	1252	CB	TRP	127	26.568	8.296	65.930	1.00	24.89	AAAA C
ATOM	1253	CG	TRP	127	27.195	7.372	64.907	1.00	34.36	AAAA C
ATOM	1254	CD2	TRP	127	28.587	7.208	64.518	1.00	28.60	AAAA C
ATOM	1255	CE2	TRP	127	28.631	6.186	63.579	1.00	29.06	AAAA C
ATOM	1256	CE3	TRP	127	29.778	7.845	64.873	1.00	35.51	AAAA C
ATOM	1257	CD1	TRP	127	26.465	6.450	64.188	1.00	18.67	AAAA C
ATOM	1258	NE1	TRP	127	27.311	5.712	63.394	1.00	42.87	AAAA N
ATOM	1260	CZ2	TRP	127	29.792	5.783	62.954	1.00	32.53	AAAA C
ATOM	1261	CZ3	TRP	127	30.972	7.445	64.285	1.00	31.51	AAAA C
ATOM	1262	CH2	TRP	127	30.937	6.405	63.336	1.00	37.86	AAAA C
ATOM	1263	C	TRP	127	26.558	9.010	68.367	1.00	36.09	AAAA C
ATOM	1264	O	TRP	127	27.382	9.977	68.497	1.00	40.87	AAAA O
ATOM	1265	N	SER	128	25.493	8.931	69.171	1.00	31.24	AAAA N
ATOM	1267	CA	SER	128	25.201	10.041	70.081	1.00	34.04	AAAA C
ATOM	1268	CB	SER	128	23.757	10.042	70.603	1.00	36.87	AAAA C
ATOM	1269	OG	SER	128	23.433	8.917	71.424	1.00	28.96	AAAA O
ATOM	1271	C	SER	128	26.133	9.975	71.292	1.00	32.39	AAAA C
ATOM	1272	O	SER	128	26.212	10.857	72.134	1.00	30.91	AAAA O
ATOM	1273	N	LEU	129	26.662	8.792	71.549	1.00	27.18	AAAA N
ATOM	1275	CA	LEU	129	27.701	8.607	72.526	1.00	36.73	AAAA C
ATOM	1276	CB	LEU	129	27.920	7.132	72.741	1.00	32.53	AAAA C
ATOM	1277	CG	LEU	129	26.795	6.324	73.371	1.00	39.28	AAAA C
ATOM	1278	CD1	LEU	129	27.292	5.024	73.975	1.00	32.54	AAAA C
ATOM	1279	CD2	LEU	129	26.237	7.117	74.560	1.00	32.12	AAAA C
ATOM	1280	C	LEU	129	29.054	9.226	72.113	1.00	38.94	AAAA C
ATOM	1281	O	LEU	129	29.645	10.001	72.874	1.00	34.50	AAAA O
ATOM	1282	N	ILE	130	29.316	9.217	70.907	1.00	42.09	AAAA N
ATOM	1284	CA	ILE	130	30.480	9.743	70.144	1.00	41.35	AAAA C
ATOM	1285	CB	ILE	130	30.793	8.886	68.901	1.00	41.73	AAAA C
ATOM	1286	CG2	ILE	130	31.992	9.434	68.176	1.00	31.95	AAAA C
ATOM	1287	CG1	ILE	130	30.969	7.413	69.347	1.00	26.64	AAAA C
ATOM	1289	CD1	ILE	130	31.053	6.457	68.165	1.00	42.68	AAAA C
ATOM	1289	C	ILE	130	30.305	11.178	69.679	1.00	46.48	AAAA C
ATOM	1290	O	ILE	130	31.224	11.985	69.966	1.00	38.46	AAAA O
ATOM	1291	N	LEU	131	29.089	11.495	69.193	1.00	45.14	AAAA N
ATOM	1293	CA	LEU	131	28.995	12.965	68.651	1.00	41.45	AAAA C
ATOM	1294	CB	LEU	131	28.499	12.816	67.259	1.00	46.81	AAAA C
ATOM	1295	CG	LEU	131	28.823	13.905	66.878	1.00	36.79	AAAA C
ATOM	1296	CD1	LEU	131	29.128	11.405	65.324	1.00	30.15	AAAA C
ATOM	1297	CD2	LEU	131	27.625	13.581	65.334	1.00	19.92	AAAA C
ATOM	1298	C	LEU	131	27.661	13.525	69.295	1.00	39.29	AAAA C
ATOM	1299	O	LEU	131	26.599	12.967	69.311	1.00	37.75	AAAA O
ATOM	1300	N	ASP	132	27.742	14.811	69.518	1.00	33.73	AAAA N
ATOM	1302	CA	ASP	132	26.610	15.542	70.003	1.00	38.20	AAAA C
ATOM	1303	CB	ASP	132	27.017	16.944	70.381	1.00	43.17	AAAA C
ATOM	1304	CG	ASP	132	27.349	17.137	71.834	1.00	43.29	AAAA C
ATOM	1305	OD1	ASP	132	27.536	16.122	72.521	1.00	47.12	AAAA O
ATOM	1306	OD2	ASP	132	27.413	18.331	72.208	1.00	60.58	AAAA O
ATOM	1307	C	ASP	132	25.520	15.659	68.946	1.00	43.46	AAAA C
ATOM	1308	O	ASP	132	24.481	15.032	68.939	1.00	49.32	AAAA O
ATOM	1309	N	ALA	133	25.754	16.398	67.900	1.00	45.03	AAAA N
ATOM	1311	CA	ALA	133	24.947	16.776	66.773	1.00	38.62	AAAA C
ATOM	1312	CB	ALA	133	25.628	17.987	66.092	1.00	33.92	AAAA C
ATOM	1313	C	ALA	133	24.694	15.669	65.775	1.00	33.33	AAAA C
ATOM	1314	O	ALA	133	24.777	15.791	64.517	1.00	33.71	AAAA O
ATOM	1315	N	VAL	134	24.115	14.565	66.219	1.00	27.88	AAAA N
ATOM	1317	CA	VAL	134	23.813	13.440	65.377	1.00	29.90	AAAA C
ATOM	1318	CB	VAL	134	23.202	12.241	66.120	1.00	40.63	AAAA C
ATOM	1319	CG1	VAL	134	24.265	11.441	66.855	1.00	35.20	AAAA C
ATOM	1320	CG2	VAL	134	22.095	12.701	67.068	1.00	30.84	AAAA C
ATOM	1321	C	VAL	134	22.735	13.732	64.353	1.00	36.98	AAAA C
ATOM	1322	O	VAL	134	22.616	13.106	63.292	1.00	32.95	AAAA O
ATOM	1323	N	SER	135	21.920	14.777	64.626	1.00	39.65	AAAA N
ATOM	1325	CA	SER	135	20.886	15.139	63.692	1.00	43.12	AAAA C
ATOM	1326	CB	SER	135	20.093	16.277	64.305	1.00	45.19	AAAA C
ATOM	1327	OG	SER	135	20.882	17.369	64.684	1.00	39.25	AAAA O
ATOM	1329	C	SER	135	21.396	15.516	62.309	1.00	41.15	AAAA C
ATOM	1330	O	SER	135	20.615	15.642	61.359	1.00	43.81	AAAA O
ATOM	1331	N	ASN	136	22.615	15.911	62.165	1.00	41.11	AAAA N
ATOM	1333	CA	ASN	136	23.298	16.353	60.978	1.00	37.21	AAAA C
ATOM	1334	CB	ASN	136	24.324	17.372	61.399	1.00	39.66	AAAA C
ATOM	1335	CG	ASN	136	23.724	18.709	61.717	1.00	36.59	AAAA C
ATOM	1336	OD1	ASN	136	22.695	19.079	61.149	1.00	50.81	AAAA O

ATOM	1337	ND2	ASN	136	24.379	19.441	62.585	1.00	47.85	AAAA N
ATOM	1340	C	ASN	136	24.031	15.230	60.259	1.00	35.31	AAAA C
ATOM	1341	O	ASN	136	24.535	15.484	59.194	1.00	38.70	AAAA O
ATOM	1342	N	ASN	137	24.057	14.035	60.793	1.00	29.11	AAAA N
ATOM	1344	CA	ASN	137	24.721	12.959	60.126	1.00	32.98	AAAA C
ATOM	1345	CB	ASN	137	24.737	11.703	61.033	1.00	24.45	AAAA C
ATOM	1346	CG	ASN	137	25.631	11.965	62.217	1.00	26.63	AAAA C
ATOM	1347	OD1	ASN	137	26.070	13.121	62.369	1.00	30.22	AAAA O
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ATOM	1351	C	ASN	137	23.950	12.749	58.817	1.00	35.89	AAAA C
ATOM	1352	O	ASN	137	22.716	12.755	58.855	1.00	38.57	AAAA O
ATOM	1353	N	TYR	138	24.592	12.251	57.785	1.00	32.86	AAAA N
ATOM	1355	CA	TYR	138	24.093	11.983	56.489	1.00	30.25	AAAA C
ATOM	1356	CB	TYR	138	24.682	12.861	55.421	1.00	27.10	AAAA C
ATOM	1357	CG	TYR	138	24.018	12.741	54.078	1.00	37.89	AAAA C
ATOM	1358	CD1	TYR	138	23.083	13.671	53.648	1.00	39.22	AAAA C
ATOM	1359	CE1	TYR	138	22.510	13.579	52.392	1.00	37.65	AAAA C
ATOM	1360	CD2	TYR	138	24.357	11.717	53.195	1.00	44.28	AAAA C
ATOM	1361	CE2	TYR	138	23.801	11.615	51.951	1.00	41.97	AAAA C
ATOM	1362	CZ	TYR	138	22.868	12.562	51.564	1.00	39.42	AAAA C
ATOM	1363	OH	TYR	138	22.296	12.504	50.318	1.00	45.48	AAAA O
ATOM	1365	C	TYR	138	24.373	10.578	56.051	1.00	31.33	AAAA C
ATOM	1366	O	TYR	138	25.505	10.317	55.797	1.00	37.76	AAAA O
ATOM	1367	N	ILE	139	23.461	9.660	56.116	1.00	35.40	AAAA N
ATOM	1369	CA	ILE	139	23.637	8.249	55.935	1.00	34.04	AAAA C
ATOM	1370	CB	ILE	139	23.234	7.450	57.171	1.00	28.66	AAAA C
ATOM	1371	CG2	ILE	139	23.640	5.984	57.093	1.00	21.99	AAAA C
ATOM	1372	CG1	ILE	139	23.711	8.057	58.469	1.00	42.81	AAAA C
ATOM	1373	CD1	ILE	139	24.455	7.100	59.389	1.00	52.23	AAAA C
ATOM	1374	C	ILE	139	22.729	7.708	54.830	1.00	35.73	AAAA C
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ATOM	1376	N	VAL	140	23.286	6.997	53.873	1.00	35.29	AAAA N
ATOM	1378	CA	VAL	140	22.533	6.481	52.755	1.00	32.39	AAAA C
ATOM	1379	CB	VAL	140	21.967	7.627	51.881	1.00	36.05	AAAA C
ATOM	1380	CG1	VAL	140	22.800	8.375	50.881	1.00	25.89	AAAA C
ATOM	1381	CG2	VAL	140	20.807	7.034	51.047	1.00	34.96	AAAA C
ATOM	1382	C	VAL	140	23.422	5.670	51.874	1.00	41.96	AAAA C
ATOM	1383	O	VAL	140	24.537	6.172	51.637	1.00	44.03	AAAA O
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ATOM	1392	CB	ASN	142	25.257	1.774	54.187	1.00	43.12	AAAA C
ATOM	1393	CG	ASN	142	26.131	3.022	54.152	1.00	42.00	AAAA C
ATOM	1394	OD1	ASN	142	26.984	3.077	53.269	1.00	40.47	AAAA O
ATOM	1395	ND2	ASN	142	25.948	4.022	55.019	1.00	41.98	AAAA N
ATOM	1398	C	ASN	142	24.153	0.066	52.687	1.00	45.84	AAAA C
ATOM	1399	O	ASN	142	23.113	-0.015	52.055	1.00	49.65	AAAA O
ATOM	1400	N	LYS	143	24.674	-0.990	53.272	1.00	45.23	AAAA N
ATOM	1402	CA	LYS	143	24.073	-2.299	53.195	1.00	49.14	AAAA C
ATOM	1403	CB	LYS	143	25.166	-3.328	53.433	1.00	41.49	AAAA C
ATOM	1404	CG	LYS	143	24.750	-4.686	53.832	1.00	44.96	AAAA C
ATOM	1405	CD	LYS	143	25.512	-5.743	53.100	1.00	48.66	AAAA C
ATOM	1406	CE	LYS	143	25.043	-7.131	53.558	1.00	38.35	AAAA C
ATOM	1407	NZ	LYS	143	26.080	-8.093	53.040	1.00	53.83	AAAA N
ATOM	1411	C	LYS	143	22.902	-2.431	54.169	1.00	52.85	AAAA C
ATOM	1412	O	LYS	143	22.960	-2.099	55.360	1.00	55.21	AAAA O
ATOM	1413	N	PRO	144	21.806	-3.047	53.731	1.00	52.39	AAAA N
ATOM	1414	CD	PRO	144	21.617	-3.469	52.315	1.00	52.58	AAAA C
ATOM	1415	CA	PRO	144	20.559	-3.118	54.489	1.00	48.30	AAAA C
ATOM	1416	CB	PRO	144	19.549	-3.602	53.455	1.00	51.41	AAAA C
ATOM	1417	CG	PRO	144	20.134	-3.299	52.099	1.00	50.41	AAAA C
ATOM	1419	C	PRO	144	20.621	-4.050	55.659	1.00	44.65	AAAA C
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ATOM	1421	CD	PRO	145	20.123	-2.054	57.094	1.00	38.17	AAAA C
ATOM	1422	CA	PRO	145	20.448	-4.233	58.128	1.00	40.19	AAAA C
ATOM	1423	CB	PRO	145	19.704	-3.288	59.099	1.00	37.08	AAAA C
ATOM	1424	CG	PRO	145	20.040	-1.910	58.602	1.00	33.65	AAAA C
ATOM	1425	C	PRO	145	19.993	-5.655	58.155	1.00	47.17	AAAA C
ATOM	1426	O	PRO	145	20.556	-6.592	58.768	1.00	49.05	AAAA O
ATOM	1427	N	LYS	146	18.879	-5.924	57.499	1.00	53.72	AAAA N
ATOM	1429	CA	LYS	146	18.268	-7.229	57.295	1.00	56.94	AAAA C
ATOM	1430	CB	LYS	146	16.894	-7.050	56.647	1.00	65.44	AAAA C
ATOM	1431	CG	LYS	146	16.220	-8.232	55.982	1.00	64.32	AAAA C
ATOM	1432	CD	LYS	146	14.797	-8.422	56.451	0.01	62.75	AAAA C
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ATOM	1434	NZ	LYS	146	12.720	-9.610	55.753	0.01	61.38	AAAA N
ATOM	1438	C	LYS	146	19.138	-8.138	56.446	1.00	61.40	AAAA C
ATOM	1439	O	LYS	146	19.237	-9.346	56.732	1.00	66.22	AAAA O
ATOM	1440	N	GLU	147	19.779	-7.649	55.389	1.00	62.92	AAAA N
ATOM	1442	CA	GLU	147	20.827	-8.446	54.742	1.00	67.00	AAAA C
ATOM	1443	CB	GLU	147	21.101	-8.070	53.294	1.00	62.32	AAAA C

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ATOM   1444  CG  GLU   147      19.867  -7.679  52.567  1.00 73.15      AAAA C
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ATOM   1446  OE1 GLU   147      21.339  -7.636  50.701  1.00 95.25      AAAA O
ATOM   1447  OE2 GLU   147      19.201  -7.053  50.376  1.00 87.47      AAAA O
ATOM   1448  C   GLU   147      22.136  -8.470  55.541  1.00 69.40      AAAA C
ATOM   1449  O   GLU   147      22.883  -9.437  55.361  1.00 72.86      AAAA O
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ATOM   1451  CA  CYS   148      23.693  -7.588  57.183  1.00 64.65      AAAA C
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ATOM   1454  O   CYS   148      24.473  -9.524  58.414  1.00 65.89      AAAA O
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ATOM   1456  SG  CYS   148      24.565  -5.091  56.808  1.00 59.22      AAAA S
ATOM   1457  N   GLY   149      22.514  -8.743  58.977  1.00 67.88      AAAA N
ATOM   1459  CA  GLY   149      22.387  -9.744  60.029  1.00 62.15      AAAA C
ATOM   1460  C   GLY   149      23.443  -9.627  61.120  1.00 59.18      AAAA C
ATOM   1461  O   GLY   149      23.925 -10.603  61.699  1.00 61.11      AAAA O
ATOM   1462  N   ASP   150      23.717  -8.426  61.596  1.00 54.88      AAAA N
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ATOM   1465  CB  ASP   150      25.041  -6.703  62.750  1.00 49.10      AAAA C
ATOM   1466  CG  ASP   150      25.320  -6.034  61.410  1.00 58.50      AAAA C
ATOM   1467  OD1 ASP   150      25.726  -6.796  60.480  1.00 57.73      AAAA O
ATOM   1468  OD2 ASP   150      25.102  -4.819  61.363  1.00 49.69      AAAA O
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ATOM   1473  CA  LEU   151      25.314  -9.908  65.853  1.00 52.79      AAAA C
ATOM   1474  CB  LEU   151      25.208 -11.409  65.806  1.00 58.55      AAAA C
ATOM   1475  CG  LEU   151      24.063 -12.101  65.092  1.00 69.45      AAAA C
ATOM   1476  CD1 LEU   151      24.515 -13.421  64.489  1.00 65.26      AAAA C
ATOM   1477  CD2 LEU   151      22.837 -12.372  65.951  1.00 65.43      AAAA C
ATOM   1478  C   LEU   151      26.409  -9.454  66.805  1.00 51.93      AAAA C
ATOM   1479  O   LEU   151      27.598  -9.734  66.634  1.00 55.59      AAAA O
ATOM   1480  N   CYS   152      26.024  -8.773  67.849  1.00 48.62      AAAA N
ATOM   1482  CA  CYS   152      26.992  -8.189  68.740  1.00 56.73      AAAA C
ATOM   1483  C   CYS   152      27.650  -9.325  69.493  1.00 63.58      AAAA C
ATOM   1484  O   CYS   152      27.074 -10.405  69.575  1.00 62.40      AAAA O
ATOM   1485  CB  CYS   152      26.358  -7.144  69.657  1.00 41.99      AAAA C
ATOM   1486  SG  CYS   152      25.985  -5.635  68.703  1.00 55.83      AAAA S
ATOM   1487  N   PRO   153      28.826  -9.072  70.059  1.00 68.05      AAAA N
ATOM   1488  CD  PRO   153      29.618  -7.838  69.903  1.00 66.66      AAAA C
ATOM   1489  CA  PRO   153      29.497 -10.094  70.851  1.00 70.60      AAAA C
ATOM   1491  CB  PRO   153      30.601  -9.323  71.557  1.00 69.98      AAAA C
ATOM   1492  CG  PRO   153      30.861  -8.159  70.690  1.00 70.58      AAAA C
ATOM   1493  C   PRO   153      28.543 -10.734  71.850  1.00 69.64      AAAA C
ATOM   1494  O   PRO   153      27.859 -10.075  72.615  1.00 69.58      AAAA O
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ATOM   1497  C   GLY   154      26.245 -13.230  72.223  1.00 81.75      AAAA C
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ATOM   1502  CB  THR   155      24.016 -11.661  69.705  1.00 85.07      AAAA C
ATOM   1503  OG1 THR   155      24.063 -10.417  70.420  1.00 84.51      AAAA O
ATOM   1505  CG2 THR   155      22.686 -11.995  69.092  1.00 82.27      AAAA C
ATOM   1506  C   THR   155      24.060 -14.094  70.353  1.00 93.69      AAAA C
ATOM   1507  O   THR   155      23.005 -14.664  70.617  1.00 95.92      AAAA O
ATOM   1508  N   MET   156      25.003 -14.655  69.617  1.00 97.23      AAAA N
ATOM   1510  CA  MET   156      24.884 -15.973  69.024  1.00 99.05      AAAA C
ATOM   1511  CB  MET   156      25.907 -16.190  67.896  1.00100.40      AAAA C
ATOM   1512  CG  MET   156      25.456 -15.675  66.542  0.01 99.75      AAAA C
ATOM   1513  SD  MET   156      23.687 -15.857  66.255  0.01 99.72      AAAA S
ATOM   1514  CE  MET   156      23.664 -17.214  65.087  0.01 99.59      AAAA C
ATOM   1515  C   MET   156      25.027 -17.106  70.032  1.00100.57      AAAA C
ATOM   1516  O   MET   156      24.353 -18.122  69.835  1.00101.64      AAAA O
ATOM   1517  N   ALA   157      25.974 -17.057  70.967  1.00100.53      AAAA N
ATOM   1519  CA  ALA   157      26.022 -18.102  71.986  1.00101.00      AAAA C
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ATOM   1527  CG  GLU   158      21.687 -17.546  75.560  1.00113.87      AAAA C
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ATOM   1530  OE2 GLU   158      21.199 -15.317  76.282  1.00117.79      AAAA O
ATOM   1531  C   GLU   158      24.434 -15.915  76.025  1.00 95.00      AAAA C
ATOM   1532  O   GLU   158      23.988 -16.117  77.145  1.00 95.89      AAAA O
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ATOM   1536  CB  SER   159      26.989 -14.805  77.517  1.00 97.37      AAAA C
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ATOM   1539  C   SER   159      26.228 -12.793  76.226  1.00 91.47      AAAA C
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ATOM   1541  N   PRO   160      25.196 -12.007  75.932  1.00 88.65      AAAA N
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ATOM	1542	CD	PRO	160	23.789	-12.122	76.395	1.00	86.67	AAAA C
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ATOM	1545	CG	PRO	160	23.370	-10.671	76.515	1.00	84.62	AAAA C
ATOM	1546	C	PRO	160	26.503	-10.025	76.236	1.00	79.60	AAAA C
ATOM	1547	O	PRO	160	26.319	-9.934	77.456	1.00	79.70	AAAA O
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ATOM	1551	CB	MET	161	29.924	-9.178	76.038	1.00	69.93	AAAA C
ATOM	1552	CG	MET	161	30.118	-10.630	75.706	1.00	71.43	AAAA C
ATOM	1553	SD	MET	161	30.716	-11.621	77.094	1.00	85.25	AAAA S
ATOM	1554	CE	MET	161	29.841	-10.905	78.471	1.00	69.31	AAAA C
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ATOM	1559	CA	CYS	162	27.493	-5.384	74.938	1.00	49.76	AAAA C
ATOM	1560	C	CYS	162	26.306	-4.777	75.670	1.00	51.52	AAAA C
ATOM	1561	O	CYS	162	25.224	-5.324	75.928	1.00	53.89	AAAA O
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ATOM	1568	CG	GLU	163	26.476	-1.364	78.465	1.00	62.30	AAAA C
ATOM	1569	CD	GLU	163	25.817	-0.135	79.116	1.00	81.67	AAAA C
ATOM	1570	OE1	GLU	163	26.470	0.473	80.016	1.00	73.22	AAAA O
ATOM	1571	OE2	GLU	163	24.646	0.208	78.721	1.00	80.93	AAAA O
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ATOM	1573	O	GLU	163	24.488	-2.423	74.234	1.00	45.90	AAAA O
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ATOM	1576	CA	LYS	164	22.011	-1.499	75.081	1.00	43.92	AAAA C
ATOM	1577	CB	LYS	164	20.714	-2.244	75.450	1.00	44.48	AAAA C
ATOM	1578	CG	LYS	164	20.560	-3.639	74.870	1.00	48.65	AAAA C
ATOM	1579	CD	LYS	164	19.480	-4.432	75.622	1.00	49.04	AAAA C
ATOM	1580	CE	LYS	164	18.409	-5.012	74.720	1.00	49.21	AAAA C
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ATOM	1596	O	LYS	164	21.466	0.484	76.282	1.00	45.69	AAAA O
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ATOM	1599	CA	THR	165	20.775	1.943	74.077	1.00	43.13	AAAA C
ATOM	1600	CB	THR	165	21.831	2.952	73.553	1.00	47.81	AAAA C
ATOM	1601	OG1	THR	165	22.053	2.689	72.127	1.00	39.13	AAAA O
ATOM	1603	CG2	THR	165	23.119	2.842	74.362	1.00	40.40	AAAA C
ATOM	1604	C	THR	165	19.532	1.881	73.189	1.00	40.92	AAAA C
ATOM	1605	O	THR	165	19.346	0.897	72.414	1.00	35.91	AAAA O
ATOM	1606	N	THR	166	18.781	2.985	73.173	1.00	39.18	AAAA N
ATOM	1608	CA	THR	166	17.689	3.991	72.182	1.00	42.97	AAAA C
ATOM	1609	CB	THR	166	16.297	3.096	72.833	1.00	55.99	AAAA C
ATOM	1610	OG1	THR	166	15.662	4.385	72.819	1.00	41.42	AAAA O
ATOM	1612	CG2	THR	166	16.157	2.740	74.313	1.00	42.93	AAAA C
ATOM	1613	C	THR	166	17.983	4.051	71.137	1.00	40.17	AAAA C
ATOM	1614	O	THR	166	18.219	5.206	71.509	1.00	35.72	AAAA O
ATOM	1615	N	ILE	167	17.912	3.725	69.866	1.00	42.21	AAAA N
ATOM	1617	CA	ILE	167	18.182	4.672	68.777	1.00	41.05	AAAA C
ATOM	1618	CB	ILE	167	19.437	4.335	67.904	1.00	39.50	AAAA C
ATOM	1619	CG2	ILE	167	19.589	5.346	66.716	1.00	15.26	AAAA C
ATOM	1620	CG1	ILE	167	20.722	4.305	68.724	1.00	36.20	AAAA C
ATOM	1621	CD1	ILE	167	21.899	3.665	67.966	1.00	35.70	AAAA C
ATOM	1623	C	ILE	167	16.937	4.524	67.882	1.00	40.94	AAAA C
ATOM	1624	O	ILE	167	16.655	3.435	67.394	1.00	35.51	AAAA O
ATOM	1625	N	ASN	168	16.318	5.635	67.537	1.00	42.29	AAAA N
ATOM	1627	CA	ASN	168	15.112	5.633	66.713	1.00	45.22	AAAA C
ATOM	1628	CB	ASN	168	15.526	5.253	65.292	1.00	45.69	AAAA C
ATOM	1629	CG	ASN	168	14.497	5.696	64.244	1.00	51.19	AAAA C
ATOM	1630	OD1	ASN	168	14.344	5.112	63.150	1.00	41.75	AAAA O
ATOM	1631	ND2	ASN	168	13.749	6.763	64.522	1.00	48.89	AAAA N
ATOM	1634	C	ASN	168	13.954	4.739	67.141	1.00	46.55	AAAA C
ATOM	1635	O	ASN	168	13.544	3.879	66.326	1.00	45.95	AAAA O
ATOM	1636	N	ASN	169	13.644	4.728	68.433	1.00	45.12	AAAA N
ATOM	1638	CA	ASN	169	12.717	3.759	69.007	1.00	43.67	AAAA C
ATOM	1639	CB	ASN	169	11.315	4.106	68.540	1.00	36.84	AAAA C
ATOM	1640	CG	ASN	169	10.943	5.487	69.093	1.00	42.75	AAAA C
ATOM	1641	OD1	ASN	169	10.917	5.779	70.280	1.00	36.67	AAAA O
ATOM	1642	ND2	ASN	169	10.658	6.448	68.213	1.00	40.74	AAAA N
ATOM	1645	C	ASN	169	13.003	2.306	68.719	1.00	44.69	AAAA C
ATOM	1646	O	ASN	169	12.100	1.544	68.383	1.00	45.72	AAAA O
ATOM	1647	N	GLU	170	14.226	1.907	68.862	1.00	41.64	AAAA N
ATOM	1649	CA	GLU	170	14.655	0.513	68.850	1.00	45.88	AAAA C
ATOM	1650	CB	GLU	170	15.283	0.278	67.524	1.00	55.92	AAAA C
ATOM	1651	CG	GLU	170	15.028	-0.953	66.702	1.00	67.08	AAAA C
ATOM	1652	CD	GLU	170	14.517	-0.605	65.294	1.00	74.56	AAAA C
ATOM	1653	OE1	GLU	170	13.869	0.466	65.049	1.00	77.75	AAAA O
ATOM	1654	OE2	GLU	170	14.763	-1.437	64.389	1.00	70.71	AAAA O
ATOM	1655	C	GLU	170	15.647	0.379	70.010	1.00	47.10	AAAA C
ATOM	1656	O	GLU	170	16.582	1.172	70.213	1.00	49.92	AAAA O

ATOM	1646	N	TYR	171	15.344	-0.462	70.952	1.00	49.19	AAAA N
ATOM	1647	CA	TYR	171	16.231	-0.688	72.097	1.00	51.81	AAAA C
ATOM	1648	CB	TYR	171	15.434	-0.861	73.359	1.00	49.94	AAAA C
ATOM	1649	CG	TYR	171	16.175	-1.168	74.620	1.00	48.90	AAAA C
ATOM	1650	CD1	TYR	171	16.980	-0.210	75.237	1.00	46.46	AAAA C
ATOM	1651	CE1	TYR	171	17.634	-0.469	76.407	1.00	41.17	AAAA C
ATOM	1652	CD2	TYR	171	16.065	-2.429	75.194	1.00	43.62	AAAA C
ATOM	1653	CE2	TYR	171	16.734	-2.675	76.366	1.00	44.44	AAAA C
ATOM	1654	CZ	TYR	171	17.516	-1.718	76.973	1.00	43.58	AAAA C
ATOM	1655	OH	TYR	171	18.174	-2.017	78.146	1.00	40.16	AAAA O
ATOM	1656	C	TYR	171	17.058	-1.938	71.832	1.00	51.41	AAAA C
ATOM	1657	O	TYR	171	16.519	-3.024	71.889	1.00	52.59	AAAA O
ATOM	1658	N	ASN	172	18.331	-1.752	71.493	1.00	53.70	AAAA N
ATOM	1659	CA	ASN	172	19.203	-2.898	71.193	1.00	52.36	AAAA C
ATOM	1660	CB	ASN	172	19.085	-3.278	69.709	1.00	55.43	AAAA C
ATOM	1661	CG	ASN	172	18.939	-4.766	69.498	1.00	61.75	AAAA C
ATOM	1662	OD1	ASN	172	19.233	-5.646	70.304	1.00	61.61	AAAA O
ATOM	1663	ND2	ASN	172	18.449	-5.048	68.295	1.00	57.97	AAAA N
ATOM	1664	C	ASN	172	20.665	-2.712	71.560	1.00	43.81	AAAA C
ATOM	1665	O	ASN	172	21.163	-1.760	72.213	1.00	39.38	AAAA O
ATOM	1666	N	TYR	173	21.373	-3.796	71.393	1.00	43.20	AAAA N
ATOM	1667	CA	TYR	173	22.794	-3.929	71.698	1.00	44.76	AAAA C
ATOM	1668	CB	TYR	173	23.223	-5.374	71.514	1.00	41.66	AAAA C
ATOM	1669	CG	TYR	173	22.759	-6.274	72.630	1.00	45.18	AAAA C
ATOM	1670	CD1	TYR	173	21.931	-7.316	72.237	1.00	46.48	AAAA C
ATOM	1671	CE1	TYR	173	21.438	-8.191	73.193	1.00	51.36	AAAA C
ATOM	1672	CD2	TYR	173	23.081	-6.132	73.978	1.00	44.86	AAAA C
ATOM	1673	CE2	TYR	173	22.583	-7.016	74.916	1.00	46.92	AAAA C
ATOM	1674	CZ	TYR	173	21.757	-8.038	74.535	1.00	50.33	AAAA C
ATOM	1675	OH	TYR	173	21.171	-9.006	75.328	1.00	50.64	AAAA O
ATOM	1676	C	TYR	173	23.673	-3.099	70.762	1.00	46.94	AAAA C
ATOM	1677	O	TYR	173	23.389	-2.983	69.567	1.00	49.76	AAAA O
ATOM	1678	N	ARG	174	24.579	-2.318	71.366	1.00	47.79	AAAA N
ATOM	1679	CA	ARG	174	25.517	-1.496	70.577	1.00	49.13	AAAA C
ATOM	1680	CB	ARG	174	25.537	-0.132	71.233	1.00	44.32	AAAA C
ATOM	1681	CG	ARG	174	24.210	0.623	71.234	1.00	48.14	AAAA C
ATOM	1682	CD	ARG	174	23.372	0.344	70.003	1.00	51.47	AAAA C
ATOM	1683	NE	ARG	174	21.974	0.760	70.039	1.00	48.35	AAAA N
ATOM	1684	CZ	ARG	174	21.144	0.870	69.017	1.00	48.23	AAAA C
ATOM	1685	NH1	ARG	174	21.477	0.022	67.864	1.00	38.96	AAAA N
ATOM	1686	NH2	ARG	174	19.909	1.022	69.197	1.00	54.65	AAAA N
ATOM	1687	C	ARG	174	26.921	-2.094	70.461	1.00	45.98	AAAA C
ATOM	1688	O	ARG	174	27.548	-2.557	71.406	1.00	44.97	AAAA O
ATOM	1689	N	CYS	175	27.493	-2.183	69.294	1.00	46.21	AAAA N
ATOM	1690	CA	CYS	175	28.787	-2.758	68.997	1.00	45.60	AAAA C
ATOM	1691	C	CYS	175	29.407	-2.395	67.665	1.00	46.23	AAAA C
ATOM	1692	O	CYS	175	28.755	-2.018	66.665	1.00	44.79	AAAA O
ATOM	1693	CB	CYS	175	28.576	-4.253	69.167	1.00	35.62	AAAA C
ATOM	1694	SG	CYS	175	27.812	-5.191	67.827	1.00	51.92	AAAA S
ATOM	1695	N	TRP	176	30.764	-2.517	67.583	1.00	48.16	AAAA N
ATOM	1696	CA	TRP	176	31.430	-2.091	66.325	1.00	42.49	AAAA C
ATOM	1697	CB	TRP	176	32.769	-1.409	66.564	1.00	36.38	AAAA C
ATOM	1698	CG	TRP	176	32.689	-0.069	67.203	1.00	25.56	AAAA C
ATOM	1699	CD2	TRP	176	32.588	1.186	66.480	1.00	23.71	AAAA C
ATOM	1700	CE2	TRP	176	32.558	2.217	67.422	1.00	32.40	AAAA C
ATOM	1701	CE3	TRP	176	32.535	1.520	65.141	1.00	24.31	AAAA C
ATOM	1702	CD1	TRP	176	32.730	0.257	68.525	1.00	28.37	AAAA C
ATOM	1703	NE1	TRP	176	32.636	1.636	68.678	1.00	37.21	AAAA N
ATOM	1704	CZ2	TRP	176	32.441	3.565	67.088	1.00	28.51	AAAA C
ATOM	1705	CZ3	TRP	176	32.447	2.822	64.789	1.00	22.23	AAAA C
ATOM	1706	CH2	TRP	176	32.406	3.817	65.745	1.00	29.51	AAAA C
ATOM	1707	C	TRP	176	31.631	-3.268	65.408	1.00	39.30	AAAA C
ATOM	1708	O	TRP	176	31.703	-3.121	64.199	1.00	39.15	AAAA O
ATOM	1709	N	THR	177	31.682	-4.460	66.005	1.00	41.33	AAAA N
ATOM	1710	CA	THR	177	31.964	-5.644	65.161	1.00	49.28	AAAA C
ATOM	1711	CB	THR	177	33.480	-6.062	65.162	1.00	43.66	AAAA C
ATOM	1712	OG1	THR	177	34.309	-5.025	64.613	1.00	47.85	AAAA O
ATOM	1713	CG2	THR	177	33.676	-7.271	64.283	1.00	58.51	AAAA C
ATOM	1714	C	THR	177	31.290	-6.814	65.858	1.00	48.76	AAAA C
ATOM	1715	O	THR	177	30.982	-6.539	67.001	1.00	51.53	AAAA O
ATOM	1716	N	THR	178	31.269	-8.000	65.331	1.00	51.96	AAAA N
ATOM	1717	CA	THR	178	30.924	-9.236	65.946	1.00	58.95	AAAA C
ATOM	1718	CB	THR	178	31.253	-10.500	65.082	1.00	66.55	AAAA C
ATOM	1719	OG1	THR	178	31.505	-10.066	63.734	1.00	75.70	AAAA O
ATOM	1720	CG2	THR	178	30.104	-11.499	65.148	1.00	74.23	AAAA C
ATOM	1721	C	THR	178	31.714	-9.539	67.213	1.00	60.25	AAAA C
ATOM	1722	O	THR	178	31.204	-10.202	68.135	1.00	66.05	AAAA O
ATOM	1723	N	ASN	179	32.977	-9.130	67.253	1.00	57.56	AAAA N
ATOM	1724	CA	ASN	179	33.793	-9.392	68.443	1.00	53.39	AAAA C
ATOM	1725	CB	ASN	179	35.130	-10.024	68.068	1.00	48.46	AAAA C
ATOM	1726	CG	ASN	179	34.897	-11.218	67.126	1.00	56.25	AAAA C
ATOM	1727	OD1	ASN	179	34.412	-12.294	67.553	1.00	51.38	AAAA O
ATOM	1728	ND2	ASN	179	35.229	-11.063	65.863	1.00	48.10	AAAA N
ATOM	1752	C	ASN	179	34.096	-8.190	69.285	1.00	50.78	AAAA C
ATOM	1753	O	ASN	179	34.556	-8.377	70.426	1.00	57.97	AAAA O

ATOM	1756	N	ARG	180	33.626	-7.022	68.913	1.00	47.06	AAAA N
ATOM	1756	CA	ARG	180	33.808	-5.820	69.691	1.00	48.25	AAAA C
ATOM	1757	CB	ARG	180	34.925	-4.962	69.074	1.00	49.72	AAAA C
ATOM	1758	CG	ARG	180	36.324	-5.501	69.285	1.00	60.92	AAAA C
ATOM	1759	CD	ARG	180	37.288	-4.948	68.279	1.00	70.83	AAAA C
ATOM	1760	NE	ARG	180	38.569	-5.605	68.203	1.00	76.18	AAAA N
ATOM	1762	CZ	ARG	180	39.298	-5.895	69.276	1.00	76.59	AAAA C
ATOM	1763	NH1	ARG	180	38.877	-5.608	70.498	1.00	80.82	AAAA N
ATOM	1766	NH2	ARG	180	40.474	-6.478	69.180	1.00	79.33	AAAA N
ATOM	1769	C	ARG	180	32.530	-4.977	69.821	1.00	48.10	AAAA C
ATOM	1770	O	ARG	180	31.862	-4.476	68.905	1.00	46.99	AAAA O
ATOM	1771	N	CYS	181	32.230	-4.728	71.063	1.00	44.80	AAAA N
ATOM	1773	CA	CYS	181	31.199	-3.924	71.619	1.00	45.20	AAAA C
ATOM	1774	C	CYS	181	31.646	-2.463	71.692	1.00	44.50	AAAA C
ATOM	1775	O	CYS	181	32.835	-2.227	71.724	1.00	47.09	AAAA O
ATOM	1776	CB	CYS	181	30.940	-4.282	73.110	1.00	43.88	AAAA C
ATOM	1777	SG	CYS	181	30.363	-5.944	73.346	1.00	56.08	AAAA S
ATOM	1778	N	GLN	182	30.659	-1.600	71.690	1.00	39.30	AAAA N
ATOM	1780	CA	GLN	182	30.948	-0.177	71.690	1.00	43.43	AAAA C
ATOM	1781	CB	GLN	182	29.749	0.619	71.196	1.00	23.99	AAAA C
ATOM	1782	CG	GLN	182	29.809	2.085	71.435	1.00	28.57	AAAA C
ATOM	1783	CD	GLN	182	28.757	2.867	70.733	1.00	29.35	AAAA C
ATOM	1784	OE1	GLN	182	27.898	2.304	70.033	1.00	38.55	AAAA O
ATOM	1785	NE2	GLN	182	28.857	4.164	70.912	1.00	28.14	AAAA N
ATOM	1788	C	GLN	182	31.218	0.089	73.162	1.00	46.07	AAAA C
ATOM	1789	O	GLN	182	30.458	-0.327	74.041	1.00	47.01	AAAA O
ATOM	1790	N	LYS	183	32.213	0.866	73.524	1.00	46.98	AAAA N
ATOM	1792	CA	LYS	183	32.479	1.064	74.934	1.00	45.26	AAAA C
ATOM	1793	CB	LYS	183	33.966	1.275	75.185	1.00	48.68	AAAA C
ATOM	1794	CG	LYS	183	34.865	0.267	74.482	1.00	47.95	AAAA C
ATOM	1795	CD	LYS	183	36.337	0.734	74.523	1.00	48.06	AAAA C
ATOM	1796	CE	LYS	183	37.178	-0.208	73.684	1.00	46.78	AAAA C
ATOM	1797	NZ	LYS	183	38.499	-0.654	74.158	1.00	44.00	AAAA N
ATOM	1801	C	LYS	183	31.659	2.205	75.477	1.00	48.13	AAAA C
ATOM	1802	O	LYS	183	31.679	3.305	74.946	1.00	48.84	AAAA O
ATOM	1803	N	MET	184	31.165	2.014	76.699	1.00	52.59	AAAA N
ATOM	1805	CA	MET	184	30.388	3.041	77.413	1.00	53.22	AAAA C
ATOM	1806	CB	MET	184	28.927	2.613	77.537	1.00	54.27	AAAA C
ATOM	1807	CG	MET	184	27.855	2.955	76.536	1.00	56.16	AAAA C
ATOM	1808	SD	MET	184	26.911	1.601	75.912	1.00	57.56	AAAA S
ATOM	1809	CE	MET	184	26.738	1.855	74.171	1.00	46.57	AAAA C
ATOM	1810	C	MET	184	31.051	3.200	78.770	1.00	50.55	AAAA C
ATOM	1811	O	MET	184	31.770	2.292	79.116	1.00	48.82	AAAA O
ATOM	1812	N	CYS	185	30.796	4.195	79.565	1.00	53.97	AAAA N
ATOM	1814	CA	CYS	185	31.342	4.365	80.892	1.00	58.63	AAAA C
ATOM	1815	C	CYS	185	30.297	4.320	81.989	1.00	65.16	AAAA C
ATOM	1816	O	CYS	185	29.133	4.649	81.761	1.00	65.87	AAAA O
ATOM	1817	CB	CYS	185	31.965	5.772	81.000	1.00	60.37	AAAA C
ATOM	1818	SG	CYS	185	33.623	5.771	80.312	1.00	60.09	AAAA S
ATOM	1819	N	PRO	186	30.688	3.979	83.206	1.00	69.41	AAAA N
ATOM	1820	CD	PRO	186	32.066	3.777	83.702	1.00	71.11	AAAA C
ATOM	1821	CA	PRO	186	29.717	3.933	84.304	1.00	69.11	AAAA C
ATOM	1822	CB	PRO	186	30.523	3.487	85.503	1.00	68.03	AAAA C
ATOM	1823	CG	PRO	186	31.910	3.920	85.198	1.00	71.02	AAAA C
ATOM	1824	C	PRO	186	29.120	5.320	84.431	1.00	69.47	AAAA C
ATOM	1825	O	PRO	186	29.820	6.345	84.507	1.00	65.93	AAAA O
ATOM	1826	N	SER	187	27.801	5.367	84.546	1.00	68.78	AAAA N
ATOM	1828	CA	SER	187	27.050	6.592	84.750	1.00	69.29	AAAA C
ATOM	1829	CB	SER	187	25.594	6.287	85.129	1.00	78.29	AAAA C
ATOM	1830	OG	SER	187	25.474	4.935	85.566	1.00	91.78	AAAA O
ATOM	1832	C	SER	187	27.630	7.476	85.836	1.00	67.19	AAAA C
ATOM	1833	O	SER	187	27.606	8.708	85.803	1.00	63.98	AAAA O
ATOM	1834	N	THR	188	28.108	6.853	86.908	1.00	68.20	AAAA N
ATOM	1836	CA	THR	188	28.870	7.507	87.963	1.00	68.39	AAAA C
ATOM	1837	CB	THR	188	29.805	6.459	88.618	1.00	73.84	AAAA C
ATOM	1838	OG1	THR	188	28.943	5.365	89.016	1.00	89.33	AAAA O
ATOM	1840	CG2	THR	188	30.605	7.048	89.759	1.00	73.71	AAAA C
ATOM	1841	C	THR	188	29.802	8.583	87.429	1.00	67.52	AAAA C
ATOM	1842	O	THR	188	29.843	9.739	87.834	1.00	68.30	AAAA O
ATOM	1843	N	CYS	189	30.643	8.247	86.446	1.00	63.89	AAAA N
ATOM	1845	CA	CYS	189	31.583	9.116	85.817	1.00	57.29	AAAA C
ATOM	1846	C	CYS	189	30.951	10.331	85.195	1.00	57.70	AAAA C
ATOM	1847	O	CYS	189	31.648	11.327	85.017	1.00	57.56	AAAA O
ATOM	1848	CB	CYS	189	32.416	9.372	84.769	1.00	58.67	AAAA C
ATOM	1849	SG	CYS	189	33.347	7.001	85.535	1.00	53.46	AAAA S
ATOM	1850	N	GLY	190	29.689	10.322	84.806	1.00	56.91	AAAA N
ATOM	1852	CA	GLY	190	29.038	11.521	84.323	1.00	57.28	AAAA C
ATOM	1853	C	GLY	190	29.444	11.834	82.886	1.00	59.62	AAAA C
ATOM	1854	O	GLY	190	29.609	10.932	82.082	1.00	57.91	AAAA O
ATOM	1855	N	LYS	191	29.842	13.052	82.624	1.00	62.78	AAAA N
ATOM	1857	CA	LYS	191	30.359	13.520	81.364	1.00	67.72	AAAA C
ATOM	1858	CB	LYS	191	30.058	15.035	81.214	1.00	72.76	AAAA C
ATOM	1859	CG	LYS	191	28.568	15.288	81.002	1.00	84.69	AAAA C
ATOM	1860	CD	LYS	191	28.207	16.733	80.723	1.00	90.15	AAAA C
ATOM	1861	CE	LYS	191	26.713	16.806	80.471	1.00	91.83	AAAA C

ATOM	1965	HZ	LYS	191	26.368	16.182	79.152	1.00	97.62	AAAA N
ATOM	1966	C	LYS	191	31.868	13.299	81.270	1.00	70.13	AAAA C
ATOM	1967	O	LYS	191	32.486	13.935	80.415	1.00	71.76	AAAA O
ATOM	1968	N	ARG	192	32.488	12.441	82.079	1.00	66.29	AAAA N
ATOM	1970	CA	ARG	192	33.885	12.171	82.044	1.00	59.95	AAAA C
ATOM	1971	CB	ARG	192	34.505	12.070	83.432	1.00	66.58	AAAA C
ATOM	1972	CG	ARG	192	34.670	13.400	84.131	1.00	71.59	AAAA C
ATOM	1973	CD	ARG	192	34.386	13.330	85.625	1.00	73.91	AAAA C
ATOM	1974	NE	ARG	192	35.622	13.280	86.377	1.00	85.74	AAAA N
ATOM	1976	CZ	ARG	192	35.968	12.407	87.330	1.00	90.67	AAAA C
ATOM	1977	NH1	ARG	192	35.026	11.486	87.600	1.00	88.49	AAAA N
ATOM	1980	NH2	ARG	192	37.162	12.463	87.950	1.00	72.95	AAAA N
ATOM	1983	C	ARG	192	34.221	10.851	81.337	1.00	58.83	AAAA C
ATOM	1984	O	ARG	192	33.336	10.007	81.176	1.00	55.13	AAAA O
ATOM	1985	N	ALA	193	35.521	10.795	80.968	1.00	50.19	AAAA N
ATOM	1987	CA	ALA	193	35.962	9.557	80.355	1.00	46.24	AAAA C
ATOM	1988	CB	ALA	193	37.167	9.921	79.541	1.00	45.15	AAAA C
ATOM	1989	C	ALA	193	36.221	8.525	81.451	1.00	48.97	AAAA C
ATOM	1990	O	ALA	193	36.220	8.908	82.616	1.00	44.80	AAAA O
ATOM	1991	N	CYS	194	36.544	7.304	81.065	1.00	50.30	AAAA N
ATOM	1993	CA	CYS	194	36.836	6.302	82.043	1.00	57.50	AAAA C
ATOM	1994	C	CYS	194	37.834	5.304	81.448	1.00	61.25	AAAA C
ATOM	1995	O	CYS	194	37.952	5.291	80.216	1.00	61.52	AAAA O
ATOM	1996	CB	CYS	194	35.510	5.741	82.504	1.00	57.96	AAAA C
ATOM	1997	SG	CYS	194	34.785	4.524	81.402	1.00	54.49	AAAA S
ATOM	1999	N	THR	195	38.422	4.499	82.311	1.00	58.51	AAAA N
ATOM	2000	CA	THR	195	39.462	3.584	81.913	1.00	57.42	AAAA C
ATOM	2001	CB	THR	195	40.237	3.142	83.188	1.00	65.73	AAAA C
ATOM	2002	OG1	THR	195	40.288	4.248	84.091	1.00	70.15	AAAA O
ATOM	2004	CG2	THR	195	41.684	2.864	82.745	1.00	77.91	AAAA C
ATOM	2005	C	THR	195	38.857	2.404	81.226	1.00	54.59	AAAA C
ATOM	2006	O	THR	195	37.633	2.315	81.318	1.00	58.75	AAAA O
ATOM	2007	N	GLU	196	39.610	1.408	80.882	1.00	55.95	AAAA N
ATOM	2009	CA	GLU	196	39.139	0.145	80.364	1.00	60.07	AAAA C
ATOM	2010	CB	GLU	196	40.395	-0.612	79.914	1.00	68.06	AAAA C
ATOM	2011	CG	GLU	196	40.479	-1.146	78.526	1.00	73.96	AAAA C
ATOM	2012	CD	GLU	196	39.235	-0.983	77.671	1.00	83.08	AAAA C
ATOM	2013	OE1	GLU	196	38.356	-1.884	77.687	1.00	81.19	AAAA O
ATOM	2014	OE2	GLU	196	39.060	0.041	76.939	1.00	82.10	AAAA O
ATOM	2015	C	GLU	196	38.382	-0.579	81.467	1.00	63.91	AAAA C
ATOM	2016	O	GLU	196	37.690	-1.537	81.159	1.00	63.51	AAAA O
ATOM	2017	N	ASN	197	38.666	-0.312	82.739	1.00	67.40	AAAA N
ATOM	2019	CA	ASN	197	38.025	-0.947	83.886	1.00	69.21	AAAA C
ATOM	2020	CB	ASN	197	39.021	-1.394	84.966	1.00	68.49	AAAA C
ATOM	2021	CG	ASN	197	39.722	-2.692	84.672	0.01	69.09	AAAA C
ATOM	2022	OD1	ASN	197	40.364	-3.273	85.551	0.01	69.04	AAAA O
ATOM	2023	ND2	ASN	197	39.622	-3.183	83.443	0.01	68.97	AAAA N
ATOM	2026	C	ASN	197	37.033	0.043	84.486	1.00	69.01	AAAA C
ATOM	2027	O	ASN	197	36.945	0.281	85.664	1.00	68.24	AAAA O
ATOM	2029	N	ASN	198	36.384	0.795	83.607	1.00	69.91	AAAA N
ATOM	2030	CA	ASN	198	35.356	1.734	84.048	1.00	68.48	AAAA C
ATOM	2031	CB	ASN	198	34.120	0.880	84.373	1.00	60.12	AAAA C
ATOM	2032	CG	ASN	198	33.806	0.095	83.102	1.00	69.29	AAAA C
ATOM	2033	OD1	ASN	198	33.475	0.654	82.054	1.00	73.20	AAAA O
ATOM	2034	ND2	ASN	198	33.980	-1.206	83.268	1.00	65.34	AAAA N
ATOM	2037	C	ASN	198	35.784	2.563	85.228	1.00	64.01	AAAA C
ATOM	2038	O	ASN	198	34.992	2.827	86.117	1.00	64.20	AAAA O
ATOM	2039	N	GLU	199	36.955	3.164	85.157	1.00	64.75	AAAA N
ATOM	2041	CA	GLU	199	37.342	4.054	86.255	1.00	64.64	AAAA C
ATOM	2042	CB	GLU	199	38.702	3.624	86.744	1.00	66.11	AAAA C
ATOM	2043	CG	GLU	199	38.846	3.717	88.233	1.00	77.15	AAAA C
ATOM	2044	CD	GLU	199	39.579	2.532	88.832	1.00	80.24	AAAA C
ATOM	2045	OE1	GLU	199	39.385	2.406	90.066	1.00	81.65	AAAA O
ATOM	2046	OE2	GLU	199	40.282	1.821	88.079	1.00	77.94	AAAA O
ATOM	2047	C	GLU	199	37.314	5.463	85.690	1.00	62.92	AAAA C
ATOM	2048	O	GLU	199	37.922	5.676	84.632	1.00	63.62	AAAA O
ATOM	2049	N	CYS	200	36.605	6.393	86.313	1.00	56.16	AAAA N
ATOM	2051	CA	CYS	200	36.600	7.721	85.740	1.00	55.11	AAAA C
ATOM	2052	C	CYS	200	37.978	8.315	85.521	1.00	57.77	AAAA C
ATOM	2053	O	CYS	200	38.884	8.058	86.300	1.00	63.79	AAAA O
ATOM	2054	CB	CYS	200	35.824	8.664	86.648	1.00	62.70	AAAA C
ATOM	2055	SG	CYS	200	34.196	8.100	87.098	1.00	55.85	AAAA S
ATOM	2056	N	CYS	201	38.124	9.192	84.540	1.00	54.50	AAAA N
ATOM	2058	CA	CYS	201	39.338	9.889	84.202	1.00	48.19	AAAA C
ATOM	2059	C	CYS	201	39.236	11.287	84.786	1.00	42.34	AAAA C
ATOM	2060	O	CYS	201	38.165	11.704	85.166	1.00	54.32	AAAA O
ATOM	2061	CB	CYS	201	39.590	10.070	82.695	1.00	40.90	AAAA C
ATOM	2062	SG	CYS	201	39.644	8.597	81.747	1.00	51.42	AAAA S
ATOM	2063	N	HIS	202	40.254	12.075	84.675	1.00	39.12	AAAA N
ATOM	2065	CA	HIS	202	40.290	13.461	85.128	1.00	41.55	AAAA C
ATOM	2066	C	HIS	202	39.284	14.184	84.289	1.00	46.59	AAAA C
ATOM	2067	O	HIS	202	39.176	13.851	83.103	1.00	51.64	AAAA O
ATOM	2068	CB	HIS	202	41.712	13.952	84.810	1.00	45.20	AAAA C
ATOM	2069	CG	HIS	202	41.996	15.330	85.267	1.00	38.71	AAAA C
ATOM	2070	ND1	HIS	202	41.501	16.404	84.550	1.00	51.32	AAAA N

ATOM	1971	CB1	HIS	202	41.987	17.528	85.178	1.00	47.62	AAAA C
ATOM	1972	CD2	HIS	202	42.665	15.813	86.340	1.00	39.59	AAAA C
ATOM	1973	NE2	HIS	202	42.563	17.207	86.258	1.00	43.48	AAAA N
ATOM	1975	N	PRO	203	38.738	15.293	84.711	1.00	47.74	AAAA N
ATOM	1976	CD	PRO	203	38.758	15.840	86.082	1.00	46.97	AAAA C
ATOM	1977	CA	PRO	203	37.780	15.987	83.879	1.00	46.44	AAAA C
ATOM	1978	CB	PRO	203	37.248	17.107	84.742	1.00	39.47	AAAA C
ATOM	1979	CG	PRO	203	38.131	17.210	85.910	1.00	43.37	AAAA C
ATOM	1980	C	PRO	203	38.440	16.519	82.607	1.00	53.27	AAAA C
ATOM	1981	O	PRO	203	37.698	17.045	81.731	1.00	53.16	AAAA O
ATOM	1982	N	GLU	204	39.792	16.535	82.561	1.00	50.34	AAAA N
ATOM	1984	CA	GLU	204	40.439	17.139	81.381	1.00	50.52	AAAA C
ATOM	1985	CB	GLU	204	41.727	17.891	81.804	1.00	48.58	AAAA C
ATOM	1986	CG	GLU	204	41.397	19.251	82.397	1.00	43.74	AAAA C
ATOM	1987	CD	GLU	204	40.778	20.282	81.501	1.00	55.26	AAAA C
ATOM	1988	OE1	GLU	204	40.766	20.344	80.248	1.00	64.04	AAAA O
ATOM	1989	OE2	GLU	204	40.226	21.198	82.141	1.00	57.66	AAAA O
ATOM	1990	C	GLU	204	40.718	16.084	80.319	1.00	45.71	AAAA C
ATOM	1991	O	GLU	204	41.238	16.405	79.251	1.00	46.56	AAAA O
ATOM	1992	N	CYS	205	40.612	14.830	80.735	1.00	42.05	AAAA N
ATOM	1994	CA	CYS	205	40.997	13.764	79.838	1.00	45.81	AAAA C
ATOM	1995	C	CYS	205	39.892	13.628	78.819	1.00	49.20	AAAA C
ATOM	1996	O	CYS	205	38.746	13.920	79.133	1.00	50.34	AAAA O
ATOM	1997	CB	CYS	205	41.288	12.491	80.572	1.00	51.55	AAAA C
ATOM	1998	SG	CYS	205	42.923	12.246	81.251	1.00	52.89	AAAA S
ATOM	1999	N	LEU	206	40.232	13.579	77.520	1.00	49.88	AAAA N
ATOM	2001	CA	LEU	206	39.169	13.446	76.533	1.00	41.49	AAAA C
ATOM	2002	CB	LEU	206	39.266	14.505	75.462	1.00	48.66	AAAA C
ATOM	2003	CG	LEU	206	38.274	14.365	74.305	1.00	47.45	AAAA C
ATOM	2004	CD1	LEU	206	36.879	14.243	74.895	1.00	45.79	AAAA C
ATOM	2005	CD2	LEU	206	38.331	15.599	73.420	1.00	50.71	AAAA C
ATOM	2006	C	LEU	206	39.310	12.109	75.912	1.00	38.44	AAAA C
ATOM	2007	O	LEU	206	40.400	11.568	75.813	1.00	36.59	AAAA O
ATOM	2008	N	GLY	207	38.264	11.359	75.681	1.00	42.41	AAAA N
ATOM	2010	CA	GLY	207	38.403	10.099	74.979	1.00	40.57	AAAA C
ATOM	2011	C	GLY	207	38.466	9.061	76.059	1.00	47.15	AAAA C
ATOM	2012	O	GLY	207	37.668	9.102	76.057	1.00	45.04	AAAA O
ATOM	2013	N	SER	208	39.622	9.079	76.760	1.00	50.36	AAAA N
ATOM	2015	CA	SER	208	39.832	7.838	77.660	1.00	48.27	AAAA C
ATOM	2016	CB	SER	208	39.909	6.631	76.787	1.00	35.77	AAAA C
ATOM	2017	OG	SER	208	40.600	5.597	77.461	1.00	61.34	AAAA O
ATOM	2019	C	SER	208	41.144	8.068	78.377	1.00	49.17	AAAA C
ATOM	2020	O	SER	208	41.781	9.084	78.163	1.00	48.24	AAAA O
ATOM	2021	N	CYS	209	41.599	7.123	79.199	1.00	52.04	AAAA N
ATOM	2023	CA	CYS	209	42.924	7.307	79.964	1.00	55.98	AAAA C
ATOM	2024	C	CYS	209	43.453	6.035	80.484	1.00	57.41	AAAA C
ATOM	2025	O	CYS	209	42.962	4.963	80.423	1.00	58.33	AAAA O
ATOM	2026	CB	CYS	209	42.629	8.258	81.146	1.00	52.51	AAAA C
ATOM	2027	SG	CYS	209	41.380	7.602	82.261	1.00	58.22	AAAA S
ATOM	2029	N	SER	210	44.734	6.145	80.883	1.00	59.37	AAAA N
ATOM	2030	CA	SER	210	45.506	4.950	81.319	1.00	58.10	AAAA C
ATOM	2031	CB	SER	210	47.022	5.083	81.105	1.00	55.07	AAAA C
ATOM	2032	OG	SER	210	47.546	6.204	81.819	1.00	64.49	AAAA O
ATOM	2034	C	SER	210	45.331	4.713	82.826	1.00	56.34	AAAA C
ATOM	2035	O	SER	210	45.529	3.614	83.336	1.00	54.42	AAAA O
ATOM	2036	N	ALA	211	45.105	5.806	83.548	1.00	52.79	AAAA N
ATOM	2038	CA	ALA	211	44.980	5.684	85.004	1.00	56.60	AAAA C
ATOM	2039	CB	ALA	211	46.333	5.926	85.649	1.00	63.41	AAAA C
ATOM	2040	C	ALA	211	43.962	6.747	85.395	1.00	56.58	AAAA C
ATOM	2041	O	ALA	211	43.957	7.792	84.711	1.00	50.78	AAAA O
ATOM	2042	N	PRO	212	43.117	6.416	86.359	1.00	55.93	AAAA N
ATOM	2043	CD	PRO	212	43.042	5.166	87.115	1.00	55.86	AAAA C
ATOM	2044	CA	PRO	212	41.951	7.257	86.575	1.00	55.50	AAAA C
ATOM	2045	CB	PRO	212	41.104	6.470	87.556	1.00	59.65	AAAA C
ATOM	2046	CG	PRO	212	42.021	5.483	88.175	1.00	54.56	AAAA C
ATOM	2047	C	PRO	212	42.409	8.535	87.177	1.00	53.64	AAAA C
ATOM	2048	O	PRO	212	43.611	8.725	87.393	1.00	57.48	AAAA O
ATOM	2049	N	ALA	213	41.537	9.492	87.347	1.00	53.87	AAAA N
ATOM	2051	CA	ALA	213	41.912	10.710	88.057	1.00	59.41	AAAA C
ATOM	2052	CB	ALA	213	41.783	10.255	89.541	1.00	66.40	AAAA C
ATOM	2053	C	ALA	213	43.289	11.300	87.907	1.00	61.40	AAAA C
ATOM	2054	O	ALA	213	43.728	12.202	88.652	1.00	60.03	AAAA O
ATOM	2055	N	ASN	214	44.068	10.999	86.899	1.00	64.80	AAAA N
ATOM	2057	CA	ASN	214	45.366	11.551	86.596	1.00	63.36	AAAA C
ATOM	2063	C	ASN	214	45.300	12.294	85.251	1.00	61.56	AAAA C
ATOM	2064	O	ASN	214	45.198	11.794	84.117	1.00	58.38	AAAA O
ATOM	2058	CB	ASN	214	46.336	10.379	86.608	1.00	67.32	AAAA C
ATOM	2059	CG	ASN	214	47.697	10.896	86.362	1.00	75.48	AAAA C
ATOM	2060	OD1	ASN	214	48.254	11.105	85.302	1.00	83.64	AAAA O
ATOM	2061	ND2	ASN	214	48.513	11.170	87.427	1.00	90.05	AAAA N
ATOM	2065	N	ASP	215	45.666	13.565	85.305	1.00	59.78	AAAA N
ATOM	2067	CA	ASP	215	45.618	14.432	84.143	1.00	56.47	AAAA C
ATOM	2068	CB	ASP	215	45.430	15.926	84.446	1.00	40.19	AAAA C
ATOM	2069	CG	ASP	215	46.671	16.543	84.986	1.00	56.36	AAAA C
ATOM	2070	OD1	ASP	215	46.590	17.699	85.473	1.00	56.17	AAAA O

ATOM	2071	HD2	ASP	215	47.766	15.926	84.941	1.00	60.51	AAAA O
ATOM	2072	C	ASP	215	46.818	14.315	83.221	1.00	53.78	AAAA C
ATOM	2073	O	ASP	215	46.998	15.148	82.322	1.00	53.58	AAAA O
ATOM	2074	N	THR	216	47.719	13.425	83.511	1.00	50.87	AAAA N
ATOM	2076	CA	THR	216	48.883	13.114	82.734	1.00	45.76	AAAA C
ATOM	2077	CB	THR	216	50.201	13.176	83.529	1.00	53.46	AAAA C
ATOM	2078	OG1	THR	216	50.403	11.977	84.335	1.00	45.14	AAAA O
ATOM	2080	CG2	THR	216	50.436	14.314	84.518	1.00	41.38	AAAA C
ATOM	2081	C	THR	216	48.681	11.712	82.158	1.00	48.34	AAAA C
ATOM	2082	O	THR	216	49.596	11.282	81.444	1.00	47.49	AAAA O
ATOM	2083	N	ALA	217	47.559	11.057	82.476	1.00	49.65	AAAA N
ATOM	2085	CA	ALA	217	47.259	9.760	81.845	1.00	51.83	AAAA C
ATOM	2086	CB	ALA	217	46.908	8.775	82.943	1.00	52.62	AAAA C
ATOM	2087	C	ALA	217	46.207	9.747	80.709	1.00	50.60	AAAA C
ATOM	2088	O	ALA	217	45.775	8.632	80.335	1.00	49.13	AAAA O
ATOM	2089	N	CYS	218	45.744	10.905	80.226	1.00	43.56	AAAA N
ATOM	2091	CA	CYS	218	44.802	11.030	79.157	1.00	48.09	AAAA C
ATOM	2092	C	CYS	218	45.166	10.331	77.869	1.00	47.06	AAAA C
ATOM	2093	O	CYS	218	46.300	9.967	77.642	1.00	55.57	AAAA O
ATOM	2094	CB	CYS	218	44.536	12.501	78.775	1.00	51.54	AAAA C
ATOM	2095	SG	CYS	218	44.256	13.494	80.302	1.00	56.98	AAAA S
ATOM	2096	N	VAL	219	44.226	10.085	76.978	1.00	43.40	AAAA N
ATOM	2098	CA	VAL	219	44.575	9.547	75.654	1.00	35.22	AAAA C
ATOM	2099	CB	VAL	219	43.693	8.427	75.242	1.00	32.26	AAAA C
ATOM	2100	CG1	VAL	219	43.952	7.873	73.886	1.00	36.19	AAAA C
ATOM	2101	CG2	VAL	219	43.811	7.144	76.071	1.00	45.51	AAAA C
ATOM	2102	C	VAL	219	44.453	10.750	74.735	1.00	32.06	AAAA C
ATOM	2103	O	VAL	219	45.303	10.897	73.874	1.00	42.27	AAAA O
ATOM	2104	N	ALA	220	43.728	11.759	75.187	1.00	24.24	AAAA N
ATOM	2106	CA	ALA	220	43.630	12.985	74.385	1.00	27.99	AAAA C
ATOM	2107	CB	ALA	220	42.536	12.919	73.331	1.00	28.42	AAAA C
ATOM	2108	C	ALA	220	43.292	14.071	75.390	1.00	29.21	AAAA C
ATOM	2109	O	ALA	220	42.846	13.604	76.455	1.00	37.88	AAAA O
ATOM	2110	N	CYS	221	43.285	15.334	75.058	1.00	30.27	AAAA N
ATOM	2112	CA	CYS	221	42.753	16.392	75.875	1.00	35.55	AAAA C
ATOM	2113	C	CYS	221	41.460	17.055	75.452	1.00	47.06	AAAA C
ATOM	2114	O	CYS	221	41.265	17.598	74.369	1.00	49.57	AAAA O
ATOM	2115	CB	CYS	221	43.804	17.479	76.063	1.00	47.45	AAAA C
ATOM	2116	SG	CYS	221	45.494	16.935	76.538	1.00	47.06	AAAA S
ATOM	2117	N	ARG	222	40.503	17.133	76.396	1.00	51.47	AAAA N
ATOM	2119	CA	ARG	222	39.281	17.906	76.338	1.00	51.86	AAAA C
ATOM	2120	CB	ARG	222	38.647	19.074	77.712	1.00	54.53	AAAA C
ATOM	2121	CG	ARG	222	37.314	19.687	77.854	1.00	45.56	AAAA C
ATOM	2122	CD	ARG	222	36.538	19.338	79.087	1.00	54.45	AAAA C
ATOM	2123	NE	ARG	222	36.272	16.947	79.269	1.00	65.53	AAAA N
ATOM	2125	CZ	ARG	222	35.534	16.080	78.617	1.00	67.60	AAAA C
ATOM	2126	NH1	ARG	222	34.925	16.599	77.533	1.00	70.26	AAAA N
ATOM	2129	NH2	ARG	222	35.342	14.780	78.901	1.00	54.11	AAAA N
ATOM	2132	C	ARG	222	39.562	19.296	75.740	1.00	50.66	AAAA C
ATOM	2133	O	ARG	222	38.737	19.845	75.009	1.00	58.34	AAAA O
ATOM	2134	N	HIS	223	40.556	19.981	76.190	1.00	45.65	AAAA N
ATOM	2136	CA	HIS	223	40.988	21.291	75.821	1.00	46.93	AAAA C
ATOM	2137	CB	HIS	223	41.057	22.251	77.011	1.00	49.51	AAAA C
ATOM	2139	CG	HIS	223	39.710	22.344	77.647	1.00	58.83	AAAA C
ATOM	2139	CD2	HIS	223	38.820	23.360	77.556	1.00	61.08	AAAA C
ATOM	2140	ND1	HIS	223	39.082	21.388	78.425	1.00	63.28	AAAA N
ATOM	2142	CE1	HIS	223	37.881	21.815	78.759	1.00	58.01	AAAA C
ATOM	2143	NE2	HIS	223	37.681	23.010	78.232	1.00	48.56	AAAA N
ATOM	2145	C	HIS	223	42.363	21.260	75.122	1.00	50.78	AAAA C
ATOM	2146	O	HIS	223	42.506	20.753	74.003	1.00	47.43	AAAA O
ATOM	2147	N	TYR	224	43.359	21.847	75.769	1.00	49.20	AAAA N
ATOM	2149	CA	TYR	224	44.712	21.992	75.259	1.00	48.17	AAAA C
ATOM	2150	CB	TYR	224	45.144	23.430	75.426	1.00	44.07	AAAA C
ATOM	2151	CG	TYR	224	44.318	24.234	74.417	1.00	51.77	AAAA C
ATOM	2152	CD1	TYR	224	43.193	24.869	74.904	1.00	48.94	AAAA C
ATOM	2153	CE1	TYR	224	42.401	25.633	74.089	1.00	48.41	AAAA C
ATOM	2154	CD2	TYR	224	44.623	24.358	73.065	1.00	54.82	AAAA C
ATOM	2155	CE2	TYR	224	43.847	25.131	72.233	1.00	56.09	AAAA C
ATOM	2156	CZ	TYR	224	42.739	25.745	72.766	1.00	54.23	AAAA C
ATOM	2157	OH	TYR	224	41.915	26.522	72.017	1.00	61.70	AAAA O
ATOM	2159	C	TYR	224	45.725	21.095	75.892	1.00	48.19	AAAA C
ATOM	2160	O	TYR	224	45.776	20.913	77.111	1.00	55.75	AAAA O
ATOM	2161	N	TYR	225	46.584	20.514	75.077	1.00	48.79	AAAA N
ATOM	2163	CA	TYR	225	47.655	19.653	75.555	1.00	43.02	AAAA C
ATOM	2164	CB	TYR	225	48.020	18.639	74.548	1.00	42.32	AAAA C
ATOM	2165	CG	TYR	225	49.286	17.926	74.954	1.00	46.95	AAAA C
ATOM	2166	CD1	TYR	225	49.299	16.859	75.817	1.00	43.57	AAAA C
ATOM	2167	CE1	TYR	225	50.450	16.221	76.173	1.00	47.26	AAAA C
ATOM	2168	CD2	TYR	225	50.487	18.407	74.421	1.00	52.82	AAAA C
ATOM	2169	CE2	TYR	225	51.656	17.791	74.781	1.00	53.94	AAAA C
ATOM	2170	CZ	TYR	225	51.639	16.707	75.644	1.00	52.31	AAAA C
ATOM	2171	OH	TYR	225	52.886	16.186	75.905	1.00	50.71	AAAA O
ATOM	2173	C	TYR	225	48.872	20.507	75.793	1.00	47.13	AAAA C
ATOM	2174	O	TYR	225	49.080	21.514	75.150	1.00	53.97	AAAA O
ATOM	2175	N	TYR	226	49.634	20.253	76.821	1.00	56.84	AAAA N

ATOM	2177	CA	TYR	226	50.814	21.061	77.172	1.00	56.83	AAAA C
ATOM	2179	CB	TYR	226	50.455	22.343	77.785	1.00	59.51	AAAA C
ATOM	2179	CG	TYR	226	51.741	23.126	77.941	1.00	65.45	AAAA C
ATOM	2180	CD1	TYR	226	52.121	23.557	79.197	1.00	69.12	AAAA C
ATOM	2181	CE1	TYR	226	53.289	24.275	79.400	1.00	70.77	AAAA C
ATOM	2182	CD2	TYR	226	52.580	23.409	76.864	1.00	69.38	AAAA C
ATOM	2183	CE2	TYR	226	53.758	24.118	77.020	1.00	70.94	AAAA C
ATOM	2184	CZ	TYR	226	54.099	24.549	78.301	1.00	72.96	AAAA C
ATOM	2185	OH	TYR	226	55.267	25.254	78.435	1.00	70.84	AAAA O
ATOM	2187	C	TYR	226	51.784	20.356	78.165	1.00	57.55	AAAA C
ATOM	2188	O	TYR	226	51.492	20.133	79.350	1.00	56.90	AAAA O
ATOM	2189	N	ALA	227	52.978	20.080	77.642	1.00	53.82	AAAA N
ATOM	2191	CA	ALA	227	54.061	19.557	78.440	1.00	51.82	AAAA C
ATOM	2192	CB	ALA	227	54.528	20.620	79.428	1.00	55.81	AAAA C
ATOM	2193	C	ALA	227	53.600	18.309	79.170	1.00	53.56	AAAA C
ATOM	2194	O	ALA	227	53.663	18.218	80.413	1.00	49.63	AAAA O
ATOM	2195	N	GLY	228	53.076	17.360	78.393	1.00	50.68	AAAA N
ATOM	2197	CA	GLY	228	52.585	16.135	79.028	1.00	49.02	AAAA C
ATOM	2198	C	GLY	228	51.312	16.330	79.861	1.00	51.61	AAAA C
ATOM	2199	O	GLY	228	51.028	15.538	80.776	1.00	51.10	AAAA O
ATOM	2200	N	VAL	229	50.643	17.495	79.791	1.00	47.09	AAAA N
ATOM	2202	CA	VAL	229	49.489	17.671	80.635	1.00	51.11	AAAA C
ATOM	2203	CB	VAL	229	49.908	18.610	81.774	1.00	56.52	AAAA C
ATOM	2204	CG1	VAL	229	48.627	18.896	82.566	1.00	38.39	AAAA C
ATOM	2205	CG2	VAL	229	51.002	18.035	82.682	1.00	50.16	AAAA C
ATOM	2206	C	VAL	229	48.255	18.173	79.873	1.00	51.37	AAAA C
ATOM	2207	O	VAL	229	48.344	19.279	79.309	1.00	53.71	AAAA O
ATOM	2208	N	CYS	230	47.100	17.518	80.036	1.00	42.21	AAAA N
ATOM	2210	CA	CYS	230	45.881	18.117	79.471	1.00	40.32	AAAA C
ATOM	2211	C	CYS	230	45.456	19.350	80.228	1.00	38.42	AAAA C
ATOM	2212	O	CYS	230	44.964	19.248	81.321	1.00	41.62	AAAA O
ATOM	2213	CB	CYS	230	44.746	17.132	79.370	1.00	31.54	AAAA C
ATOM	2214	SG	CYS	230	45.149	15.753	78.266	1.00	43.61	AAAA S
ATOM	2215	N	VAL	231	45.637	20.534	79.731	1.00	39.83	AAAA N
ATOM	2217	CA	VAL	231	45.445	21.769	80.462	1.00	46.57	AAAA C
ATOM	2218	CB	VAL	231	46.619	22.736	80.088	1.00	50.99	AAAA C
ATOM	2219	CG1	VAL	231	46.798	23.878	81.053	1.00	50.41	AAAA C
ATOM	2220	CG2	VAL	231	47.839	21.913	80.506	1.00	44.95	AAAA C
ATOM	2221	C	VAL	231	44.111	22.321	80.057	1.00	52.59	AAAA C
ATOM	2222	O	VAL	231	43.599	22.193	78.936	1.00	55.30	AAAA O
ATOM	2223	N	PRO	232	43.482	23.105	80.913	1.00	54.29	AAAA N
ATOM	2224	CD	PRO	232	43.830	23.385	82.320	1.00	54.25	AAAA C
ATOM	2225	CA	PRO	232	42.153	23.625	80.575	1.00	54.39	AAAA C
ATOM	2226	CB	PRO	232	41.537	23.877	81.928	1.00	53.73	AAAA C
ATOM	2227	CG	PRO	232	42.683	24.287	82.765	1.00	55.00	AAAA C
ATOM	2228	C	PRO	232	42.361	24.913	79.795	1.00	56.37	AAAA C
ATOM	2229	O	PRO	232	41.498	25.492	79.137	1.00	55.79	AAAA O
ATOM	2230	N	ALA	233	43.615	25.400	79.901	1.00	54.76	AAAA N
ATOM	2232	CA	ALA	233	43.998	26.569	79.124	1.00	49.93	AAAA C
ATOM	2233	CB	ALA	233	43.440	27.907	79.746	1.00	35.43	AAAA C
ATOM	2234	C	ALA	233	45.502	26.662	79.974	1.00	49.79	AAAA C
ATOM	2235	O	ALA	233	46.195	25.879	79.616	1.00	51.41	AAAA O
ATOM	2236	N	CYS	234	45.984	27.508	78.072	1.00	45.07	AAAA N
ATOM	2238	CA	CYS	234	47.430	27.518	77.907	1.00	48.63	AAAA C
ATOM	2239	C	CYS	234	48.001	28.340	79.076	1.00	50.93	AAAA C
ATOM	2240	O	CYS	234	47.650	29.513	79.250	1.00	47.57	AAAA O
ATOM	2241	CB	CYS	234	47.816	28.034	76.511	1.00	43.10	AAAA C
ATOM	2242	SG	CYS	234	47.608	26.789	75.226	1.00	43.04	AAAA S
ATOM	2243	N	PRO	235	49.127	27.853	79.599	1.00	49.55	AAAA N
ATOM	2244	CD	PRO	235	49.692	26.557	79.207	1.00	48.75	AAAA C
ATOM	2245	CA	PRO	235	49.911	28.569	80.599	1.00	51.69	AAAA C
ATOM	2246	CB	PRO	235	50.984	27.581	80.975	1.00	50.80	AAAA C
ATOM	2247	CG	PRO	235	50.912	26.417	80.077	1.00	50.06	AAAA C
ATOM	2248	C	PRO	235	50.487	29.852	80.050	1.00	57.11	AAAA C
ATOM	2249	O	PRO	235	50.848	29.957	78.870	1.00	59.60	AAAA O
ATOM	2250	N	PRO	236	50.676	30.875	80.887	1.00	59.85	AAAA N
ATOM	2251	CD	PRO	236	50.405	30.822	82.363	1.00	55.85	AAAA C
ATOM	2252	CA	PRO	236	51.323	32.143	80.493	1.00	52.27	AAAA C
ATOM	2253	CB	PRO	236	51.695	32.814	81.826	1.00	53.62	AAAA C
ATOM	2254	CG	PRO	236	50.652	32.277	82.754	1.00	56.73	AAAA C
ATOM	2255	C	PRO	236	52.545	31.886	79.671	1.00	44.21	AAAA C
ATOM	2256	O	PRO	236	53.218	30.892	79.928	1.00	43.40	AAAA O
ATOM	2257	N	ASN	237	52.837	32.757	78.716	1.00	46.54	AAAA N
ATOM	2259	CA	ASN	237	53.895	32.623	77.716	1.00	45.94	AAAA C
ATOM	2260	CB	ASN	237	55.258	32.653	78.456	1.00	58.65	AAAA C
ATOM	2261	CG	ASN	237	55.357	33.855	79.371	1.00	58.51	AAAA C
ATOM	2262	OD1	ASN	237	56.044	33.783	80.379	1.00	72.25	AAAA O
ATOM	2263	ND2	ASN	237	54.631	34.910	79.051	1.00	62.99	AAAA N
ATOM	2266	C	ASN	237	53.897	31.425	76.788	1.00	46.87	AAAA C
ATOM	2267	O	ASN	237	54.962	30.935	76.326	1.00	54.50	AAAA O
ATOM	2268	N	THR	238	52.817	30.657	76.692	1.00	42.91	AAAA N
ATOM	2270	CA	THR	238	52.617	29.567	75.780	1.00	40.20	AAAA C
ATOM	2271	CB	THR	238	52.461	28.248	76.466	1.00	42.62	AAAA C
ATOM	2272	OG1	THR	238	51.227	28.343	77.237	1.00	50.89	AAAA O
ATOM	2274	CG2	THR	238	53.552	27.886	77.424	1.00	34.84	AAAA C

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ATOM   2275  C   THR   238      51.279  29.875  75.078  1.00 42.59      AAAA C
ATOM   2276  O   THR   238      50.669  30.864  75.509  1.00 42.51      AAAA O
ATOM   2277  N   TYR   239      51.051  29.488  73.830  1.00 42.62      AAAA N
ATOM   2279  CA  TYR   239      49.949  29.959  73.024  1.00 41.87      AAAA C
ATOM   2280  CB  TYR   239      50.457  30.907  71.931  1.00 44.86      AAAA C
ATOM   2281  CG  TYR   239      51.099  32.125  72.564  1.00 42.05      AAAA C
ATOM   2282  CD1 TYR   239      52.467  32.086  72.815  1.00 39.41      AAAA C
ATOM   2283  CE1 TYR   239      53.092  33.152  73.415  1.00 43.27      AAAA C
ATOM   2284  CD2 TYR   239      50.376  33.230  72.923  1.00 44.15      AAAA C
ATOM   2285  CE2 TYR   239      50.972  34.310  73.536  1.00 46.22      AAAA C
ATOM   2286  CZ  TYR   239      52.339  34.243  73.779  1.00 50.49      AAAA C
ATOM   2287  OH  TYR   239      53.013  35.289  74.387  1.00 55.47      AAAA O
ATOM   2289  C   TYR   239      49.232  28.813  72.315  1.00 45.54      AAAA C
ATOM   2290  O   TYR   239      49.922  27.810  72.021  1.00 46.66      AAAA O
ATOM   2291  N   ARG   240      47.895  28.990  72.126  1.00 40.62      AAAA N
ATOM   2293  CA  ARG   240      47.177  27.892  71.426  1.00 38.78      AAAA C
ATOM   2294  CB  ARG   240      45.675  28.127  71.452  1.00 39.77      AAAA C
ATOM   2295  CG  ARG   240      45.116  28.944  72.588  1.00 43.37      AAAA C
ATOM   2296  CD  ARG   240      43.573  28.957  72.683  1.00 38.60      AAAA C
ATOM   2297  NE  ARG   240      43.114  29.683  71.455  1.00 53.98      AAAA N
ATOM   2299  CZ  ARG   240      43.123  31.015  71.530  1.00 48.07      AAAA C
ATOM   2300  NH1 ARG   240      43.513  31.562  72.668  1.00 47.65      AAAA N
ATOM   2303  NH2 ARG   240      42.788  31.778  70.533  1.00 51.03      AAAA N
ATOM   2306  C   ARG   240      47.627  27.737  69.979  1.00 31.72      AAAA C
ATOM   2307  O   ARG   240      47.937  28.730  69.302  1.00 32.37      AAAA O
ATOM   2308  N   PHE   241      47.779  26.542  69.549  1.00 27.95      AAAA N
ATOM   2310  CA  PHE   241      48.182  26.269  68.183  1.00 30.41      AAAA C
ATOM   2311  CB  PHE   241      49.678  25.940  68.151  1.00 34.83      AAAA C
ATOM   2312  CG  PHE   241      50.235  25.653  66.773  1.00 26.84      AAAA C
ATOM   2313  CD1 PHE   241      50.165  26.567  65.753  1.00 25.31      AAAA C
ATOM   2314  CD2 PHE   241      50.785  24.417  66.573  1.00 27.38      AAAA C
ATOM   2315  CE1 PHE   241      50.676  26.232  64.509  1.00 37.24      AAAA C
ATOM   2316  CE2 PHE   241      51.294  24.101  65.320  1.00 38.45      AAAA C
ATOM   2317  CZ  PHE   241      51.281  25.010  64.281  1.00 21.17      AAAA C
ATOM   2318  C   PHE   241      47.382  25.089  67.621  1.00 35.77      AAAA C
ATOM   2319  O   PHE   241      47.543  24.013  68.186  1.00 36.77      AAAA O
ATOM   2320  N   GLU   242      46.739  25.301  66.468  1.00 32.30      AAAA N
ATOM   2322  CA  GLU   242      45.964  24.269  65.805  1.00 35.43      AAAA C
ATOM   2323  CB  GLU   242      46.953  23.144  65.472  1.00 37.98      AAAA C
ATOM   2324  CG  GLU   242      47.867  23.415  64.314  1.00 39.63      AAAA C
ATOM   2325  CD  GLU   242      47.207  23.965  63.075  1.00 39.27      AAAA C
ATOM   2326  OE1 GLU   242      46.380  23.205  62.517  1.00 42.79      AAAA O
ATOM   2327  OE2 GLU   242      47.354  25.109  62.626  1.00 36.36      AAAA O
ATOM   2328  C   GLU   242      44.752  23.771  66.600  1.00 34.36      AAAA C
ATOM   2329  O   GLU   242      44.390  22.611  66.511  1.00 28.53      AAAA O
ATOM   2330  N   GLY   243      44.135  24.589  67.449  1.00 36.94      AAAA N
ATOM   2332  CA  GLY   243      43.048  24.154  68.303  1.00 34.57      AAAA C
ATOM   2333  C   GLY   243      43.429  23.107  69.319  1.00 37.76      AAAA C
ATOM   2334  O   GLY   243      42.474  22.473  69.746  1.00 43.00      AAAA O
ATOM   2335  N   TRP   244      44.637  22.636  69.611  1.00 39.53      AAAA N
ATOM   2337  CA  TRP   244      44.797  21.536  70.566  1.00 40.85      AAAA C
ATOM   2338  CB  TRP   244      44.774  20.271  69.764  1.00 26.76      AAAA C
ATOM   2339  CG  TRP   244      46.012  19.885  69.028  1.00 43.19      AAAA C
ATOM   2340  CD2 TRP   244      47.019  18.983  69.498  1.00 39.55      AAAA C
ATOM   2341  CE2 TRP   244      47.998  18.906  68.489  1.00 36.50      AAAA C
ATOM   2342  CE3 TRP   244      47.186  18.254  70.692  1.00 32.18      AAAA C
ATOM   2343  CD1 TRP   244      46.424  20.308  67.779  1.00 43.37      AAAA C
ATOM   2344  NE1 TRP   244      47.595  19.727  67.469  1.00 38.89      AAAA N
ATOM   2346  CZ2 TRP   244      49.150  18.128  68.620  1.00 39.01      AAAA C
ATOM   2347  CZ3 TRP   244      48.336  17.478  70.815  1.00 43.98      AAAA C
ATOM   2348  CH2 TRP   244      49.322  17.425  69.784  1.00 42.50      AAAA C
ATOM   2349  C   TRP   244      45.998  21.517  71.509  1.00 42.98      AAAA C
ATOM   2350  O   TRP   244      46.253  20.501  72.146  1.00 42.70      AAAA O
ATOM   2351  N   ARG   245      46.888  22.485  71.435  1.00 44.16      AAAA N
ATOM   2353  CA  ARG   245      48.168  22.472  72.095  1.00 46.47      AAAA C
ATOM   2354  CB  ARG   245      49.203  21.602  71.367  1.00 47.30      AAAA C
ATOM   2355  CG  ARG   245      49.885  22.309  70.203  1.00 48.97      AAAA C
ATOM   2356  CD  ARG   245      51.129  21.552  69.819  1.00 39.28      AAAA C
ATOM   2357  NE  ARG   245      51.586  21.665  68.444  1.00 50.96      AAAA N
ATOM   2359  CZ  ARG   245      52.629  21.044  67.895  1.00 46.73      AAAA C
ATOM   2360  NH1 ARG   245      53.344  20.236  68.653  1.00 50.15      AAAA N
ATOM   2363  NH2 ARG   245      53.072  21.126  66.638  1.00 41.69      AAAA N
ATOM   2366  C   ARG   245      48.771  23.963  72.271  1.00 46.01      AAAA C
ATOM   2367  O   ARG   245      48.394  24.793  71.541  1.00 47.44      AAAA O
ATOM   2368  N   CYS   246      49.625  23.881  73.317  1.00 42.08      AAAA N
ATOM   2370  CA  CYS   246      50.246  25.199  73.628  1.00 43.48      AAAA C
ATOM   2371  C   CYS   246      51.695  25.217  73.183  1.00 43.38      AAAA C
ATOM   2372  O   CYS   246      52.476  24.239  73.320  1.00 42.51      AAAA O
ATOM   2373  CB  CYS   246      50.102  25.392  75.138  1.00 48.91      AAAA C
ATOM   2374  SG  CYS   246      48.386  25.049  75.797  1.00 43.68      AAAA S
ATOM   2375  N   VAL   247      52.121  26.288  72.564  1.00 41.21      AAAA N
ATOM   2377  CA  VAL   247      53.417  26.468  71.982  1.00 36.51      AAAA C
ATOM   2378  CB  VAL   247      53.568  26.357  70.444  1.00 36.87      AAAA C
ATOM   2379  CG1 VAL   247      53.089  24.988  70.024  1.00 32.71      AAAA C
ATOM   2380  CG2 VAL   247      53.129  27.602  69.729  1.00 28.20      AAAA C
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ATOM	2381	C	VAL	247	53.969	27.812	72.373	1.00	39.37	AAAA C
ATOM	2382	O	VAL	247	53.230	28.770	72.540	1.00	38.80	AAAA O
ATOM	2383	N	ASP	248	55.291	27.820	72.711	1.00	45.21	AAAA N
ATOM	2385	CA	ASP	248	55.895	29.115	73.098	1.00	40.19	AAAA C
ATOM	2386	CB	ASP	248	57.091	28.946	73.953	1.00	42.63	AAAA C
ATOM	2387	CG	ASP	248	58.126	27.997	73.394	1.00	58.81	AAAA C
ATOM	2388	OD1	ASP	248	59.067	27.795	74.187	1.00	53.06	AAAA O
ATOM	2389	OD2	ASP	248	58.167	27.395	72.313	1.00	69.51	AAAA O
ATOM	2390	C	ASP	248	56.315	29.883	71.839	1.00	36.99	AAAA C
ATOM	2391	O	ASP	248	56.292	29.288	70.772	1.00	39.70	AAAA O
ATOM	2392	N	ARG	249	56.545	31.163	71.918	1.00	30.72	AAAA N
ATOM	2394	CA	ARG	249	56.950	32.057	70.906	1.00	36.17	AAAA C
ATOM	2395	CB	ARG	249	57.223	33.485	71.491	1.00	21.29	AAAA C
ATOM	2396	CG	ARG	249	57.594	34.424	70.326	1.00	24.96	AAAA C
ATOM	2397	CD	ARG	249	57.814	35.811	70.843	1.00	21.23	AAAA C
ATOM	2398	NE	ARG	249	56.658	36.150	71.689	1.00	39.75	AAAA N
ATOM	2400	CZ	ARG	249	55.632	36.823	71.101	1.00	39.35	AAAA C
ATOM	2401	NH1	ARG	249	55.642	37.118	69.801	1.00	25.41	AAAA N
ATOM	2404	NH2	ARG	249	54.641	37.118	71.946	1.00	44.04	AAAA N
ATOM	2407	C	ARG	249	58.134	31.685	70.010	1.00	40.63	AAAA C
ATOM	2408	O	ARG	249	58.086	31.923	68.797	1.00	44.79	AAAA O
ATOM	2409	N	ASP	250	59.149	30.974	70.468	1.00	41.87	AAAA N
ATOM	2411	CA	ASP	250	60.287	30.739	69.606	1.00	46.90	AAAA C
ATOM	2412	CB	ASP	250	61.740	30.726	70.154	1.00	53.11	AAAA C
ATOM	2413	CG	ASP	250	62.421	32.122	70.081	1.00	71.49	AAAA C
ATOM	2414	OD1	ASP	250	63.124	32.682	69.176	1.00	58.53	AAAA O
ATOM	2415	OD2	ASP	250	62.272	32.928	71.071	1.00	70.30	AAAA O
ATOM	2416	C	ASP	250	59.881	29.536	68.771	1.00	41.22	AAAA C
ATOM	2417	O	ASP	250	60.291	29.443	67.616	1.00	39.06	AAAA O
ATOM	2418	N	PHE	251	59.116	28.609	69.299	1.00	36.13	AAAA N
ATOM	2420	CA	PHE	251	58.457	27.601	68.489	1.00	34.88	AAAA C
ATOM	2421	CB	PHE	251	57.468	26.746	69.256	1.00	29.82	AAAA C
ATOM	2422	CG	PHE	251	56.701	25.801	68.385	1.00	41.50	AAAA C
ATOM	2423	CD1	PHE	251	57.101	24.479	68.263	1.00	30.66	AAAA C
ATOM	2424	CD2	PHE	251	55.559	26.213	67.686	1.00	37.78	AAAA C
ATOM	2425	CE1	PHE	251	56.414	23.597	67.424	1.00	29.30	AAAA C
ATOM	2426	CE2	PHE	251	54.847	25.372	66.856	1.00	36.09	AAAA C
ATOM	2427	CZ	PHE	251	55.294	24.070	66.715	1.00	36.21	AAAA C
ATOM	2428	C	PHE	251	57.624	28.290	67.338	1.00	39.28	AAAA C
ATOM	2429	O	PHE	251	57.911	28.010	66.144	1.00	30.27	AAAA O
ATOM	2430	N	CYS	252	56.734	29.225	67.713	1.00	35.13	AAAA N
ATOM	2432	CA	CYS	252	55.895	29.870	66.728	1.00	38.80	AAAA C
ATOM	2433	C	CYS	252	56.827	30.599	65.747	1.00	44.73	AAAA C
ATOM	2434	O	CYS	252	56.552	30.534	64.536	1.00	43.20	AAAA O
ATOM	2435	CB	CYS	252	54.903	30.778	67.379	1.00	35.65	AAAA C
ATOM	2436	SG	CYS	252	53.562	31.544	66.459	1.00	39.03	AAAA S
ATOM	2437	N	ALA	253	57.872	31.256	66.285	1.00	41.53	AAAA N
ATOM	2439	CA	ALA	253	58.687	32.071	65.415	1.00	40.39	AAAA C
ATOM	2440	CB	ALA	253	59.529	33.098	66.172	1.00	36.07	AAAA C
ATOM	2441	C	ALA	253	59.551	31.167	64.539	1.00	42.89	AAAA C
ATOM	2442	O	ALA	253	60.147	31.735	63.640	1.00	47.42	AAAA O
ATOM	2443	N	ASN	254	59.657	29.859	64.700	1.00	38.75	AAAA N
ATOM	2445	CA	ASN	254	60.546	29.073	63.928	1.00	42.94	AAAA C
ATOM	2446	CB	ASN	254	61.667	28.497	64.847	1.00	48.09	AAAA C
ATOM	2447	CG	ASN	254	62.696	29.635	65.031	1.00	49.54	AAAA C
ATOM	2448	OD1	ASN	254	63.468	29.940	64.081	1.00	61.38	AAAA O
ATOM	2449	ND2	ASN	254	62.607	30.321	66.144	1.00	48.38	AAAA N
ATOM	2452	C	ASN	254	59.907	27.959	63.135	1.00	53.72	AAAA C
ATOM	2453	O	ASN	254	60.552	26.965	62.804	1.00	51.19	AAAA O
ATOM	2454	N	ILE	255	58.612	28.136	62.766	1.00	57.77	AAAA N
ATOM	2456	CA	ILE	255	57.828	27.107	62.134	1.00	53.28	AAAA C
ATOM	2457	CB	ILE	255	56.329	27.322	62.304	1.00	50.41	AAAA C
ATOM	2458	CG2	ILE	255	55.477	26.595	61.246	1.00	51.95	AAAA C
ATOM	2459	CG1	ILE	255	55.778	26.675	63.553	1.00	40.59	AAAA C
ATOM	2460	CD1	ILE	255	54.479	27.317	64.006	1.00	38.97	AAAA C
ATOM	2461	C	ILE	255	58.127	26.886	60.651	1.00	52.62	AAAA C
ATOM	2462	O	ILE	255	58.196	25.709	60.252	1.00	53.96	AAAA O
ATOM	2463	N	LEU	256	58.290	27.960	59.918	1.00	49.96	AAAA N
ATOM	2465	CA	LEU	256	58.680	27.764	58.516	1.00	63.68	AAAA C
ATOM	2466	CB	LEU	256	58.175	29.012	57.799	1.00	56.80	AAAA C
ATOM	2467	CG	LEU	256	56.671	29.196	57.864	1.00	59.11	AAAA C
ATOM	2468	CD1	LEU	256	56.310	30.654	57.645	1.00	43.31	AAAA C
ATOM	2469	CD2	LEU	256	55.965	28.222	56.928	1.00	55.88	AAAA C
ATOM	2470	C	LEU	256	60.193	27.622	58.355	1.00	66.23	AAAA C
ATOM	2471	O	LEU	256	60.691	27.511	57.245	1.00	70.29	AAAA O
ATOM	2472	N	SER	257	60.942	27.559	59.430	1.00	64.61	AAAA N
ATOM	2474	CA	SER	257	62.352	27.529	59.534	1.00	69.23	AAAA C
ATOM	2475	CB	SER	257	62.924	27.318	60.955	1.00	62.45	AAAA C
ATOM	2476	OG	SER	257	63.381	25.980	61.074	1.00	56.18	AAAA O
ATOM	2478	C	SER	257	62.973	26.497	58.610	1.00	70.77	AAAA C
ATOM	2479	O	SER	257	64.127	26.731	58.246	1.00	72.50	AAAA O
ATOM	2480	N	ALA	258	62.322	25.389	58.320	1.00	74.61	AAAA N
ATOM	2482	CA	ALA	258	62.933	24.498	57.343	1.00	76.34	AAAA C
ATOM	2483	CB	ALA	258	62.570	23.039	57.584	1.00	80.82	AAAA C
ATOM	2484	C	ALA	258	62.663	24.964	55.921	1.00	78.21	AAAA C

ATOM	2485	O	ALA	258	62.880	24.139	55.029	1.00	79.60	AAAA	O
ATOM	2486	N	GLU	259	62.069	26.109	55.651	1.00	79.05	AAAA	N
ATOM	2488	CA	GLU	259	61.742	26.621	54.349	1.00	83.84	AAAA	C
ATOM	2489	CB	GLU	259	60.226	26.457	54.135	1.00	86.99	AAAA	C
ATOM	2490	CG	GLU	259	59.687	25.049	54.314	1.00	89.38	AAAA	C
ATOM	2491	CD	GLU	259	58.364	25.032	55.057	1.00	97.77	AAAA	C
ATOM	2492	OE1	GLU	259	58.080	24.088	55.838	1.00	101.45	AAAA	O
ATOM	2493	OE2	GLU	259	57.598	26.002	54.837	1.00	94.58	AAAA	O
ATOM	2494	C	GLU	259	62.117	28.078	54.083	1.00	85.43	AAAA	C
ATOM	2495	O	GLU	259	62.059	29.009	54.903	1.00	88.01	AAAA	O
ATOM	2496	N	SER	260	62.298	28.338	52.799	1.00	84.66	AAAA	N
ATOM	2498	CA	SER	260	62.725	29.625	52.254	1.00	84.03	AAAA	C
ATOM	2499	CB	SER	260	63.753	29.269	51.173	1.00	87.24	AAAA	C
ATOM	2500	OG	SER	260	63.306	29.419	49.835	1.00	93.65	AAAA	O
ATOM	2502	C	SER	260	61.558	30.466	51.789	1.00	80.84	AAAA	C
ATOM	2503	O	SER	260	61.496	30.889	50.635	1.00	81.31	AAAA	O
ATOM	2504	N	SER	261	60.617	30.785	52.685	1.00	78.56	AAAA	N
ATOM	2506	CA	SER	261	59.423	31.540	52.308	1.00	72.13	AAAA	C
ATOM	2507	CB	SER	261	58.179	31.297	53.170	1.00	67.30	AAAA	C
ATOM	2508	OG	SER	261	57.436	30.334	52.451	1.00	74.74	AAAA	O
ATOM	2510	C	SER	261	59.683	33.032	52.318	1.00	66.90	AAAA	C
ATOM	2511	O	SER	261	60.048	33.588	53.334	1.00	63.24	AAAA	O
ATOM	2512	N	ASP	262	59.364	33.659	51.204	1.00	65.30	AAAA	N
ATOM	2514	CA	ASP	262	59.358	35.071	50.915	1.00	58.55	AAAA	C
ATOM	2515	CB	ASP	262	59.268	35.285	49.400	1.00	64.85	AAAA	C
ATOM	2516	CG	ASP	262	59.389	36.713	48.931	1.00	76.42	AAAA	C
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ATOM	2519	C	ASP	262	58.121	35.706	51.529	1.00	56.88	AAAA	C
ATOM	2520	O	ASP	262	57.851	36.918	51.510	1.00	52.48	AAAA	O
ATOM	2521	N	SER	263	57.259	34.849	52.118	1.00	53.43	AAAA	N
ATOM	2523	CA	SER	263	56.047	35.352	52.734	1.00	52.84	AAAA	C
ATOM	2524	CB	SER	263	55.020	34.245	52.885	1.00	46.60	AAAA	C
ATOM	2525	OG	SER	263	55.149	33.348	51.791	1.00	66.80	AAAA	O
ATOM	2527	C	SER	263	56.310	36.965	54.117	1.00	49.52	AAAA	C
ATOM	2528	O	SER	263	57.396	36.737	54.709	1.00	42.33	AAAA	O
ATOM	2529	N	GLU	264	55.320	36.783	54.549	1.00	38.93	AAAA	N
ATOM	2531	CA	GLU	264	55.362	37.222	55.921	1.00	36.70	AAAA	C
ATOM	2532	CB	GLU	264	54.359	38.337	56.208	1.00	43.71	AAAA	C
ATOM	2533	CG	GLU	264	54.575	39.482	55.218	1.00	37.74	AAAA	C
ATOM	2534	CD	GLU	264	55.374	40.632	55.793	1.00	34.36	AAAA	C
ATOM	2535	OE1	GLU	264	55.493	41.600	57.034	1.00	41.55	AAAA	O
ATOM	2536	OE2	GLU	264	55.832	41.576	55.146	1.00	39.60	AAAA	O
ATOM	2537	C	GLU	264	55.099	36.056	56.827	1.00	35.84	AAAA	C
ATOM	2538	O	GLU	264	54.366	35.151	56.355	1.00	39.60	AAAA	O
ATOM	2539	N	GLY	265	55.801	35.938	57.962	1.00	35.64	AAAA	N
ATOM	2541	CA	GLY	265	55.671	34.690	58.727	1.00	40.30	AAAA	C
ATOM	2542	C	GLY	265	54.622	34.716	59.829	1.00	39.81	AAAA	C
ATOM	2543	O	GLY	265	53.981	35.699	60.135	1.00	37.20	AAAA	O
ATOM	2544	N	PHE	266	54.537	33.569	60.516	1.00	35.75	AAAA	N
ATOM	2546	CA	PHE	266	53.637	33.434	61.625	1.00	33.70	AAAA	C
ATOM	2547	CB	PHE	266	53.924	32.155	62.386	1.00	28.20	AAAA	C
ATOM	2548	CG	PHE	266	53.356	30.958	61.671	1.00	37.07	AAAA	C
ATOM	2549	CD1	PHE	266	53.760	30.618	60.377	1.00	34.72	AAAA	C
ATOM	2550	CD2	PHE	266	52.383	30.185	62.313	1.00	25.65	AAAA	C
ATOM	2551	CE1	PHE	266	53.225	29.506	59.760	1.00	37.72	AAAA	C
ATOM	2552	CE2	PHE	266	51.879	29.094	61.672	1.00	24.63	AAAA	C
ATOM	2553	CZ	PHE	266	52.260	28.708	60.402	1.00	23.58	AAAA	C
ATOM	2554	C	PHE	266	53.571	34.570	62.608	1.00	35.82	AAAA	C
ATOM	2555	O	PHE	266	54.446	35.372	62.879	1.00	39.23	AAAA	O
ATOM	2556	N	VAL	267	52.360	34.763	63.161	1.00	37.10	AAAA	N
ATOM	2558	CA	VAL	267	52.118	35.812	64.113	1.00	36.09	AAAA	C
ATOM	2559	CB	VAL	267	51.315	36.974	63.567	1.00	39.01	AAAA	C
ATOM	2560	CG1	VAL	267	51.626	37.601	62.230	1.00	31.10	AAAA	C
ATOM	2561	CG2	VAL	267	49.890	36.400	63.570	1.00	36.88	AAAA	C
ATOM	2562	C	VAL	267	51.506	35.260	65.400	1.00	33.55	AAAA	C
ATOM	2563	O	VAL	267	51.202	34.098	65.515	1.00	32.41	AAAA	O
ATOM	2564	N	ILE	268	51.539	36.088	66.477	1.00	35.88	AAAA	N
ATOM	2566	CA	ILE	268	50.867	35.573	67.681	1.00	39.79	AAAA	C
ATOM	2567	CB	ILE	268	51.791	35.232	68.849	1.00	31.17	AAAA	C
ATOM	2568	CG2	ILE	268	50.922	35.253	70.150	1.00	32.66	AAAA	C
ATOM	2569	CG1	ILE	268	52.403	33.966	68.724	1.00	23.56	AAAA	C
ATOM	2570	CD1	ILE	268	53.421	33.546	69.806	1.00	25.93	AAAA	C
ATOM	2571	C	ILE	268	49.806	36.628	68.060	1.00	42.44	AAAA	C
ATOM	2572	O	ILE	268	50.116	37.767	68.327	1.00	39.99	AAAA	O
ATOM	2573	N	HIS	269	48.528	36.292	67.864	1.00	44.26	AAAA	N
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ATOM	2576	CB	HIS	269	46.885	37.876	66.901	1.00	45.48	AAAA	C
ATOM	2577	CG	HIS	269	45.915	38.986	67.079	1.00	54.33	AAAA	C
ATOM	2578	CD2	HIS	269	44.551	39.014	67.096	1.00	46.61	AAAA	C
ATOM	2579	ND1	HIS	269	46.356	40.280	67.307	1.00	51.86	AAAA	N
ATOM	2581	CE1	HIS	269	45.282	41.057	67.437	1.00	55.17	AAAA	C
ATOM	2582	NE2	HIS	269	44.175	40.324	67.309	1.00	46.97	AAAA	N
ATOM	2584	C	HIS	269	46.423	36.740	69.074	1.00	45.54	AAAA	C
ATOM	2585	O	HIS	269	46.076	35.552	69.027	1.00	42.94	AAAA	O

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ATOM   2586  N   ASP  270      45.952  37.526  70.059  1.00 42.82      AAAA N
ATOM   2587  CA  ASP  270      44.948  37.025  71.001  1.00 48.03      AAAA C
ATOM   2588  CB  ASP  270      43.573  37.014  70.338  1.00 63.63      AAAA C
ATOM   2589  CG  ASP  270      42.919  38.393  70.294  1.00 80.82      AAAA C
ATOM   2590  OD1 ASP  270      41.737  38.379  69.835  1.00 90.92      AAAA O
ATOM   2591  OD2 ASP  270      43.407  39.494  70.652  1.00 86.49      AAAA O
ATOM   2592  C   ASP  270      45.226  35.667  71.594  1.00 44.66      AAAA C
ATOM   2593  O   ASP  270      44.357  34.782  71.576  1.00 45.54      AAAA O
ATOM   2594  N   GLY  271      46.477  35.379  71.924  1.00 41.63      AAAA N
ATOM   2595  CA  GLY  271      46.839  34.117  72.506  1.00 37.20      AAAA C
ATOM   2596  C   GLY  271      46.818  32.998  71.537  1.00 39.15      AAAA C
ATOM   2597  O   GLY  271      46.775  31.865  72.039  1.00 46.56      AAAA O
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ATOM   2600  CB  GLU  272      45.752  31.737  68.876  1.00 37.58      AAAA C
ATOM   2601  CG  GLU  272      45.778  30.600  67.839  1.00 45.30      AAAA C
ATOM   2602  CD  GLU  272      44.413  30.528  67.149  1.00 36.92      AAAA C
ATOM   2603  OE1 GLU  272      43.545  31.345  67.533  1.00 48.41      AAAA O
ATOM   2604  OE2 GLU  272      44.223  29.696  66.286  1.00 44.10      AAAA O
ATOM   2605  C   GLU  272      48.211  32.324  68.335  1.00 40.32      AAAA C
ATOM   2606  O   GLU  272      48.445  33.447  67.896  1.00 37.04      AAAA O
ATOM   2607  N   CYS  273      48.942  31.237  68.138  1.00 38.83      AAAA N
ATOM   2608  CA  CYS  273      50.046  31.187  67.188  1.00 40.27      AAAA C
ATOM   2609  C   CYS  273      49.321  30.810  65.883  1.00 42.16      AAAA C
ATOM   2610  O   CYS  273      48.713  29.712  65.831  1.00 40.86      AAAA O
ATOM   2611  CB  CYS  273      51.098  30.148  67.529  1.00 40.21      AAAA C
ATOM   2612  SG  CYS  273      52.337  29.825  66.260  1.00 39.79      AAAA S
ATOM   2613  N   MET  274      49.373  31.749  64.933  1.00 33.70      AAAA N
ATOM   2614  CA  MET  274      48.586  31.351  63.720  1.00 36.68      AAAA C
ATOM   2615  CB  MET  274      47.136  31.861  63.847  1.00 29.11      AAAA C
ATOM   2616  CG  MET  274      46.923  33.379  63.691  1.00 36.51      AAAA C
ATOM   2617  SD  MET  274      45.477  33.921  64.677  1.00 40.00      AAAA S
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ATOM   2619  C   MET  274      49.426  31.900  62.608  1.00 39.35      AAAA C
ATOM   2620  O   MET  274      50.167  32.880  62.672  1.00 41.00      AAAA O
ATOM   2621  N   GLN  275      49.378  31.353  61.428  1.00 42.55      AAAA N
ATOM   2622  CA  GLN  275      50.041  31.934  60.232  1.00 37.69      AAAA C
ATOM   2623  CB  GLN  275      49.619  30.765  59.242  1.00 34.01      AAAA C
ATOM   2624  CG  GLN  275      49.329  31.274  57.864  1.00 56.40      AAAA C
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ATOM   2626  OE1 GLN  275      49.941  29.151  56.910  1.00 67.24      AAAA O
ATOM   2627  NE2 GLN  275      48.451  30.436  55.799  1.00 78.29      AAAA N
ATOM   2628  C   GLN  275      49.721  33.195  59.720  1.00 35.41      AAAA C
ATOM   2629  O   GLN  275      50.526  33.831  59.064  1.00 35.95      AAAA O
ATOM   2630  N   GLU  276      48.566  33.754  60.056  1.00 41.70      AAAA N
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ATOM   2632  CB  GLU  276      47.387  34.884  58.245  1.00 42.40      AAAA C
ATOM   2633  CG  GLU  276      47.154  36.269  57.650  1.00 53.84      AAAA C
ATOM   2634  CD  GLU  276      48.359  37.198  57.460  1.00 61.37      AAAA C
ATOM   2635  OE1 GLU  276      49.356  36.595  56.943  1.00 67.32      AAAA O
ATOM   2636  OE2 GLU  276      48.242  38.411  57.811  1.00 45.10      AAAA O
ATOM   2637  C   GLU  276      47.444  35.935  60.540  1.00 39.74      AAAA C
ATOM   2638  O   GLU  276      46.760  35.449  61.444  1.00 45.06      AAAA O
ATOM   2639  N   CYS  277      47.495  37.235  60.500  1.00 38.69      AAAA N
ATOM   2640  CA  CYS  277      46.718  38.089  61.332  1.00 46.11      AAAA C
ATOM   2641  C   CYS  277      45.205  37.938  60.994  1.00 52.70      AAAA C
ATOM   2642  O   CYS  277      44.760  37.511  59.936  1.00 49.43      AAAA O
ATOM   2643  CB  CYS  277      47.039  39.537  61.111  1.00 45.56      AAAA C
ATOM   2644  SG  CYS  277      48.629  40.083  61.645  1.00 52.86      AAAA S
ATOM   2645  N   PRO  278      44.380  38.261  61.993  1.00 54.63      AAAA N
ATOM   2646  CD  PRO  278      44.824  38.778  63.311  1.00 57.20      AAAA C
ATOM   2647  CA  PRO  278      42.946  38.185  61.899  1.00 55.82      AAAA C
ATOM   2648  CB  PRO  278      42.445  38.635  63.267  1.00 55.61      AAAA C
ATOM   2649  CG  PRO  278      43.605  38.670  64.153  1.00 55.58      AAAA C
ATOM   2650  C   PRO  278      42.487  39.116  60.781  1.00 52.55      AAAA C
ATOM   2651  O   PRO  278      43.083  40.195  60.631  1.00 48.76      AAAA O
ATOM   2652  N   SER  279      41.370  38.845  60.143  1.00 49.35      AAAA N
ATOM   2653  CA  SER  279      40.815  39.720  59.140  1.00 52.03      AAAA C
ATOM   2654  CB  SER  279      39.280  39.572  58.975  1.00 47.62      AAAA C
ATOM   2655  OG  SER  279      39.320  39.778  57.785  1.00 68.16      AAAA O
ATOM   2656  C   SER  279      41.003  41.209  59.173  1.00 55.40      AAAA C
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ATOM   2658  N   GLY  280      40.775  41.962  60.247  1.00 55.32      AAAA N
ATOM   2659  CA  GLY  280      40.968  43.406  59.868  1.00 48.58      AAAA C
ATOM   2660  C   GLY  280      42.248  43.890  60.479  1.00 55.98      AAAA C
ATOM   2661  O   GLY  280      42.249  45.097  60.772  1.00 56.00      AAAA O
ATOM   2662  N   PHE  281      43.213  42.983  60.742  1.00 55.42      AAAA N
ATOM   2663  CA  PHE  281      44.506  43.411  61.262  1.00 52.94      AAAA C
ATOM   2664  CB  PHE  281      44.938  42.644  62.523  1.00 61.20      AAAA C
ATOM   2665  CG  PHE  281      43.958  42.792  63.637  1.00 53.66      AAAA C
ATOM   2666  CD1 PHE  281      44.142  43.702  64.630  1.00 60.47      AAAA C
ATOM   2667  CD2 PHE  281      42.839  41.992  63.712  1.00 60.98      AAAA C
ATOM   2668  CE1 PHE  281      43.272  43.901  65.678  1.00 64.71      AAAA C
ATOM   2669  CE2 PHE  281      41.931  42.162  64.756  1.00 63.18      AAAA C
ATOM   2670  CZ  PHE  281      42.141  43.115  65.744  1.00 58.88      AAAA C
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ATOM   2685  C   PHE  281      45.630  43.217  60.240  1.00 48.00      AAAA C
ATOM   2686  O   PHE  281      45.738  42.395  59.327  1.00 38.84      AAAA O
ATOM   2687  N   ILE  282      46.670  43.990  60.557  1.00 49.55      AAAA N
ATOM   2689  CA  ILE  282      47.907  43.984  59.748  1.00 45.00      AAAA C
ATOM   2690  CB  ILE  282      47.945  45.198  58.799  1.00 30.25      AAAA C
ATOM   2691  CG2 ILE  282      48.041  46.494  59.507  1.00 24.60      AAAA C
ATOM   2692  CG1 ILE  282      49.092  45.022  57.795  1.00 38.71      AAAA C
ATOM   2693  CD1 ILE  282      49.194  46.043  56.669  1.00 33.38      AAAA C
ATOM   2694  C   ILE  282      49.081  43.889  60.673  1.00 44.30      AAAA C
ATOM   2695  O   ILE  282      49.078  44.447  61.759  1.00 48.49      AAAA O
ATOM   2696  N   ARG  283      50.126  43.153  60.298  1.00 48.68      AAAA N
ATOM   2698  CA  ARG  283      51.396  43.094  61.048  1.00 39.30      AAAA C
ATOM   2699  CB  ARG  283      52.300  42.200  60.286  1.00 41.10      AAAA C
ATOM   2700  CG  ARG  283      52.295  40.696  60.515  1.00 29.19      AAAA C
ATOM   2701  CD  ARG  283      53.078  39.986  59.451  1.00 29.85      AAAA C
ATOM   2702  NE  ARG  283      52.823  38.545  59.404  1.00 29.39      AAAA N
ATOM   2704  CZ  ARG  283      51.862  38.024  58.646  1.00 37.61      AAAA C
ATOM   2705  NH1 ARG  283      51.065  38.846  57.944  1.00 31.41      AAAA N
ATOM   2708  NH2 ARG  283      51.651  36.722  58.596  1.00 31.97      AAAA N
ATOM   2711  C   ARG  283      51.945  44.498  61.190  1.00 42.27      AAAA C
ATOM   2712  O   ARG  283      51.931  45.228  60.173  1.00 43.42      AAAA O
ATOM   2713  N   ASN  284      52.362  44.886  62.422  1.00 39.49      AAAA N
ATOM   2715  CA  ASN  284      52.733  46.311  62.574  1.00 42.07      AAAA C
ATOM   2721  C   ASN  284      54.078  46.656  61.929  1.00 41.64      AAAA C
ATOM   2722  O   ASN  284      54.431  47.798  61.742  1.00 39.01      AAAA O
ATOM   2716  CB  ASN  284      52.734  46.760  64.032  1.00 37.33      AAAA C
ATOM   2717  CG  ASN  284      53.917  46.028  64.611  1.00 50.21      AAAA C
ATOM   2719  OD1 ASN  284      54.609  45.104  64.192  1.00 44.30      AAAA O
ATOM   2719  ND2 ASN  284      54.323  46.432  65.842  1.00 42.46      AAAA N
ATOM   2723  N   GLY  285      54.931  45.699  61.562  1.00 40.10      AAAA N
ATOM   2725  CA  GLY  285      55.971  45.815  60.593  1.00 26.91      AAAA C
ATOM   2726  C   GLY  285      56.091  44.468  59.848  1.00 33.12      AAAA C
ATOM   2727  O   GLY  285      55.584  43.331  60.187  1.00 29.51      AAAA O
ATOM   2728  N   SER  286      56.915  44.619  59.766  1.00 26.53      AAAA N
ATOM   2730  CA  SER  286      57.109  43.395  57.975  1.00 32.67      AAAA C
ATOM   2731  CB  SER  286      57.944  43.691  56.757  1.00 33.19      AAAA C
ATOM   2732  OG  SER  286      58.283  42.490  56.014  1.00 31.95      AAAA O
ATOM   2734  C   SER  286      57.759  42.310  58.836  1.00 34.57      AAAA C
ATOM   2735  O   SER  286      58.700  42.495  59.607  1.00 44.29      AAAA O
ATOM   2736  N   GLN  287      57.227  41.148  58.940  1.00 34.45      AAAA N
ATOM   2738  CA  GLN  287      57.738  40.005  59.634  1.00 35.25      AAAA C
ATOM   2739  CB  GLN  287      59.139  39.610  59.083  1.00 27.97      AAAA C
ATOM   2740  CG  GLN  287      59.037  39.234  57.664  1.00 26.61      AAAA C
ATOM   2741  CD  GLN  287      58.539  37.963  57.130  1.00 21.25      AAAA C
ATOM   2742  OE1 GLN  287      58.192  37.023  57.845  1.00 28.18      AAAA O
ATOM   2743  NE2 GLN  287      58.492  37.839  55.782  1.00 27.55      AAAA N
ATOM   2746  C   GLN  287      57.773  40.296  61.111  1.00 30.25      AAAA C
ATOM   2747  O   GLN  287      58.163  39.415  61.909  1.00 32.78      AAAA O
ATOM   2748  N   SER  288      57.021  41.317  61.624  1.00 32.49      AAAA N
ATOM   2750  CA  SER  288      56.696  41.322  63.043  1.00 28.98      AAAA C
ATOM   2751  CB  SER  288      56.024  42.675  63.313  1.00 35.79      AAAA C
ATOM   2752  OG  SER  288      55.639  42.812  64.701  1.00 36.61      AAAA O
ATOM   2754  C   SER  288      55.665  40.285  63.442  1.00 28.96      AAAA C
ATOM   2755  O   SER  288      54.993  39.776  62.553  1.00 31.16      AAAA O
ATOM   2756  N   MET  289      55.774  39.720  64.621  1.00 32.51      AAAA N
ATOM   2758  CA  MET  289      54.875  38.697  65.105  1.00 34.53      AAAA C
ATOM   2759  CB  MET  289      55.507  37.823  66.153  1.00 30.31      AAAA C
ATOM   2760  CG  MET  289      56.571  36.872  65.680  1.00 40.50      AAAA C
ATOM   2761  SD  MET  289      56.977  35.623  66.881  1.00 31.65      AAAA S
ATOM   2762  CE  MET  289      55.745  34.315  66.508  1.00 30.47      AAAA C
ATOM   2763  C   MET  289      53.557  39.286  65.703  1.00 35.55      AAAA C
ATOM   2764  O   MET  289      52.630  38.512  66.014  1.00 38.37      AAAA O
ATOM   2765  N   TYR  290      53.380  40.565  65.742  1.00 29.54      AAAA N
ATOM   2767  CA  TYR  290      52.363  41.358  66.297  1.00 38.81      AAAA C
ATOM   2768  CB  TYR  290      52.947  42.589  67.042  1.00 36.72      AAAA C
ATOM   2769  CG  TYR  290      53.570  42.184  68.351  1.00 41.94      AAAA C
ATOM   2770  CD1 TYR  290      54.932  41.780  68.350  1.00 37.79      AAAA C
ATOM   2771  CE1 TYR  290      55.548  41.369  69.503  1.00 32.60      AAAA C
ATOM   2772  CD2 TYR  290      52.887  42.157  69.570  1.00 39.93      AAAA C
ATOM   2773  CE2 TYR  290      53.501  41.750  70.748  1.00 36.16      AAAA C
ATOM   2774  CZ  TYR  290      54.822  41.355  70.693  1.00 38.85      AAAA C
ATOM   2775  OH  TYR  290      55.581  40.923  71.751  1.00 43.41      AAAA O
ATOM   2777  C   TYR  290      51.361  41.955  65.270  1.00 45.54      AAAA C
ATOM   2778  O   TYR  290      51.733  42.520  64.227  1.00 47.10      AAAA O
ATOM   2779  N   CYS  291      50.071  41.699  65.537  1.00 44.68      AAAA N
ATOM   2781  CA  CYS  291      49.017  42.205  64.685  1.00 47.20      AAAA C
ATOM   2782  C   CYS  291      48.295  43.434  65.194  1.00 46.06      AAAA C
ATOM   2783  O   CYS  291      47.892  43.550  66.343  1.00 49.45      AAAA O
ATOM   2784  CB  CYS  291      47.973  41.103  64.483  1.00 43.44      AAAA C
ATOM   2785  SG  CYS  291      48.766  39.715  63.683  1.00 45.49      AAAA S
ATOM   2786  N   ILE  292      48.136  44.453  64.365  1.00 46.82      AAAA N
ATOM   2788  CA  ILE  292      47.399  45.651  64.755  1.00 50.64      AAAA C
ATOM   2789  CB  ILE  292      48.267  46.932  64.779  1.00 39.19      AAAA C
ATOM   2790  CG2 ILE  292      49.291  46.885  65.861  1.00 44.39      AAAA C
ATOM   2791  CG1 ILE  292      48.920  47.095  63.402  1.00 44.25      AAAA C
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ATOM	2792	CD1	ILE	292	49.234	48.568	63.108	1.00	32.80	AAAA C
ATOM	2793	C	ILE	292	46.240	46.003	63.806	1.00	50.01	AAAA C
ATOM	2794	O	ILE	292	46.165	45.526	62.670	1.00	46.64	AAAA O
ATOM	2795	N	PRO	293	45.150	46.507	64.385	1.00	51.86	AAAA N
ATOM	2796	CD	PRO	293	45.009	46.804	65.839	1.00	51.05	AAAA C
ATOM	2797	CA	PRO	293	43.958	46.930	63.675	1.00	51.40	AAAA C
ATOM	2798	CB	PRO	293	43.170	47.784	64.681	1.00	49.00	AAAA C
ATOM	2799	CG	PRO	293	43.533	47.112	65.951	1.00	53.73	AAAA C
ATOM	2800	C	PRO	293	44.253	47.870	62.525	1.00	51.68	AAAA C
ATOM	2801	O	PRO	293	45.053	48.788	62.737	1.00	51.92	AAAA O
ATOM	2802	N	CYS	294	43.607	47.621	61.408	1.00	50.66	AAAA N
ATOM	2804	CA	CYS	294	43.811	48.464	60.254	1.00	57.90	AAAA C
ATOM	2805	C	CYS	294	43.219	49.848	60.345	1.00	59.59	AAAA C
ATOM	2806	O	CYS	294	43.744	50.814	59.785	1.00	60.87	AAAA O
ATOM	2807	CB	CYS	294	43.229	47.686	59.046	1.00	57.59	AAAA C
ATOM	2808	SG	CYS	294	44.408	46.460	58.563	1.00	51.12	AAAA S
ATOM	2809	N	ALA	295	42.009	50.031	60.854	1.00	65.87	AAAA N
ATOM	2811	CA	ALA	295	41.391	51.386	60.804	1.00	71.19	AAAA C
ATOM	2812	CB	ALA	295	42.311	52.459	61.393	1.00	63.82	AAAA C
ATOM	2813	C	ALA	295	40.971	51.770	59.370	1.00	69.17	AAAA C
ATOM	2814	O	ALA	295	41.421	52.717	58.762	1.00	64.70	AAAA O
ATOM	2815	N	GLY	296	40.153	50.920	58.775	1.00	71.30	AAAA N
ATOM	2817	CA	GLY	296	39.640	51.049	57.416	1.00	72.66	AAAA C
ATOM	2818	C	GLY	296	39.895	49.686	56.769	1.00	74.20	AAAA C
ATOM	2819	O	GLY	296	40.408	48.819	57.490	1.00	75.04	AAAA O
ATOM	2820	N	PRO	297	39.561	49.540	55.497	1.00	71.88	AAAA N
ATOM	2821	CD	PRO	297	38.928	50.561	54.637	1.00	72.15	AAAA C
ATOM	2822	CA	PRO	297	39.958	48.344	54.777	1.00	68.23	AAAA C
ATOM	2823	CB	PRO	297	39.488	48.603	53.369	1.00	72.57	AAAA C
ATOM	2824	CG	PRO	297	38.470	49.687	53.490	1.00	74.04	AAAA C
ATOM	2825	C	PRO	297	41.480	48.306	54.860	1.00	65.78	AAAA C
ATOM	2826	O	PRO	297	42.147	49.323	54.997	1.00	62.72	AAAA O
ATOM	2827	N	CYS	298	42.039	47.135	55.073	1.00	63.85	AAAA N
ATOM	2829	CA	CYS	298	43.464	46.953	55.248	1.00	54.47	AAAA C
ATOM	2830	C	CYS	298	44.109	47.303	53.908	1.00	54.56	AAAA C
ATOM	2831	O	CYS	298	43.621	47.030	52.820	1.00	54.83	AAAA O
ATOM	2832	CB	CYS	298	43.665	45.544	55.669	1.00	47.65	AAAA C
ATOM	2833	SG	CYS	298	43.501	45.115	57.371	1.00	46.12	AAAA S
ATOM	2834	N	PRO	299	45.310	47.876	53.967	1.00	49.83	AAAA N
ATOM	2835	CD	PRO	299	46.087	48.168	55.194	1.00	48.14	AAAA C
ATOM	2836	CA	PRO	299	46.055	48.212	52.787	1.00	43.67	AAAA C
ATOM	2837	CB	PRO	299	47.267	48.965	53.281	1.00	44.08	AAAA C
ATOM	2838	CG	PRO	299	47.454	48.361	54.628	1.00	51.38	AAAA C
ATOM	2839	C	PRO	299	46.341	46.969	52.010	1.00	39.86	AAAA C
ATOM	2840	O	PRO	299	46.372	45.874	52.546	1.00	42.85	AAAA O
ATOM	2841	N	LYS	300	46.310	47.073	50.712	1.00	38.30	AAAA N
ATOM	2843	CA	LYS	300	46.484	45.959	49.812	1.00	42.62	AAAA C
ATOM	2844	CB	LYS	300	45.176	45.226	49.595	1.00	34.28	AAAA C
ATOM	2845	CG	LYS	300	45.346	43.901	49.920	1.00	41.45	AAAA C
ATOM	2846	CD	LYS	300	44.013	43.413	48.378	1.00	48.31	AAAA C
ATOM	2847	CE	LYS	300	44.388	42.027	47.787	1.00	48.57	AAAA C
ATOM	2848	NZ	LYS	300	43.662	42.031	46.478	1.00	63.70	AAAA N
ATOM	2852	C	LYS	300	46.964	46.479	49.432	1.00	48.72	AAAA C
ATOM	2853	O	LYS	300	46.413	47.383	47.776	1.00	46.09	AAAA O
ATOM	2854	N	VAL	301	48.150	45.994	48.054	1.00	48.15	AAAA N
ATOM	2856	CA	VAL	301	48.802	46.462	46.871	1.00	44.52	AAAA C
ATOM	2857	CB	VAL	301	50.292	46.729	47.074	1.00	51.52	AAAA C
ATOM	2858	CG1	VAL	301	51.008	47.200	45.796	1.00	43.07	AAAA C
ATOM	2859	CG2	VAL	301	50.495	47.794	48.141	1.00	49.50	AAAA C
ATOM	2860	C	VAL	301	48.526	45.410	45.837	1.00	44.59	AAAA C
ATOM	2861	O	VAL	301	48.913	44.291	46.060	1.00	43.70	AAAA O
ATOM	2862	N	CYS	302	47.910	45.816	44.718	1.00	47.98	AAAA N
ATOM	2864	CA	CYS	302	47.645	44.735	43.739	1.00	55.19	AAAA C
ATOM	2865	C	CYS	302	48.594	44.968	42.583	1.00	57.64	AAAA C
ATOM	2866	O	CYS	302	48.852	46.152	42.343	1.00	60.23	AAAA O
ATOM	2867	CB	CYS	302	46.186	44.630	43.330	1.00	68.30	AAAA C
ATOM	2868	SG	CYS	302	45.070	44.360	44.751	1.00	70.31	AAAA S
ATOM	2869	N	GLU	303	49.183	43.921	42.075	1.00	58.15	AAAA N
ATOM	2871	CA	GLU	303	50.174	43.932	41.034	1.00	62.85	AAAA C
ATOM	2872	CB	GLU	303	51.603	44.006	41.595	1.00	67.85	AAAA C
ATOM	2873	CG	GLU	303	51.760	43.487	43.014	0.01	67.46	AAAA C
ATOM	2874	CD	GLU	303	51.989	41.992	43.097	0.01	67.94	AAAA C
ATOM	2875	OE1	GLU	303	53.011	41.514	42.561	0.01	67.67	AAAA O
ATOM	2876	OE2	GLU	303	51.147	41.290	43.697	0.01	67.65	AAAA O
ATOM	2877	C	GLU	303	50.096	42.662	40.194	1.00	64.12	AAAA C
ATOM	2878	O	GLU	303	50.162	41.562	40.708	1.00	65.08	AAAA O
ATOM	2879	N	GLU	304	49.867	42.794	38.904	1.00	67.37	AAAA N
ATOM	2881	CA	GLU	304	49.672	41.583	38.094	1.00	74.63	AAAA C
ATOM	2882	CB	GLU	304	48.285	41.596	37.458	1.00	71.71	AAAA C
ATOM	2883	CG	GLU	304	47.339	42.663	38.031	1.00	84.54	AAAA C
ATOM	2884	CD	GLU	304	45.930	42.152	39.185	1.00	87.56	AAAA C
ATOM	2885	OE1	GLU	304	45.438	41.571	37.179	1.00	89.13	AAAA O
ATOM	2886	OE2	GLU	304	45.249	42.269	39.233	1.00	93.19	AAAA O
ATOM	2887	C	GLU	304	50.866	41.307	37.190	1.00	76.10	AAAA C
ATOM	2888	O	GLU	304	51.911	41.962	37.217	1.00	74.78	AAAA O

ATOM	2889	N	GLU	305	50.899	40.126	36.568	1.00	77.31	AAAA N
ATOM	2891	CA	GLU	305	51.932	39.656	35.674	1.00	75.90	AAAA C
ATOM	2892	CB	GLU	305	51.467	38.380	34.970	1.00	79.95	AAAA C
ATOM	2893	CG	GLU	305	52.307	37.937	33.807	1.00	87.28	AAAA C
ATOM	2894	CD	GLU	305	51.758	36.891	32.886	0.01	83.39	AAAA C
ATOM	2895	OE1	GLU	305	50.762	36.234	33.252	0.01	83.66	AAAA O
ATOM	2896	OE2	GLU	305	52.310	36.700	31.780	0.01	83.73	AAAA O
ATOM	2897	C	GLU	305	52.276	40.737	34.666	1.00	75.97	AAAA C
ATOM	2898	O	GLU	305	53.381	41.268	34.613	1.00	76.54	AAAA O
ATOM	2899	N	LYS	306	51.291	41.181	33.888	1.00	78.22	AAAA N
ATOM	2901	CA	LYS	306	51.479	42.328	33.004	1.00	75.99	AAAA C
ATOM	2902	CB	LYS	306	50.467	42.253	31.855	1.00	79.78	AAAA C
ATOM	2903	CG	LYS	306	51.208	42.227	30.527	1.00	94.52	AAAA C
ATOM	2904	CD	LYS	306	50.313	42.191	29.314	1.00	92.78	AAAA C
ATOM	2905	CE	LYS	306	50.740	43.227	28.261	1.00	97.10	AAAA C
ATOM	2906	NZ	LYS	306	50.938	44.554	28.929	1.00	84.87	AAAA N
ATOM	2910	C	LYS	306	51.381	43.669	33.703	1.00	73.85	AAAA C
ATOM	2911	O	LYS	306	50.703	43.862	34.718	1.00	76.08	AAAA O
ATOM	2912	N	LYS	307	52.000	44.700	33.180	1.00	71.15	AAAA N
ATOM	2914	CA	LYS	307	51.934	46.053	33.692	1.00	69.45	AAAA C
ATOM	2915	CB	LYS	307	53.022	46.903	33.008	1.00	79.64	AAAA C
ATOM	2916	CG	LYS	307	54.419	46.837	33.564	1.00	78.88	AAAA C
ATOM	2917	CD	LYS	307	55.257	48.084	33.374	1.00	85.84	AAAA C
ATOM	2918	CE	LYS	307	55.708	48.215	31.924	1.00	97.07	AAAA C
ATOM	2919	NZ	LYS	307	54.649	48.840	31.067	1.00	97.80	AAAA N
ATOM	2923	C	LYS	307	50.562	46.716	33.525	1.00	67.97	AAAA C
ATOM	2924	O	LYS	307	50.010	47.369	34.431	1.00	64.46	AAAA O
ATOM	2925	N	THR	308	49.979	46.661	32.323	1.00	65.84	AAAA N
ATOM	2927	CA	THR	308	48.709	47.319	32.091	1.00	64.56	AAAA C
ATOM	2928	CB	THR	308	48.714	47.977	30.711	1.00	59.91	AAAA C
ATOM	2929	OG1	THR	308	49.834	48.843	30.577	1.00	61.97	AAAA O
ATOM	2931	CG2	THR	308	47.392	48.742	30.561	1.00	63.64	AAAA C
ATOM	2932	C	THR	308	47.514	46.379	32.234	1.00	61.82	AAAA C
ATOM	2933	O	THR	308	47.412	45.415	31.477	1.00	62.05	AAAA O
ATOM	2934	N	LYS	309	46.675	46.719	33.211	1.00	55.66	AAAA N
ATOM	2936	CA	LYS	309	45.456	45.926	33.445	1.00	54.67	AAAA C
ATOM	2937	CB	LYS	309	45.043	45.880	34.904	1.00	56.82	AAAA C
ATOM	2938	CG	LYS	309	43.601	45.541	35.223	1.00	57.50	AAAA C
ATOM	2939	CD	LYS	309	43.390	44.039	35.086	1.00	59.50	AAAA C
ATOM	2940	CE	LYS	309	42.703	43.449	36.324	1.00	57.31	AAAA C
ATOM	2941	NZ	LYS	309	42.758	41.954	36.236	1.00	57.22	AAAA N
ATOM	2945	C	LYS	309	44.391	46.570	32.549	1.00	51.21	AAAA C
ATOM	2946	O	LYS	309	44.074	47.763	32.680	1.00	47.23	AAAA O
ATOM	2947	N	THR	310	43.895	45.772	31.610	1.00	47.67	AAAA N
ATOM	2949	CA	THR	310	42.862	46.329	30.733	1.00	51.89	AAAA C
ATOM	2950	CB	THR	310	43.161	46.015	29.266	1.00	54.81	AAAA C
ATOM	2951	OG1	THR	310	41.909	45.710	28.635	1.00	66.29	AAAA O
ATOM	2953	CG2	THR	310	44.032	44.791	29.139	1.00	55.19	AAAA C
ATOM	2954	C	THR	310	41.468	45.941	31.117	1.00	51.15	AAAA C
ATOM	2955	O	THR	310	41.162	44.690	30.991	1.00	49.27	AAAA O
ATOM	2956	N	ILE	311	40.684	46.706	31.732	1.00	50.18	AAAA N
ATOM	2958	CA	ILE	311	39.363	46.453	32.276	1.00	48.67	AAAA C
ATOM	2959	CB	ILE	311	39.120	47.396	33.462	1.00	49.27	AAAA C
ATOM	2960	CG2	ILE	311	37.655	47.596	33.799	1.00	50.72	AAAA C
ATOM	2961	CG1	ILE	311	39.896	46.930	34.699	1.00	41.34	AAAA C
ATOM	2962	CD1	ILE	311	39.847	48.073	35.739	1.00	52.22	AAAA C
ATOM	2963	C	ILE	311	38.334	46.729	31.186	1.00	45.37	AAAA C
ATOM	2964	O	ILE	311	38.132	47.875	30.758	1.00	37.14	AAAA O
ATOM	2965	N	ASP	312	37.871	45.678	30.524	1.00	50.10	AAAA N
ATOM	2967	CA	ASP	312	36.991	45.842	29.377	1.00	56.35	AAAA C
ATOM	2968	CB	ASP	312	37.546	45.152	28.128	1.00	59.45	AAAA C
ATOM	2969	CG	ASP	312	37.761	43.671	28.382	1.00	65.64	AAAA C
ATOM	2970	OD1	ASP	312	38.525	43.034	27.636	1.00	72.60	AAAA O
ATOM	2971	OD2	ASP	312	37.154	43.176	29.349	1.00	66.86	AAAA O
ATOM	2972	C	ASP	312	35.589	45.337	29.693	1.00	59.39	AAAA C
ATOM	2973	O	ASP	312	34.729	45.007	28.867	1.00	61.00	AAAA O
ATOM	2974	N	SER	313	35.278	45.290	30.976	1.00	61.17	AAAA N
ATOM	2976	CA	SER	313	34.053	44.683	31.459	1.00	55.73	AAAA C
ATOM	2977	CB	SER	313	34.121	43.201	31.083	1.00	48.22	AAAA C
ATOM	2978	OG	SER	313	34.373	42.514	32.282	1.00	57.89	AAAA O
ATOM	2980	C	SER	313	33.998	44.818	32.941	1.00	57.87	AAAA C
ATOM	2981	O	SER	313	34.802	45.506	33.537	1.00	66.47	AAAA O
ATOM	2982	N	VAL	314	33.001	44.205	33.545	1.00	64.35	AAAA N
ATOM	2984	CA	VAL	314	32.849	44.305	35.016	1.00	64.39	AAAA C
ATOM	2985	CB	VAL	314	31.360	44.340	35.343	1.00	69.57	AAAA C
ATOM	2986	CG1	VAL	314	31.024	43.693	36.681	1.00	65.60	AAAA C
ATOM	2987	CG2	VAL	314	30.927	45.823	35.319	1.00	65.27	AAAA C
ATOM	2988	C	VAL	314	33.492	43.088	35.638	1.00	62.65	AAAA C
ATOM	2989	O	VAL	314	34.029	43.141	36.704	1.00	63.92	AAAA O
ATOM	2990	N	THR	315	33.468	42.011	34.878	1.00	61.82	AAAA N
ATOM	2992	CA	THR	315	34.029	40.752	35.284	1.00	63.44	AAAA C
ATOM	2993	CB	THR	315	33.618	39.628	34.314	1.00	65.54	AAAA C
ATOM	2994	OG1	THR	315	32.403	40.004	33.634	1.00	74.05	AAAA O
ATOM	2996	CG2	THR	315	33.339	38.366	35.104	1.00	64.86	AAAA C
ATOM	2997	C	THR	315	35.541	40.871	35.323	1.00	65.62	AAAA C

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ATOM   2998  O   THR  315      36.217  40.339  36.206  1.00 66.41      AAAA O
ATOM   2999  N   SER  316      36.071  41.593  34.332  1.00 63.28      AAAA N
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ATOM   3002  CB  SER  316      37.785  42.537  32.900  1.00 52.20      AAAA C
ATOM   3003  OG  SER  316      37.298  43.859  32.933  1.00 48.04      AAAA O
ATOM   3005  C   SER  316      38.077  42.573  35.387  1.00 58.91      AAAA C
ATOM   3006  O   SER  316      39.293  42.522  35.520  1.00 59.86      AAAA O
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ATOM   3010  CB  ALA  317      36.833  45.409  37.269  1.00 54.23      AAAA C
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ATOM   3016  CB  GLN  318      36.857  39.956  39.293  1.00 74.48      AAAA C
ATOM   3017  CG  GLN  318      36.624  38.947  40.383  1.00 89.82      AAAA C
ATOM   3018  CD  GLN  318      35.265  39.080  41.048  1.00 92.69      AAAA C
ATOM   3019  OE1 GLN  318      34.256  38.807  40.391  1.00 98.57      AAAA O
ATOM   3020  NE2 GLN  318      35.356  39.509  42.308  1.00 92.51      AAAA N
ATOM   3023  C   GLN  318      38.380  41.413  40.653  1.00 72.63      AAAA C
ATOM   3024  O   GLN  318      38.294  41.855  41.804  1.00 68.92      AAAA O
ATOM   3025  N   MET  319      39.562  41.062  40.153  1.00 75.18      AAAA N
ATOM   3027  CA  MET  319      40.846  41.175  40.826  1.00 71.85      AAAA C
ATOM   3028  CB  MET  319      41.950  40.960  39.772  1.00 82.00      AAAA C
ATOM   3029  CG  MET  319      41.740  39.644  39.050  1.00 91.16      AAAA C
ATOM   3030  SD  MET  319      43.123  38.482  39.185  1.00106.72      AAAA S
ATOM   3031  CE  MET  319      42.486  37.105  38.231  1.00 97.56      AAAA C
ATOM   3032  C   MET  319      41.118  42.509  41.471  1.00 67.68      AAAA C
ATOM   3033  O   MET  319      41.597  42.541  42.612  1.00 69.73      AAAA O
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ATOM   3037  CB  LEU  320      40.440  46.085  40.623  1.00 54.93      AAAA C
ATOM   3038  CG  LEU  320      41.091  46.163  39.238  1.00 53.48      AAAA C
ATOM   3039  CD1 LEU  320      41.005  47.552  38.692  1.00 51.31      AAAA C
ATOM   3040  CD2 LEU  320      42.557  45.709  39.403  1.00 58.43      AAAA C
ATOM   3041  C   LEU  320      40.209  45.008  42.881  1.00 60.30      AAAA C
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ATOM   3043  N   GLN  321      39.267  44.106  43.112  1.00 59.62      AAAA N
ATOM   3045  CA  GLN  321      38.482  44.128  44.343  1.00 63.50      AAAA C
ATOM   3046  CB  GLN  321      37.373  43.089  44.250  1.00 62.52      AAAA C
ATOM   3047  CG  GLN  321      36.611  42.884  45.523  1.00 56.83      AAAA C
ATOM   3048  CD  GLN  321      35.337  42.064  45.291  1.00 68.77      AAAA C
ATOM   3049  OE1 GLN  321      35.362  40.969  44.718  1.00 70.37      AAAA O
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ATOM   3058  C   GLY  322      41.126  45.773  47.812  1.00 61.79      AAAA C
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ATOM   3060  N   CYS  323      41.719  46.104  46.676  1.00 60.03      AAAA N
ATOM   3062  CA  CYS  323      42.938  46.845  46.528  1.00 54.20      AAAA C
ATOM   3063  C   CYS  323      42.924  48.307  46.910  1.00 53.48      AAAA C
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ATOM   3066  SG  CYS  323      43.325  45.222  44.248  1.00 66.22      AAAA S
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ATOM   3069  CA  THR  324      44.164  50.161  47.811  1.00 52.29      AAAA C
ATOM   3070  CB  THR  324      44.623  50.324  49.264  1.00 52.84      AAAA C
ATOM   3071  OG1 THR  324      45.245  49.087  49.634  1.00 59.92      AAAA O
ATOM   3073  CG2 THR  324      43.432  50.517  50.193  1.00 60.00      AAAA C
ATOM   3074  C   THR  324      45.154  50.802  46.844  1.00 48.91      AAAA C
ATOM   3075  O   THR  324      45.277  52.016  46.710  1.00 46.90      AAAA O
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ATOM   3078  CA  ILE  325      47.114  50.511  45.445  1.00 45.10      AAAA C
ATOM   3079  CB  ILE  325      48.473  50.577  46.183  1.00 43.60      AAAA C
ATOM   3080  CG2 ILE  325      49.586  50.905  45.163  1.00 47.47      AAAA C
ATOM   3081  CG1 ILE  325      48.394  51.623  47.294  1.00 34.03      AAAA C
ATOM   3082  CD1 ILE  325      49.595  52.010  48.028  1.00 41.94      AAAA C
ATOM   3083  C   ILE  325      47.265  49.642  44.229  1.00 42.88      AAAA C
ATOM   3084  O   ILE  325      47.406  48.429  44.469  1.00 42.99      AAAA O
ATOM   3085  N   PHE  326      47.170  50.238  43.042  1.00 41.19      AAAA N
ATOM   3087  CA  PHE  326      47.312  49.334  41.880  1.00 42.89      AAAA C
ATOM   3088  CB  PHE  326      46.166  49.437  40.877  1.00 39.15      AAAA C
ATOM   3089  CG  PHE  326      46.403  48.474  39.738  1.00 38.03      AAAA C
ATOM   3090  CD1 PHE  326      46.186  47.125  39.951  1.00 39.68      AAAA C
ATOM   3091  CD2 PHE  326      46.917  48.892  38.525  1.00 37.31      AAAA C
ATOM   3092  CE1 PHE  326      46.447  46.139  39.023  1.00 36.52      AAAA C
ATOM   3093  CE2 PHE  326      47.136  47.919  37.551  1.00 45.74      AAAA C
ATOM   3094  CZ  PHE  326      46.924  46.570  37.787  1.00 39.92      AAAA C
ATOM   3095  C   PHE  326      48.682  49.673  41.280  1.00 48.78      AAAA C
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ATOM   3097  N   LYS  327      49.623  48.751  41.379  1.00 50.22      AAAA N
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ATOM   3100  CB  LYS  327      52.050  48.091  41.519  1.00 58.64      AAAA C
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ATOM   3191  CG  LYS   327      53.254  48.997  41.981  1.00 59.15      AAAA C
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ATOM   3137  CA  LEU   331      43.367  50.869  30.625  1.00 43.10      AAAA C
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ATOM   3141  CD2 LEU   331      43.844  48.834  27.367  1.00 48.76      AAAA C
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ATOM   3149  CG1 ILE   332      39.550  51.895  33.452  1.00 33.64      AAAA C
ATOM   3150  CD1 ILE   332      39.479  53.182  34.337  1.00 48.21      AAAA C
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ATOM   3315  CB  ASN   339      23.252  49.915  34.945  1.00109.15      AAAA C
ATOM   3316  CG  ASN   339      22.777  51.351  35.003  0.01107.52      AAAA C
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ATOM   3318  ND2 ASN   339      22.441  51.932  33.859  0.01107.46      AAAA N
ATOM   3321  C   ASN   339      25.697  49.237  35.007  1.00106.33      AAAA C
ATOM   3322  O   ASN   339      25.520  48.390  35.886  1.00108.82      AAAA O
ATOM   3323  N   ILE   340      26.897  49.527  34.510  1.00101.36      AAAA N
ATOM   3325  CA  ILE   340      28.136  49.101  35.138  1.00 97.43      AAAA C
ATOM   3326  CB  ILE   340      29.040  48.354  34.151  1.00 93.63      AAAA C
ATOM   3327  CG2 ILE   340      28.194  47.252  33.489  1.00 99.38      AAAA C
ATOM   3328  CG1 ILE   340      29.726  49.158  33.070  1.00 85.50      AAAA C
ATOM   3329  CD1 ILE   340      28.897  49.634  31.915  1.00 92.53      AAAA C
ATOM   3330  C   ILE   340      28.783  50.357  35.706  1.00 95.32      AAAA C
ATOM   3331  O   ILE   340      29.472  51.099  34.997  1.00 97.86      AAAA O
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ATOM   3334  CA  ALA   341      28.892  52.008  37.450  1.00 88.45      AAAA C
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ATOM   3340  CA  SER   342      27.910  50.601  40.780  1.00 82.05      AAAA C
ATOM   3341  CB  SER   342      26.426  50.667  41.112  1.00 85.51      AAAA C
ATOM   3342  OG  SER   342      26.145  51.271  42.361  1.00 86.02      AAAA O
ATOM   3344  C   SER   342      28.487  49.196  40.965  1.00 76.62      AAAA C
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ATOM   3350  CG  GLU   343      27.118  46.105  38.316  1.00 85.33      AAAA C
ATOM   3351  CD  GLU   343      26.898  45.121  37.169  1.00 92.76      AAAA C
ATOM   3352  OE1 GLU   343      27.209  43.911  37.310  1.00 96.41      AAAA O
ATOM   3353  OE2 GLU   343      26.423  45.517  36.082  1.00 98.55      AAAA O
ATOM   3354  C   GLU   343      30.526  47.319  39.804  1.00 77.75      AAAA C
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ATOM   3359  CB  LEU   344      32.760  49.697  37.809  1.00 64.33      AAAA C
ATOM   3360  CG  LEU   344      32.687  49.397  36.311  1.00 60.12      AAAA C
ATOM   3361  CD1 LEU   344      33.224  50.577  35.519  1.00 57.00      AAAA C
ATOM   3362  CD2 LEU   344      33.401  48.127  35.905  1.00 51.62      AAAA C
ATOM   3363  C   LEU   344      32.963  49.130  40.174  1.00 69.74      AAAA C
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ATOM   3368  CB  GLU   345      31.592  51.714  42.478  1.00 55.59      AAAA C
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ATOM   3370  CD  GLU   345      31.324  53.374  44.376  1.00 81.31      AAAA C
ATOM   3371  OE1 GLU   345      30.614  54.320  43.976  1.00 85.60      AAAA O
ATOM   3372  OE2 GLU   345      31.237  53.078  45.595  1.00 88.79      AAAA O
ATOM   3373  C   GLU   345      32.706  49.652  43.255  1.00 63.31      AAAA C
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ATOM   3381  ND2 ASN   346      31.155  44.092  44.444  1.00 51.10      AAAA N
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ATOM   3386  N   PHE   347      34.419  47.173  43.066  1.00 63.23      AAAA N
ATOM   3388  CA  PHE   347      35.540  46.411  42.506  1.00 61.39      AAAA C
ATOM   3389  CB  PHE   347      35.123  45.854  41.170  1.00 61.38      AAAA C
ATOM   3390  CG  PHE   347      34.457  44.534  41.142  1.00 65.57      AAAA C
ATOM   3391  CD1 PHE   347      33.090  44.438  40.982  1.00 75.25      AAAA C
ATOM   3392  CD2 PHE   347      35.148  43.351  41.267  1.00 77.15      AAAA C
ATOM   3393  CE1 PHE   347      32.425  43.224  40.951  1.00 75.55      AAAA C
ATOM   3394  CE2 PHE   347      34.512  42.130  41.249  1.00 72.86      AAAA C
ATOM   3395  CZ  PHE   347      33.152  42.051  41.095  1.00 72.74      AAAA C
ATOM   3396  C   PHE   347      36.712  47.375  42.440  1.00 57.70      AAAA C
ATOM   3397  O   PHE   347      37.770  46.920  42.354  1.00 59.92      AAAA O
ATOM   3399  N   MET   348      36.492  48.676  42.319  1.00 50.56      AAAA N
ATOM   3400  CA  MET   348      37.500  49.630  41.964  1.00 42.86      AAAA C
ATOM   3401  CB  MET   348      37.402  50.096  40.493  1.00 31.72      AAAA C
ATOM   3402  CG  MET   348      37.426  48.933  39.471  1.00 33.42      AAAA C
ATOM   3403  SD  MET   348      37.566  49.448  37.732  1.00 44.79      AAAA S
ATOM   3404  CE  MET   348      38.408  50.999  37.791  1.00 59.57      AAAA C
ATOM   3405  C   MET   348      37.368  50.831  42.867  1.00 45.88      AAAA C
ATOM   3406  O   MET   348      38.210  51.772  42.901  1.00 43.33      AAAA O
ATOM   3407  N   GLY   349      36.296  50.783  43.683  1.00 45.30      AAAA N
ATOM   3409  CA  GLY   349      35.998  51.965  44.504  1.00 49.19      AAAA C
ATOM   3410  C   GLY   349      36.980  52.189  45.620  1.00 52.77      AAAA C
ATOM   3411  O   GLY   349      37.033  53.299  46.156  1.00 53.43      AAAA O
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ATOM	3315	CB	LEU	350	38.873	49.949	47.834	1.00	49.00	AAAA C
ATOM	3316	CG	LEU	350	37.871	50.020	49.031	1.00	50.79	AAAA C
ATOM	3317	CD1	LEU	350	37.705	48.680	49.700	1.00	52.92	AAAA C
ATOM	3318	CD2	LEU	350	38.247	51.106	50.038	1.00	56.11	AAAA C
ATOM	3319	C	LEU	350	40.144	51.727	46.685	1.00	61.34	AAAA C
ATOM	3320	O	LEU	350	40.931	51.962	47.618	1.00	63.52	AAAA O
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ATOM	3324	CB	ILE	351	41.814	51.912	43.352	1.00	48.19	AAAA C
ATOM	3325	CG2	ILE	351	43.121	52.416	42.757	1.00	40.01	AAAA C
ATOM	3326	CG1	ILE	351	41.535	50.418	43.058	1.00	36.87	AAAA C
ATOM	3327	CD1	ILE	351	41.172	50.351	41.581	1.00	36.46	AAAA C
ATOM	3328	C	ILE	351	42.031	53.533	45.178	1.00	46.80	AAAA C
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ATOM	3332	CA	GLU	352	43.381	55.241	46.248	1.00	51.20	AAAA C
ATOM	3333	CB	GLU	352	43.907	55.353	47.678	1.00	52.12	AAAA C
ATOM	3334	CG	GLU	352	42.912	55.769	48.735	1.00	65.55	AAAA C
ATOM	3335	CD	GLU	352	43.034	54.834	49.947	1.00	71.49	AAAA C
ATOM	3336	OE1	GLU	352	43.881	55.244	50.765	1.00	66.09	AAAA O
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ATOM	3338	C	GLU	352	44.502	55.751	45.314	1.00	47.43	AAAA C
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ATOM	3340	N	VAL	353	45.342	54.838	44.852	1.00	43.54	AAAA N
ATOM	3342	CA	VAL	353	46.512	55.236	44.078	1.00	43.71	AAAA C
ATOM	3343	CB	VAL	353	47.759	55.540	44.911	1.00	45.01	AAAA C
ATOM	3344	CG1	VAL	353	47.766	55.261	46.387	1.00	30.84	AAAA C
ATOM	3345	CG2	VAL	353	48.988	54.844	44.310	1.00	42.55	AAAA C
ATOM	3346	C	VAL	353	46.828	54.233	42.957	1.00	41.41	AAAA C
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ATOM	3351	CB	VAL	354	46.725	54.390	39.407	1.00	40.86	AAAA C
ATOM	3352	CG1	VAL	354	47.347	53.896	38.123	1.00	36.72	AAAA C
ATOM	3353	CG2	VAL	354	45.293	53.849	39.678	1.00	35.35	AAAA C
ATOM	3354	C	VAL	354	49.043	54.510	40.388	1.00	44.56	AAAA C
ATOM	3355	O	VAL	354	49.366	55.718	40.289	1.00	43.32	AAAA O
ATOM	3356	N	THR	355	49.972	53.561	40.431	1.00	43.93	AAAA N
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ATOM	3360	OG1	THR	355	52.273	51.744	39.695	1.00	45.30	AAAA O
ATOM	3362	CG2	THR	355	52.210	52.194	42.039	1.00	38.13	AAAA C
ATOM	3363	C	THR	355	51.746	54.339	39.851	1.00	43.84	AAAA C
ATOM	3364	O	THR	355	52.463	55.334	38.697	1.00	44.26	AAAA O
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ATOM	3367	CA	GLY	356	51.358	54.073	36.470	1.00	37.81	AAAA C
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ATOM	3369	O	GLY	356	50.364	56.261	36.615	1.00	34.65	AAAA O
ATOM	3370	N	TYR	357	49.910	55.004	34.800	1.00	38.47	AAAA N
ATOM	3372	CA	TYR	357	48.982	55.973	34.205	1.00	38.03	AAAA C
ATOM	3373	CB	TYR	357	49.557	56.343	32.905	1.00	31.44	AAAA C
ATOM	3374	CG	TYR	357	49.473	55.219	31.812	1.00	33.04	AAAA C
ATOM	3375	CD1	TYR	357	48.333	54.842	31.077	1.00	32.86	AAAA C
ATOM	3376	CE1	TYR	357	48.352	53.779	30.175	1.00	32.83	AAAA C
ATOM	3377	CD2	TYR	357	50.639	54.465	31.606	1.00	34.28	AAAA C
ATOM	3378	CE2	TYR	357	50.706	53.402	30.720	1.00	32.51	AAAA C
ATOM	3379	CZ	TYR	357	49.552	53.068	30.007	1.00	37.26	AAAA C
ATOM	3380	OH	TYR	357	49.726	51.997	29.166	1.00	35.85	AAAA O
ATOM	3382	C	TYR	357	47.582	55.368	34.150	1.00	38.55	AAAA C
ATOM	3383	O	TYR	357	47.458	54.127	34.088	1.00	36.11	AAAA O
ATOM	3384	N	VAL	358	46.593	56.216	33.814	1.00	40.98	AAAA N
ATOM	3386	CA	VAL	358	45.197	55.798	33.639	1.00	38.90	AAAA C
ATOM	3387	CB	VAL	358	44.211	56.502	34.610	1.00	49.15	AAAA C
ATOM	3388	CG1	VAL	358	42.815	55.883	34.484	1.00	33.12	AAAA C
ATOM	3389	CG2	VAL	358	44.748	56.437	36.043	1.00	29.20	AAAA C
ATOM	3390	C	VAL	358	44.760	56.194	32.234	1.00	35.64	AAAA C
ATOM	3391	O	VAL	358	44.792	57.358	31.888	1.00	34.58	AAAA O
ATOM	3392	N	LYS	359	44.387	55.188	31.461	1.00	36.00	AAAA N
ATOM	3394	CA	LYS	359	43.898	55.419	30.117	1.00	41.27	AAAA C
ATOM	3395	CB	LYS	359	44.845	54.707	29.174	1.00	37.40	AAAA C
ATOM	3396	CG	LYS	359	44.340	54.473	27.770	1.00	45.19	AAAA C
ATOM	3397	CD	LYS	359	45.040	55.317	26.750	1.00	43.40	AAAA C
ATOM	3398	CE	LYS	359	45.958	54.402	25.986	1.00	43.56	AAAA C
ATOM	3399	NZ	LYS	359	45.416	53.937	24.680	1.00	47.98	AAAA N
ATOM	3403	C	LYS	359	42.423	54.979	29.939	1.00	42.14	AAAA C
ATOM	3404	O	LYS	359	42.056	53.791	30.006	1.00	40.40	AAAA O
ATOM	3405	N	ILE	360	41.602	55.974	29.572	1.00	37.16	AAAA N
ATOM	3407	CA	ILE	360	40.164	55.742	29.334	1.00	40.02	AAAA C
ATOM	3408	CB	ILE	360	39.297	56.804	30.048	1.00	38.10	AAAA C
ATOM	3409	CG2	ILE	360	37.887	56.277	29.932	1.00	39.42	AAAA C
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ATOM	3412	C	ILE	360	39.888	55.837	27.834	1.00	39.49	AAAA C

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ATOM	3414	N	ARG	361	39.567	54.721	27.221	1.00	34.34	AAAA N
ATOM	3416	CA	ARG	361	39.472	54.782	25.744	1.00	41.24	AAAA C
ATOM	3417	CB	ARG	361	40.783	54.213	25.148	1.00	47.92	AAAA C
ATOM	3418	CG	ARG	361	40.805	54.203	23.646	1.00	50.39	AAAA C
ATOM	3419	CD	ARG	361	41.943	53.357	23.116	1.00	51.36	AAAA C
ATOM	3420	NE	ARG	361	41.473	51.974	23.263	1.00	50.97	AAAA N
ATOM	3422	CZ	ARG	361	42.297	50.962	23.490	1.00	55.78	AAAA C
ATOM	3423	NH1	ARG	361	43.612	51.074	23.616	1.00	51.62	AAAA N
ATOM	3426	NH2	ARG	361	41.834	49.719	23.631	1.00	54.52	AAAA N
ATOM	3429	C	ARG	361	38.382	53.866	25.246	1.00	42.06	AAAA C
ATOM	3430	O	ARG	361	38.336	52.661	25.499	1.00	38.93	AAAA O
ATOM	3431	N	HIS	362	37.514	54.342	24.373	1.00	46.19	AAAA N
ATOM	3433	CA	HIS	362	36.372	53.555	23.885	1.00	49.34	AAAA C
ATOM	3434	CB	HIS	362	37.000	52.300	23.266	1.00	40.94	AAAA C
ATOM	3435	CG	HIS	362	37.849	52.610	22.084	1.00	42.78	AAAA C
ATOM	3436	CD2	HIS	362	38.049	53.765	21.411	1.00	48.32	AAAA C
ATOM	3437	ND1	HIS	362	38.628	51.676	21.469	1.00	43.59	AAAA N
ATOM	3439	CE1	HIS	362	39.256	52.247	20.465	1.00	46.01	AAAA C
ATOM	3440	NE2	HIS	362	38.923	53.515	20.408	1.00	49.22	AAAA N
ATOM	3442	C	HIS	362	35.295	53.113	24.913	1.00	50.32	AAAA C
ATOM	3443	O	HIS	362	34.686	52.030	24.795	1.00	41.31	AAAA O
ATOM	3444	N	SER	363	35.222	53.875	26.013	1.00	46.96	AAAA N
ATOM	3446	CA	SER	363	34.402	53.456	27.139	1.00	52.19	AAAA C
ATOM	3447	CB	SER	363	35.231	53.837	28.400	1.00	53.73	AAAA C
ATOM	3448	OG	SER	363	35.713	52.558	28.816	1.00	41.72	AAAA O
ATOM	3450	C	SER	363	33.005	54.072	27.046	1.00	49.08	AAAA C
ATOM	3451	O	SER	363	32.653	55.040	27.694	1.00	37.49	AAAA O
ATOM	3452	N	HIS	364	32.243	53.577	26.058	1.00	52.25	AAAA N
ATOM	3454	CA	HIS	364	30.954	54.173	25.717	1.00	53.66	AAAA C
ATOM	3455	C	HIS	364	29.879	53.937	26.760	1.00	48.77	AAAA C
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ATOM	3457	CB	HIS	364	30.485	53.699	24.348	1.00	49.83	AAAA C
ATOM	3458	CG	HIS	364	31.493	54.182	23.339	1.00	51.51	AAAA C
ATOM	3459	ND1	HIS	364	31.870	55.502	23.156	1.00	44.83	AAAA N
ATOM	3460	CE1	HIS	364	32.798	55.533	22.214	1.00	28.57	AAAA C
ATOM	3461	CD2	HIS	364	32.194	53.393	22.472	1.00	38.62	AAAA C
ATOM	3462	NE2	HIS	364	32.992	54.274	21.810	1.00	41.44	AAAA N
ATOM	3464	N	ALA	365	29.949	52.819	27.427	1.00	47.53	AAAA N
ATOM	3466	CA	ALA	365	29.211	52.488	28.621	1.00	44.41	AAAA C
ATOM	3467	CB	ALA	365	29.678	51.133	29.150	1.00	40.28	AAAA C
ATOM	3468	C	ALA	365	29.318	53.473	29.768	1.00	44.70	AAAA C
ATOM	3469	O	ALA	365	28.576	53.206	30.726	1.00	45.28	AAAA O
ATOM	3470	N	LEU	366	30.158	54.517	29.762	1.00	40.80	AAAA N
ATOM	3472	CA	LEU	366	30.415	55.243	30.968	1.00	42.21	AAAA C
ATOM	3473	CB	LEU	366	31.885	55.241	31.350	1.00	43.79	AAAA C
ATOM	3474	CG	LEU	366	32.740	54.037	31.667	1.00	51.52	AAAA C
ATOM	3475	CD1	LEU	366	34.192	54.373	32.043	1.00	51.77	AAAA C
ATOM	3476	CD2	LEU	366	32.118	53.305	32.834	1.00	51.13	AAAA C
ATOM	3477	C	LEU	366	29.974	56.687	30.896	1.00	46.36	AAAA C
ATOM	3478	O	LEU	366	30.305	57.248	29.849	1.00	48.40	AAAA O
ATOM	3479	N	VAL	367	29.521	57.275	32.015	1.00	43.68	AAAA N
ATOM	3481	CA	VAL	367	29.072	58.675	31.940	1.00	44.19	AAAA C
ATOM	3482	CB	VAL	367	27.557	58.727	32.376	1.00	48.80	AAAA C
ATOM	3483	CG1	VAL	367	26.923	60.073	32.571	1.00	41.69	AAAA C
ATOM	3484	CG2	VAL	367	26.697	57.949	31.365	1.00	34.00	AAAA C
ATOM	3485	C	VAL	367	29.923	59.518	32.845	1.00	44.90	AAAA C
ATOM	3486	O	VAL	367	29.965	60.751	32.720	1.00	44.75	AAAA O
ATOM	3487	N	SER	368	30.591	58.818	33.757	1.00	48.72	AAAA N
ATOM	3489	CA	SER	368	31.487	59.465	34.742	1.00	52.70	AAAA C
ATOM	3490	CB	SER	368	30.658	59.706	36.000	1.00	55.32	AAAA C
ATOM	3491	OG	SER	368	31.300	60.298	37.091	1.00	64.86	AAAA O
ATOM	3493	C	SER	368	32.590	58.497	35.179	1.00	52.76	AAAA C
ATOM	3494	O	SER	368	32.352	57.299	34.976	1.00	48.99	AAAA O
ATOM	3495	N	LEU	369	33.631	59.012	35.831	1.00	53.86	AAAA N
ATOM	3497	CA	LEU	369	34.716	58.129	36.274	1.00	60.15	AAAA C
ATOM	3498	CB	LEU	369	36.073	58.630	35.784	1.00	55.91	AAAA C
ATOM	3499	CG	LEU	369	36.325	58.736	34.271	1.00	45.96	AAAA C
ATOM	3500	CD1	LEU	369	37.669	59.428	34.154	1.00	53.97	AAAA C
ATOM	3501	CD2	LEU	369	36.207	57.384	33.619	1.00	38.77	AAAA C
ATOM	3502	C	LEU	369	34.645	58.036	37.811	1.00	62.52	AAAA C
ATOM	3503	O	LEU	369	35.569	57.700	38.595	1.00	59.33	AAAA O
ATOM	3504	N	SER	370	33.437	58.401	38.285	1.00	56.26	AAAA N
ATOM	3506	CA	SER	370	33.089	58.431	39.690	1.00	53.88	AAAA C
ATOM	3507	CB	SER	370	31.673	59.052	39.816	1.00	57.50	AAAA C
ATOM	3508	OG	SER	370	30.771	58.061	39.261	1.00	69.12	AAAA O
ATOM	3510	C	SER	370	33.060	57.085	40.412	1.00	47.97	AAAA C
ATOM	3511	O	SER	370	33.228	56.943	41.596	1.00	41.93	AAAA O
ATOM	3512	N	PHE	371	32.967	55.936	39.792	1.00	45.48	AAAA N
ATOM	3514	CA	PHE	371	33.223	54.643	40.356	1.00	46.29	AAAA C
ATOM	3515	CB	PHE	371	32.952	53.596	39.287	1.00	43.53	AAAA C
ATOM	3516	CG	PHE	371	33.724	53.629	38.012	1.00	56.45	AAAA C
ATOM	3517	CD1	PHE	371	34.805	52.807	37.764	1.00	58.95	AAAA C
ATOM	3518	CD2	PHE	371	33.371	54.515	37.004	1.00	53.92	AAAA C
ATOM	3519	CE1	PHE	371	35.498	52.842	36.570	1.00	59.50	AAAA C

ATOM	3520	CE2	PHE	371	34.048	54.546	35.817	1.00	56.49	AAAA C
ATOM	3521	CZ	PHE	371	35.119	53.716	35.579	1.00	56.39	AAAA C
ATOM	3522	C	PHE	371	34.654	54.467	40.895	1.00	54.84	AAAA C
ATOM	3523	O	PHE	371	35.005	53.592	41.728	1.00	52.23	AAAA O
ATOM	3524	N	LEU	372	35.633	55.305	40.510	1.00	50.17	AAAA N
ATOM	3526	CA	LEU	372	36.928	55.395	41.109	1.00	46.25	AAAA C
ATOM	3527	CB	LEU	372	38.171	55.812	40.276	1.00	44.82	AAAA C
ATOM	3528	CG	LEU	372	38.411	54.800	39.114	1.00	36.78	AAAA C
ATOM	3529	CD1	LEU	372	38.853	55.643	37.934	1.00	45.04	AAAA C
ATOM	3530	CD2	LEU	372	39.260	53.657	39.565	1.00	35.55	AAAA C
ATOM	3531	C	LEU	372	36.715	56.392	42.243	1.00	42.26	AAAA C
ATOM	3532	O	LEU	372	37.224	57.507	42.364	1.00	38.37	AAAA O
ATOM	3533	N	LYS	373	35.970	55.862	43.192	1.00	47.06	AAAA N
ATOM	3535	CA	LYS	373	35.527	56.509	44.415	1.00	50.19	AAAA C
ATOM	3536	CB	LYS	373	34.546	55.521	45.077	1.00	56.74	AAAA C
ATOM	3537	CG	LYS	373	33.645	56.162	46.119	1.00	59.64	AAAA C
ATOM	3538	CD	LYS	373	32.529	56.955	45.441	0.01	60.17	AAAA C
ATOM	3539	CE	LYS	373	31.674	57.687	46.460	0.01	60.45	AAAA C
ATOM	3540	NZ	LYS	373	31.083	58.933	45.899	0.01	60.38	AAAA N
ATOM	3544	C	LYS	373	36.646	56.863	45.366	1.00	49.72	AAAA C
ATOM	3545	O	LYS	373	36.636	57.960	45.907	1.00	42.42	AAAA O
ATOM	3546	N	ASN	374	37.657	55.986	45.513	1.00	54.43	AAAA N
ATOM	3548	CA	ASN	374	38.765	56.352	46.410	1.00	59.92	AAAA C
ATOM	3549	CB	ASN	374	39.080	55.154	47.314	1.00	63.16	AAAA C
ATOM	3550	CG	ASN	374	38.009	54.978	48.396	1.00	64.53	AAAA C
ATOM	3551	OD1	ASN	374	37.892	53.972	49.096	1.00	66.40	AAAA O
ATOM	3552	ND2	ASN	374	37.160	55.965	48.578	1.00	52.88	AAAA N
ATOM	3555	C	ASN	374	40.043	56.892	45.786	1.00	62.35	AAAA C
ATOM	3556	O	ASN	374	41.031	57.223	46.479	1.00	63.08	AAAA O
ATOM	3557	N	LEU	375	40.091	56.893	44.438	1.00	58.34	AAAA N
ATOM	3559	CA	LEU	375	41.305	57.374	43.795	1.00	54.73	AAAA C
ATOM	3560	CB	LEU	375	41.099	57.359	42.288	1.00	56.41	AAAA C
ATOM	3561	CG	LEU	375	42.396	57.422	41.459	1.00	54.12	AAAA C
ATOM	3562	CD1	LEU	375	43.135	56.112	41.689	1.00	37.88	AAAA C
ATOM	3563	CD2	LEU	375	42.030	57.796	40.041	1.00	40.97	AAAA C
ATOM	3564	C	LEU	375	41.712	59.754	44.245	1.00	52.37	AAAA C
ATOM	3565	O	LEU	375	41.151	59.777	43.877	1.00	52.11	AAAA O
ATOM	3566	N	ARG	376	42.801	59.874	44.982	1.00	55.16	AAAA N
ATOM	3568	CA	ARG	376	43.320	60.188	45.434	1.00	55.45	AAAA C
ATOM	3569	CB	ARG	376	43.706	60.202	46.928	1.00	58.69	AAAA C
ATOM	3570	CG	ARG	376	44.288	58.907	47.415	1.00	69.10	AAAA C
ATOM	3571	CD	ARG	376	44.286	58.917	48.944	1.00	81.17	AAAA C
ATOM	3572	NE	ARG	376	45.377	57.926	49.410	1.00	84.46	AAAA N
ATOM	3574	CZ	ARG	376	46.619	58.380	49.598	1.00	85.64	AAAA C
ATOM	3575	NH1	ARG	376	46.966	59.645	49.383	1.00	81.94	AAAA N
ATOM	3578	NH2	ARG	376	47.571	57.548	50.012	1.00	94.15	AAAA N
ATOM	3581	C	ARG	376	44.556	60.544	44.633	1.00	50.16	AAAA C
ATOM	3582	O	ARG	376	44.746	61.728	44.465	1.00	44.25	AAAA O
ATOM	3583	N	LEU	377	45.375	59.578	44.219	1.00	50.99	AAAA N
ATOM	3585	CA	LEU	377	46.526	59.942	43.379	1.00	49.40	AAAA C
ATOM	3586	CB	LEU	377	47.596	60.411	44.329	1.00	64.72	AAAA C
ATOM	3587	CG	LEU	377	48.806	59.577	44.667	1.00	70.76	AAAA C
ATOM	3588	CD1	LEU	377	50.031	60.157	43.954	1.00	63.32	AAAA C
ATOM	3589	CD2	LEU	377	49.010	59.696	46.179	1.00	68.60	AAAA C
ATOM	3590	C	LEU	377	47.043	59.022	42.311	1.00	46.33	AAAA C
ATOM	3591	O	LEU	377	46.868	57.788	42.286	1.00	45.17	AAAA O
ATOM	3592	N	ILE	378	47.448	59.675	41.199	1.00	45.12	AAAA N
ATOM	3594	CA	ILE	378	48.042	58.976	40.042	1.00	49.10	AAAA C
ATOM	3595	CB	ILE	378	47.342	59.303	38.724	1.00	46.36	AAAA C
ATOM	3596	CG2	ILE	378	48.115	58.696	37.574	1.00	34.36	AAAA C
ATOM	3597	CG1	ILE	378	45.871	58.862	38.829	1.00	38.59	AAAA C
ATOM	3598	CD1	ILE	378	44.999	59.515	37.765	1.00	37.19	AAAA C
ATOM	3599	C	ILE	378	49.524	59.381	40.003	1.00	49.87	AAAA C
ATOM	3600	O	ILE	378	49.801	60.595	40.040	1.00	44.72	AAAA O
ATOM	3601	N	LEU	379	50.454	58.423	40.067	1.00	49.97	AAAA N
ATOM	3603	CA	LEU	379	51.866	58.712	40.344	1.00	48.48	AAAA C
ATOM	3604	CB	LEU	379	52.575	57.531	41.054	1.00	48.44	AAAA C
ATOM	3605	CG	LEU	379	52.234	57.363	42.554	1.00	50.28	AAAA C
ATOM	3606	CD1	LEU	379	52.926	56.187	43.217	1.00	39.99	AAAA C
ATOM	3607	CD2	LEU	379	52.616	58.625	43.300	1.00	42.89	AAAA C
ATOM	3608	C	LEU	379	52.609	59.019	39.080	1.00	50.94	AAAA C
ATOM	3609	O	LEU	379	53.576	59.788	39.139	1.00	54.23	AAAA O
ATOM	3610	N	GLY	380	52.175	58.423	37.972	1.00	49.67	AAAA N
ATOM	3612	CA	GLY	380	52.831	58.715	36.702	1.00	49.94	AAAA C
ATOM	3613	C	GLY	380	54.249	58.155	36.624	1.00	52.70	AAAA C
ATOM	3614	O	GLY	380	55.026	58.657	35.803	1.00	49.94	AAAA O
ATOM	3615	N	GLU	381	54.549	57.033	37.272	1.00	52.51	AAAA N
ATOM	3617	CA	GLU	381	55.849	56.386	37.243	1.00	52.33	AAAA C
ATOM	3618	CB	GLU	381	56.055	55.310	38.323	1.00	45.22	AAAA C
ATOM	3619	CG	GLU	381	55.402	55.779	39.636	1.00	52.91	AAAA C
ATOM	3620	CD	GLU	381	56.050	55.192	40.873	1.00	42.11	AAAA C
ATOM	3621	OE1	GLU	381	56.160	53.966	40.890	1.00	40.26	AAAA O
ATOM	3622	OE2	GLU	381	56.379	56.014	41.754	1.00	51.32	AAAA O
ATOM	3623	C	GLU	381	56.078	55.784	35.858	1.00	55.86	AAAA C
ATOM	3624	O	GLU	381	57.216	55.652	35.345	1.00	54.61	AAAA O

ATOM	3625	N	GLU	382	54.980	55.449	35.157	1.00	53.56	AAAA N
ATOM	3627	CA	GLU	382	55.091	55.018	33.766	1.00	48.15	AAAA C
ATOM	3628	CB	GLU	382	55.051	53.550	33.532	1.00	35.27	AAAA C
ATOM	3629	CG	GLU	382	54.739	53.225	32.051	1.00	49.69	AAAA C
ATOM	3630	CD	GLU	382	54.676	51.719	31.807	1.00	56.45	AAAA C
ATOM	3631	OE1	GLU	382	55.062	50.924	32.705	1.00	61.66	AAAA O
ATOM	3632	OE2	GLU	382	54.264	51.201	30.745	1.00	57.69	AAAA O
ATOM	3633	C	GLU	382	54.006	55.732	32.973	1.00	50.84	AAAA C
ATOM	3634	O	GLU	382	53.097	56.282	33.598	1.00	49.44	AAAA O
ATOM	3635	N	GLN	383	54.347	56.256	31.780	1.00	52.25	AAAA N
ATOM	3637	CA	GLN	383	53.498	57.153	31.016	1.00	40.15	AAAA C
ATOM	3638	CB	GLN	383	53.914	58.609	31.155	1.00	28.50	AAAA C
ATOM	3639	CG	GLN	383	54.489	58.909	32.542	1.00	31.10	AAAA C
ATOM	3640	CD	GLN	383	54.950	60.301	32.752	1.00	33.19	AAAA C
ATOM	3641	OE1	GLN	383	55.186	60.840	31.683	1.00	40.34	AAAA O
ATOM	3642	NE2	GLN	383	55.043	60.943	33.934	1.00	36.30	AAAA N
ATOM	3645	C	GLN	383	53.426	56.744	29.563	1.00	40.45	AAAA C
ATOM	3646	O	GLN	383	54.131	55.858	29.139	1.00	43.45	AAAA O
ATOM	3647	N	LEU	384	52.375	57.195	28.860	1.00	42.54	AAAA N
ATOM	3649	CA	LEU	384	52.257	56.889	27.443	1.00	43.24	AAAA C
ATOM	3650	CB	LEU	384	50.814	57.011	26.949	1.00	43.79	AAAA C
ATOM	3651	CG	LEU	384	49.818	56.235	27.861	1.00	41.21	AAAA C
ATOM	3652	CD1	LEU	384	48.611	57.095	28.221	1.00	33.99	AAAA C
ATOM	3653	CD2	LEU	384	49.405	54.968	27.149	1.00	33.20	AAAA C
ATOM	3654	C	LEU	384	53.204	57.809	26.672	1.00	40.51	AAAA C
ATOM	3655	O	LEU	384	53.582	58.872	27.177	1.00	29.66	AAAA O
ATOM	3656	N	GLU	385	53.659	57.319	25.531	1.00	45.22	AAAA N
ATOM	3658	CA	GLU	385	54.410	58.116	24.570	1.00	49.98	AAAA C
ATOM	3659	CB	GLU	385	54.424	57.475	23.174	1.00	60.50	AAAA C
ATOM	3660	CG	GLU	385	55.045	56.095	23.106	1.00	68.76	AAAA C
ATOM	3661	CD	GLU	385	54.195	54.951	23.592	1.00	72.07	AAAA C
ATOM	3662	OE1	GLU	385	53.150	55.213	24.244	1.00	81.88	AAAA O
ATOM	3663	OE2	GLU	385	54.565	53.786	23.301	1.00	73.13	AAAA O
ATOM	3664	C	GLU	385	53.828	59.515	24.450	1.00	47.41	AAAA C
ATOM	3665	O	GLU	385	52.635	59.706	24.184	1.00	54.43	AAAA O
ATOM	3666	N	GLY	386	54.614	60.470	24.902	1.00	43.69	AAAA N
ATOM	3668	CA	GLY	386	54.191	61.870	24.897	1.00	40.34	AAAA C
ATOM	3669	C	GLY	386	54.286	62.449	26.309	1.00	40.65	AAAA C
ATOM	3670	O	GLY	386	53.930	63.615	26.491	1.00	39.75	AAAA O
ATOM	3671	N	ASN	387	54.441	61.637	27.272	1.00	40.75	AAAA N
ATOM	3673	CA	ASN	387	54.479	61.912	28.675	1.00	49.18	AAAA C
ATOM	3674	CB	ASN	387	55.500	63.004	28.874	1.00	44.41	AAAA C
ATOM	3675	CG	ASN	387	56.925	62.541	28.722	1.00	61.51	AAAA C
ATOM	3676	OD1	ASN	387	57.199	61.313	28.677	1.00	57.85	AAAA O
ATOM	3677	ND2	ASN	387	58.063	63.251	28.592	1.00	61.96	AAAA N
ATOM	3680	C	ASN	387	53.095	62.100	29.299	1.00	48.46	AAAA C
ATOM	3681	O	ASN	387	52.836	62.991	30.218	1.00	48.99	AAAA O
ATOM	3682	N	TYR	388	52.214	61.116	29.058	1.00	46.29	AAAA N
ATOM	3684	CA	TYR	388	50.846	61.199	29.540	1.00	45.09	AAAA C
ATOM	3685	CB	TYR	388	49.823	60.957	28.399	1.00	40.70	AAAA C
ATOM	3686	CG	TYR	388	49.925	62.056	27.373	1.00	42.24	AAAA C
ATOM	3687	CD1	TYR	388	50.343	61.854	26.064	1.00	44.38	AAAA C
ATOM	3688	CE1	TYR	388	50.401	62.885	25.157	1.00	35.51	AAAA C
ATOM	3689	CD2	TYR	388	49.625	63.356	27.709	1.00	44.67	AAAA C
ATOM	3690	CE2	TYR	388	49.699	64.428	26.830	1.00	38.14	AAAA C
ATOM	3691	CZ	TYR	388	50.087	64.148	25.555	1.00	41.27	AAAA C
ATOM	3692	OH	TYR	388	50.151	65.181	24.604	1.00	50.18	AAAA O
ATOM	3694	C	TYR	388	50.563	60.288	30.714	1.00	41.88	AAAA C
ATOM	3695	O	TYR	388	50.727	59.092	30.511	1.00	32.99	AAAA O
ATOM	3696	N	SER	389	50.020	60.917	31.763	1.00	45.42	AAAA N
ATOM	3698	CA	SER	389	49.591	60.131	32.931	1.00	50.13	AAAA C
ATOM	3699	CB	SER	389	49.798	60.894	34.261	1.00	45.57	AAAA C
ATOM	3700	OG	SER	389	51.185	60.899	34.504	1.00	51.11	AAAA O
ATOM	3702	C	SER	389	48.097	59.813	32.804	1.00	48.11	AAAA C
ATOM	3703	O	SER	389	47.686	58.792	33.336	1.00	49.25	AAAA O
ATOM	3704	N	PHE	390	47.321	60.685	32.196	1.00	42.56	AAAA N
ATOM	3706	CA	PHE	390	45.867	60.595	32.146	1.00	40.76	AAAA C
ATOM	3707	CB	PHE	390	45.241	61.581	33.139	1.00	44.80	AAAA C
ATOM	3708	CG	PHE	390	43.764	61.358	33.328	1.00	40.53	AAAA C
ATOM	3709	CD1	PHE	390	43.406	60.273	34.089	1.00	40.80	AAAA C
ATOM	3710	CD2	PHE	390	42.768	62.157	32.748	1.00	35.59	AAAA C
ATOM	3711	CE1	PHE	390	42.050	59.985	34.312	1.00	47.09	AAAA C
ATOM	3712	CE2	PHE	390	41.454	61.824	32.965	1.00	44.50	AAAA C
ATOM	3713	CZ	PHE	390	41.063	60.745	33.739	1.00	34.54	AAAA C
ATOM	3714	C	PHE	390	45.372	60.929	30.720	1.00	38.54	AAAA C
ATOM	3715	O	PHE	390	45.542	61.918	30.126	1.00	40.29	AAAA O
ATOM	3716	N	TYR	391	44.819	59.818	30.096	1.00	33.48	AAAA N
ATOM	3718	CA	TYR	391	44.596	59.782	28.663	1.00	38.58	AAAA C
ATOM	3719	CB	TYR	391	45.579	58.871	27.972	1.00	38.95	AAAA C
ATOM	3720	CG	TYR	391	45.760	59.006	26.503	1.00	44.54	AAAA C
ATOM	3721	CD1	TYR	391	46.822	59.815	26.052	1.00	47.14	AAAA C
ATOM	3722	CE1	TYR	391	47.057	59.993	24.722	1.00	46.03	AAAA C
ATOM	3723	CD2	TYR	391	44.927	58.390	25.584	1.00	46.94	AAAA C
ATOM	3724	CE2	TYR	391	45.157	58.560	24.242	1.00	47.45	AAAA C
ATOM	3725	CZ	TYR	391	46.207	59.350	23.830	1.00	45.84	AAAA C

ATOM	3826	OH	TYR	391	46.374	59.492	22.481	1.00	44.70	AAAA	O
ATOM	3828	C	TYR	391	43.194	59.232	28.349	1.00	39.74	AAAA	C
ATOM	3829	O	TYR	391	42.841	58.103	28.730	1.00	38.49	AAAA	O
ATOM	3830	N	VAL	392	42.417	60.158	27.779	1.00	37.07	AAAA	N
ATOM	3832	CA	VAL	392	40.958	59.874	27.603	1.00	39.52	AAAA	C
ATOM	3833	CB	VAL	392	40.075	60.880	28.440	1.00	41.12	AAAA	C
ATOM	3834	CG1	VAL	392	38.612	60.464	28.472	1.00	37.96	AAAA	C
ATOM	3835	CG2	VAL	392	40.666	61.041	29.841	1.00	33.19	AAAA	C
ATOM	3836	C	VAL	392	40.531	60.092	26.182	1.00	31.08	AAAA	C
ATOM	3837	O	VAL	392	40.508	61.277	25.804	1.00	34.71	AAAA	O
ATOM	3838	N	LEU	393	40.299	59.113	25.383	1.00	34.62	AAAA	N
ATOM	3840	CA	LEU	393	39.948	59.259	23.977	1.00	38.12	AAAA	C
ATOM	3841	CB	LEU	393	41.200	59.036	23.096	1.00	42.49	AAAA	C
ATOM	3842	CG	LEU	393	41.023	58.649	21.586	1.00	26.48	AAAA	C
ATOM	3843	CD1	LEU	393	41.128	59.879	20.753	1.00	26.57	AAAA	C
ATOM	3844	CD2	LEU	393	42.078	57.589	21.244	1.00	29.98	AAAA	C
ATOM	3845	C	LEU	393	38.821	58.375	23.482	1.00	39.15	AAAA	C
ATOM	3846	O	LEU	393	38.760	57.173	23.799	1.00	37.90	AAAA	O
ATOM	3847	N	ASP	394	38.015	58.973	22.565	1.00	43.38	AAAA	N
ATOM	3849	CA	ASP	394	36.888	58.215	21.975	1.00	44.77	AAAA	C
ATOM	3850	CB	ASP	394	37.445	57.073	21.120	1.00	44.80	AAAA	C
ATOM	3851	CG	ASP	394	36.466	56.477	20.156	1.00	47.14	AAAA	C
ATOM	3852	OD1	ASP	394	36.750	55.577	19.333	1.00	52.81	AAAA	O
ATOM	3853	OD2	ASP	394	35.311	56.948	20.180	1.00	49.27	AAAA	O
ATOM	3854	C	ASP	394	35.936	57.619	23.021	1.00	43.17	AAAA	C
ATOM	3855	O	ASP	394	35.831	56.385	23.212	1.00	43.51	AAAA	O
ATOM	3856	N	ASN	395	35.299	58.495	23.746	1.00	39.90	AAAA	N
ATOM	3858	CA	ASN	395	34.305	58.158	24.776	1.00	46.32	AAAA	C
ATOM	3859	CB	ASN	395	34.804	58.512	26.212	1.00	42.96	AAAA	C
ATOM	3860	CG	ASN	395	35.992	57.619	26.579	1.00	36.92	AAAA	C
ATOM	3861	OD1	ASN	395	36.013	56.394	26.796	1.00	21.65	AAAA	O
ATOM	3862	ND2	ASN	395	37.075	58.409	26.558	1.00	27.87	AAAA	N
ATOM	3865	C	ASN	395	32.932	58.816	24.541	1.00	40.44	AAAA	C
ATOM	3866	O	ASN	395	32.749	59.982	24.882	1.00	37.06	AAAA	O
ATOM	3867	N	GLN	396	32.073	58.055	23.877	1.00	46.74	AAAA	N
ATOM	3869	CA	GLN	396	30.771	58.582	23.421	1.00	52.93	AAAA	C
ATOM	3870	CB	GLN	396	29.848	57.567	22.744	1.00	52.29	AAAA	C
ATOM	3871	CG	GLN	396	30.173	57.405	21.257	1.00	46.42	AAAA	C
ATOM	3872	CD	GLN	396	29.817	55.991	20.840	1.00	55.21	AAAA	C
ATOM	3873	OE1	GLN	396	28.835	55.421	21.312	1.00	61.17	AAAA	O
ATOM	3874	NE2	GLN	396	30.628	55.411	19.971	1.00	55.79	AAAA	N
ATOM	3877	C	GLN	396	29.874	59.204	24.458	1.00	48.64	AAAA	C
ATOM	3878	O	GLN	396	29.407	60.287	24.113	1.00	51.63	AAAA	O
ATOM	3879	N	ASN	397	29.717	58.681	25.633	1.00	48.95	AAAA	N
ATOM	3881	CA	ASN	397	28.783	59.196	26.632	1.00	51.72	AAAA	C
ATOM	3882	CB	ASN	397	27.969	57.959	27.093	1.00	35.94	AAAA	C
ATOM	3883	CG	ASN	397	27.231	57.430	25.860	1.00	49.09	AAAA	C
ATOM	3884	OD1	ASN	397	26.591	58.304	25.229	1.00	49.32	AAAA	O
ATOM	3885	ND2	ASN	397	27.258	56.175	25.431	1.00	43.31	AAAA	N
ATOM	3888	C	ASN	397	29.367	59.945	27.800	1.00	52.98	AAAA	C
ATOM	3889	O	ASN	397	28.586	60.344	28.627	1.00	53.33	AAAA	O
ATOM	3890	N	LEU	398	30.682	59.990	29.001	1.00	55.73	AAAA	N
ATOM	3892	CA	LEU	398	31.312	60.550	29.179	1.00	52.12	AAAA	C
ATOM	3893	CB	LEU	398	32.827	60.388	29.148	1.00	48.47	AAAA	C
ATOM	3894	CG	LEU	398	33.606	60.283	30.460	1.00	41.81	AAAA	C
ATOM	3895	CD1	LEU	398	33.417	58.939	31.136	1.00	40.35	AAAA	C
ATOM	3896	CD2	LEU	398	35.070	60.608	30.082	1.00	39.03	AAAA	C
ATOM	3897	C	LEU	398	30.923	61.995	29.353	1.00	52.35	AAAA	C
ATOM	3898	O	LEU	398	31.422	62.909	28.681	1.00	49.91	AAAA	O
ATOM	3899	N	GLN	399	30.241	62.225	30.469	1.00	58.76	AAAA	N
ATOM	3901	CA	GLN	399	29.688	63.558	30.796	1.00	60.03	AAAA	C
ATOM	3902	CB	GLN	399	28.236	63.331	31.262	1.00	59.55	AAAA	C
ATOM	3903	CG	GLN	399	27.235	63.962	30.316	1.00	73.07	AAAA	C
ATOM	3904	CD	GLN	399	25.944	63.146	30.340	1.00	78.39	AAAA	C
ATOM	3905	OE1	GLN	399	25.097	63.455	31.194	1.00	71.79	AAAA	O
ATOM	3906	NE2	GLN	399	25.856	62.158	29.440	1.00	69.88	AAAA	N
ATOM	3909	C	GLN	399	30.490	64.252	31.888	1.00	54.49	AAAA	C
ATOM	3910	O	GLN	399	30.528	65.477	32.068	1.00	51.96	AAAA	O
ATOM	3911	N	GLN	400	31.058	63.389	32.734	1.00	50.44	AAAA	N
ATOM	3913	CA	GLN	400	31.938	63.948	33.756	1.00	53.83	AAAA	C
ATOM	3914	CB	GLN	400	31.215	64.314	35.049	1.00	54.97	AAAA	C
ATOM	3915	CG	GLN	400	30.717	63.150	35.887	1.00	58.99	AAAA	C
ATOM	3916	CD	GLN	400	30.678	63.430	37.389	1.00	65.82	AAAA	C
ATOM	3917	OE1	GLN	400	30.906	64.502	37.962	1.00	68.10	AAAA	O
ATOM	3919	NE2	GLN	400	30.341	62.444	38.222	1.00	55.35	AAAA	N
ATOM	3921	C	GLN	400	33.113	63.008	34.052	1.00	52.08	AAAA	C
ATOM	3922	O	GLN	400	33.107	61.783	33.942	1.00	51.90	AAAA	O
ATOM	3923	N	LEU	401	34.073	63.580	34.751	1.00	49.58	AAAA	N
ATOM	3925	CA	LEU	401	35.175	62.844	35.334	1.00	49.57	AAAA	C
ATOM	3926	CB	LEU	401	36.378	63.803	35.260	1.00	47.94	AAAA	C
ATOM	3927	CG	LEU	401	36.638	64.237	33.772	1.00	46.61	AAAA	C
ATOM	3928	CD1	LEU	401	37.658	65.326	33.677	1.00	39.09	AAAA	C
ATOM	3929	CD2	LEU	401	36.919	63.069	32.860	1.00	40.72	AAAA	C
ATOM	3930	C	LEU	401	34.866	62.357	36.734	1.00	51.23	AAAA	C
ATOM	3931	O	LEU	401	34.258	61.299	36.892	1.00	49.06	AAAA	O

ATOM	3832	N	TRP	402	35.297	63.140	37.690	1.00	54.58	AAAA N
ATOM	3834	CA	TRP	402	34.975	63.090	39.097	1.00	59.76	AAAA C
ATOM	3835	CB	TRP	402	36.279	62.953	39.933	1.00	59.56	AAAA C
ATOM	3836	CG	TRP	402	36.971	61.624	39.737	1.00	58.17	AAAA C
ATOM	3837	CD2	TRP	402	37.981	61.243	38.784	1.00	53.18	AAAA C
ATOM	3838	CE2	TRP	402	38.286	59.897	39.002	1.00	56.61	AAAA C
ATOM	3839	CE3	TRP	402	38.643	61.917	37.764	1.00	43.25	AAAA C
ATOM	3840	CD1	TRP	402	36.719	60.517	40.459	1.00	53.50	AAAA C
ATOM	3841	NE1	TRP	402	37.488	59.467	40.032	1.00	57.66	AAAA N
ATOM	3843	CZ2	TRP	402	39.212	59.160	38.249	1.00	51.44	AAAA C
ATOM	3844	CZ3	TRP	402	39.546	61.199	37.026	1.00	53.69	AAAA C
ATOM	3845	CH2	TRP	402	39.820	59.857	37.263	1.00	50.75	AAAA C
ATOM	3846	C	TRP	402	34.223	64.389	39.429	1.00	64.09	AAAA C
ATOM	3847	O	TRP	402	34.408	65.449	38.808	1.00	61.98	AAAA O
ATOM	3848	N	ASP	403	33.503	64.418	40.551	1.00	68.85	AAAA N
ATOM	3850	CA	ASP	403	32.947	65.668	41.068	1.00	67.83	AAAA C
ATOM	3851	CB	ASP	403	31.918	65.343	42.151	1.00	72.19	AAAA C
ATOM	3852	CG	ASP	403	30.853	66.417	42.306	1.00	73.08	AAAA C
ATOM	3853	OD1	ASP	403	31.177	67.625	42.297	1.00	71.67	AAAA O
ATOM	3854	OD2	ASP	403	29.693	65.979	42.454	1.00	75.08	AAAA O
ATOM	3855	C	ASP	403	34.005	66.607	41.607	1.00	66.63	AAAA C
ATOM	3856	O	ASP	403	34.245	66.672	42.811	1.00	67.18	AAAA O
ATOM	3857	N	TRP	404	34.449	67.588	40.846	1.00	69.29	AAAA N
ATOM	3859	CA	TRP	404	35.412	68.588	41.291	1.00	77.11	AAAA C
ATOM	3860	CB	TRP	404	35.859	69.409	40.063	1.00	79.10	AAAA C
ATOM	3861	CG	TRP	404	36.504	68.509	39.047	1.00	82.59	AAAA C
ATOM	3862	CD2	TRP	404	37.294	67.346	39.322	1.00	84.82	AAAA C
ATOM	3863	CE2	TRP	404	37.686	66.813	38.081	1.00	84.56	AAAA C
ATOM	3864	CE3	TRP	404	37.703	66.710	40.506	1.00	80.95	AAAA C
ATOM	3865	CD1	TRP	404	36.460	68.622	37.694	1.00	83.37	AAAA C
ATOM	3866	NE1	TRP	404	37.165	67.617	37.111	1.00	80.33	AAAA N
ATOM	3868	CZ2	TRP	404	38.477	65.662	37.982	1.00	85.91	AAAA C
ATOM	3869	CZ3	TRP	404	38.471	65.573	40.392	1.00	86.36	AAAA C
ATOM	3870	CH2	TRP	404	38.860	65.051	39.133	1.00	85.05	AAAA C
ATOM	3871	C	TRP	404	35.034	69.517	42.420	1.00	81.60	AAAA C
ATOM	3872	O	TRP	404	35.387	70.709	42.504	1.00	84.57	AAAA O
ATOM	3873	N	ASP	405	34.281	69.063	43.393	1.00	84.45	AAAA N
ATOM	3875	CA	ASP	405	33.771	69.861	44.496	1.00	87.48	AAAA C
ATOM	3876	CB	ASP	405	32.352	70.365	44.262	1.00	88.04	AAAA C
ATOM	3877	CG	ASP	405	32.274	71.612	43.409	1.00	92.54	AAAA C
ATOM	3878	OD1	ASP	405	33.306	72.285	43.207	1.00	94.82	AAAA O
ATOM	3879	OD2	ASP	405	31.130	71.954	42.955	1.00	95.26	AAAA O
ATOM	3880	C	ASP	405	33.730	68.906	45.693	1.00	87.80	AAAA C
ATOM	3881	O	ASP	405	34.245	69.224	46.743	1.00	92.19	AAAA O
ATOM	3882	N	ALA	406	33.239	67.709	45.460	1.00	84.46	AAAA N
ATOM	3884	CA	ALA	406	33.176	66.671	46.451	1.00	82.97	AAAA C
ATOM	3885	CB	ALA	406	31.943	65.805	46.133	1.00	76.32	AAAA C
ATOM	3886	C	ALA	406	34.445	65.840	46.459	1.00	85.77	AAAA C
ATOM	3887	O	ALA	406	34.470	64.823	47.185	1.00	89.38	AAAA O
ATOM	3888	N	ARG	407	35.433	66.373	45.577	1.00	83.74	AAAA N
ATOM	3890	CA	ARG	407	36.541	65.151	45.400	1.00	79.60	AAAA C
ATOM	3891	CB	ARG	407	36.165	64.140	44.297	1.00	77.84	AAAA C
ATOM	3892	CG	ARG	407	35.457	62.950	44.921	1.00	81.91	AAAA C
ATOM	3893	CD	ARG	407	35.362	61.688	44.113	1.00	86.97	AAAA C
ATOM	3894	NE	ARG	407	36.281	60.660	44.607	1.00	86.94	AAAA N
ATOM	3896	CZ	ARG	407	37.564	60.583	44.279	1.00	92.14	AAAA C
ATOM	3897	NH1	ARG	407	38.169	61.441	43.469	1.00	97.06	AAAA N
ATOM	3900	NH2	ARG	407	38.309	59.616	44.770	1.00	96.33	AAAA N
ATOM	3903	C	ARG	407	37.880	65.749	45.048	1.00	76.72	AAAA C
ATOM	3904	O	ARG	407	37.989	66.774	44.410	1.00	77.47	AAAA O
ATOM	3905	N	ASN	408	38.958	65.081	45.453	1.00	75.75	AAAA N
ATOM	3907	CA	ASN	408	40.311	65.556	45.173	1.00	73.79	AAAA C
ATOM	3908	CB	ASN	408	40.938	66.240	46.388	1.00	74.46	AAAA C
ATOM	3909	CG	ASN	408	41.986	67.242	45.947	1.00	82.51	AAAA C
ATOM	3910	OD1	ASN	408	41.813	68.429	46.240	1.00	90.33	AAAA O
ATOM	3911	ND2	ASN	408	43.028	66.821	45.253	1.00	84.46	AAAA N
ATOM	3914	C	ASN	408	41.257	64.468	44.654	1.00	65.97	AAAA C
ATOM	3915	O	ASN	408	41.251	63.374	45.151	1.00	63.82	AAAA O
ATOM	3916	N	LEU	409	42.041	64.793	43.650	1.00	61.41	AAAA N
ATOM	3918	CA	LEU	409	42.896	63.872	42.947	1.00	60.90	AAAA C
ATOM	3919	CB	LEU	409	42.153	63.250	41.768	1.00	62.98	AAAA C
ATOM	3920	CG	LEU	409	42.992	62.553	40.704	1.00	59.77	AAAA C
ATOM	3921	CD1	LEU	409	43.488	61.205	41.197	1.00	54.06	AAAA C
ATOM	3922	CD2	LEU	409	42.094	62.445	39.486	1.00	55.74	AAAA C
ATOM	3923	C	LEU	409	44.151	64.599	42.485	1.00	61.19	AAAA C
ATOM	3924	O	LEU	409	44.141	65.809	42.370	1.00	60.64	AAAA O
ATOM	3925	N	THR	410	45.281	63.903	42.424	1.00	63.74	AAAA N
ATOM	3927	CA	THR	410	46.588	64.462	42.131	1.00	60.44	AAAA C
ATOM	3928	CB	THR	410	47.454	64.676	43.385	1.00	67.08	AAAA C
ATOM	3929	OG1	THR	410	46.870	65.746	44.157	1.00	74.29	AAAA O
ATOM	3931	CG2	THR	410	48.909	65.103	43.162	1.00	48.56	AAAA C
ATOM	3932	C	THR	410	47.426	63.565	41.218	1.00	56.62	AAAA C
ATOM	3933	O	THR	410	47.382	62.354	41.317	1.00	54.99	AAAA O
ATOM	3934	N	ILE	411	48.077	64.245	40.288	1.00	53.97	AAAA N
ATOM	3936	CA	ILE	411	48.897	63.562	39.291	1.00	53.29	AAAA C

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ATOM   3937  CB  ILE   411      48.409  63.854  37.864  1.00 49.81      AAAA C
ATOM   3938  CG2 ILE   411      49.216  63.128  36.806  1.00 30.86      AAAA C
ATOM   3939  CG1 ILE   411      46.911  63.489  37.729  1.00 40.83      AAAA C
ATOM   3940  CD1 ILE   411      46.322  63.547  36.338  1.00 38.51      AAAA C
ATOM   3941  C   ILE   411      50.319  64.018  39.568  1.00 55.38      AAAA C
ATOM   3942  O   ILE   411      50.656  65.179  39.291  1.00 57.59      AAAA O
ATOM   3943  N   SER   412      51.073  63.182  40.270  1.00 54.26      AAAA N
ATOM   3945  CA  SER   412      52.434  63.502  40.689  1.00 54.46      AAAA C
ATOM   3946  CB  SER   412      53.071  62.210  41.248  1.00 55.78      AAAA C
ATOM   3947  OG  SER   412      53.756  62.536  42.434  1.00 67.12      AAAA O
ATOM   3949  C   SER   412      53.326  63.910  39.523  1.00 55.52      AAAA C
ATOM   3950  O   SER   412      54.081  64.876  39.527  1.00 55.04      AAAA O
ATOM   3951  N   ALA   413      53.254  63.124  38.438  1.00 50.12      AAAA N
ATOM   3953  CA  ALA   413      54.064  63.402  37.281  1.00 50.01      AAAA C
ATOM   3954  CB  ALA   413      55.334  62.520  37.365  1.00 34.96      AAAA C
ATOM   3955  C   ALA   413      53.301  63.078  35.994  1.00 48.71      AAAA C
ATOM   3956  O   ALA   413      52.495  62.168  35.998  1.00 48.81      AAAA O
ATOM   3957  N   GLY   414      53.675  63.690  34.895  1.00 47.92      AAAA N
ATOM   3959  CA  GLY   414      53.057  63.454  33.607  1.00 51.75      AAAA C
ATOM   3960  C   GLY   414      52.017  64.524  33.294  1.00 52.77      AAAA C
ATOM   3961  O   GLY   414      51.684  65.370  34.114  1.00 53.23      AAAA O
ATOM   3962  N   LYS   415      51.385  64.406  32.138  1.00 56.31      AAAA N
ATOM   3964  CA  LYS   415      50.289  65.317  31.759  1.00 52.49      AAAA C
ATOM   3965  CB  LYS   415      50.884  66.358  30.833  1.00 50.94      AAAA C
ATOM   3966  CG  LYS   415      51.198  65.855  29.429  1.00 54.39      AAAA C
ATOM   3967  CD  LYS   415      52.288  66.691  28.765  1.00 53.96      AAAA C
ATOM   3968  CE  LYS   415      52.785  66.151  27.441  1.00 56.01      AAAA C
ATOM   3969  NZ  LYS   415      52.426  67.032  26.284  1.00 66.36      AAAA N
ATOM   3973  C   LYS   415      49.110  64.576  31.155  1.00 50.04      AAAA C
ATOM   3974  O   LYS   415      49.077  63.337  31.036  1.00 49.77      AAAA O
ATOM   3975  N   MET   416      48.091  65.353  30.771  1.00 48.34      AAAA N
ATOM   3977  CA  MET   416      46.890  64.734  30.186  1.00 46.77      AAAA C
ATOM   3978  CB  MET   416      45.629  65.186  30.949  1.00 42.79      AAAA C
ATOM   3979  CG  MET   416      45.836  65.880  32.273  1.00 40.91      AAAA C
ATOM   3980  SD  MET   416      44.511  65.636  33.517  1.00 56.20      AAAA S
ATOM   3981  CE  MET   416      44.002  67.366  33.690  1.00 35.94      AAAA C
ATOM   3982  C   MET   416      46.623  65.064  28.728  1.00 40.40      AAAA C
ATOM   3983  O   MET   416      46.963  66.137  28.247  1.00 34.94      AAAA O
ATOM   3984  N   TYR   417      45.993  64.169  28.104  1.00 38.49      AAAA N
ATOM   3986  CA  TYR   417      45.355  64.387  26.765  1.00 39.50      AAAA C
ATOM   3987  CB  TYR   417      46.156  63.471  25.831  1.00 32.02      AAAA C
ATOM   3988  CG  TYR   417      45.583  63.430  24.428  1.00 39.48      AAAA C
ATOM   3989  CD1 TYR   417      45.730  64.501  23.511  1.00 39.29      AAAA C
ATOM   3990  CE1 TYR   417      45.196  64.429  22.253  1.00 34.56      AAAA C
ATOM   3991  CD2 TYR   417      44.894  62.321  24.005  1.00 36.91      AAAA C
ATOM   3992  CE2 TYR   417      44.379  62.241  22.722  1.00 38.80      AAAA C
ATOM   3993  CZ  TYR   417      44.535  63.292  21.872  1.00 44.20      AAAA C
ATOM   3994  OH  TYR   417      44.053  63.361  20.582  1.00 58.10      AAAA O
ATOM   3996  C   TYR   417      43.853  64.065  26.699  1.00 44.18      AAAA C
ATOM   3997  O   TYR   417      43.376  62.974  27.135  1.00 42.19      AAAA O
ATOM   3999  N   PHE   418      43.068  64.971  26.100  1.00 45.94      AAAA N
ATOM   4000  CA  PHE   418      41.644  64.701  25.910  1.00 45.87      AAAA C
ATOM   4001  CB  PHE   418      40.772  65.657  26.730  1.00 47.19      AAAA C
ATOM   4002  CG  PHE   418      40.675  65.264  28.177  1.00 43.44      AAAA C
ATOM   4003  CD1 PHE   418      41.552  65.685  29.132  1.00 38.43      AAAA C
ATOM   4004  CD2 PHE   418      39.638  64.417  28.544  1.00 51.21      AAAA C
ATOM   4005  CE1 PHE   418      41.402  65.291  30.440  1.00 46.44      AAAA C
ATOM   4006  CE2 PHE   418      39.486  64.023  29.845  1.00 46.63      AAAA C
ATOM   4007  CZ  PHE   418      40.358  64.454  30.801  1.00 44.68      AAAA C
ATOM   4008  C   PHE   418      41.251  64.730  24.440  1.00 44.64      AAAA C
ATOM   4009  O   PHE   418      41.375  65.762  23.812  1.00 47.60      AAAA O
ATOM   4010  N   ALA   419      40.554  63.713  23.936  1.00 43.06      AAAA N
ATOM   4012  CA  ALA   419      40.015  63.793  22.607  1.00 39.21      AAAA C
ATOM   4013  CB  ALA   419      41.090  63.562  21.555  1.00 30.88      AAAA C
ATOM   4014  C   ALA   419      38.837  62.846  22.366  1.00 41.77      AAAA C
ATOM   4015  O   ALA   419      38.871  61.628  22.557  1.00 36.08      AAAA O
ATOM   4016  N   PHE   420      37.829  63.398  21.618  1.00 40.41      AAAA N
ATOM   4019  CA  PHE   420      36.742  62.621  21.070  1.00 40.03      AAAA C
ATOM   4019  CB  PHE   420      37.157  61.430  20.180  1.00 45.54      AAAA C
ATOM   4020  CG  PHE   420      37.832  61.909  18.912  1.00 54.18      AAAA C
ATOM   4021  CD1 PHE   420      39.221  61.987  18.751  1.00 49.23      AAAA C
ATOM   4022  CD2 PHE   420      37.006  62.345  17.871  1.00 47.65      AAAA C
ATOM   4023  CE1 PHE   420      39.783  62.496  17.567  1.00 46.00      AAAA C
ATOM   4024  CE2 PHE   420      37.572  62.833  16.725  1.00 51.10      AAAA C
ATOM   4025  CZ  PHE   420      38.964  62.928  16.549  1.00 44.01      AAAA C
ATOM   4026  C   PHE   420      35.762  62.146  22.126  1.00 41.65      AAAA C
ATOM   4027  O   PHE   420      35.352  60.991  22.215  1.00 38.35      AAAA O
ATOM   4028  N   ASN   421      35.459  63.024  23.049  1.00 45.35      AAAA N
ATOM   4030  CA  ASN   421      34.477  62.960  24.112  1.00 46.86      AAAA C
ATOM   4031  CB  ASN   421      35.183  63.276  25.449  1.00 43.60      AAAA C
ATOM   4032  CG  ASN   421      36.407  62.401  25.654  1.00 47.90      AAAA C
ATOM   4033  OD1 ASN   421      36.426  61.147  25.714  1.00 44.83      AAAA O
ATOM   4034  ND2 ASN   421      37.541  63.101  25.732  1.00 37.46      AAAA N
ATOM   4037  C   ASN   421      33.432  64.069  23.835  1.00 47.83      AAAA C
ATOM   4038  O   ASN   421      33.617  65.233  24.237  1.00 38.85      AAAA O
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ATOM	4039	N	PRO	422	32.453	63.777	22.968	1.00	47.86	AAAA N
ATOM	4040	CD	PRO	422	32.213	62.423	22.372	1.00	44.11	AAAA C
ATOM	4041	CA	PRO	422	31.463	64.776	22.605	1.00	47.85	AAAA C
ATOM	4042	CB	PRO	422	30.731	64.084	21.446	1.00	44.86	AAAA C
ATOM	4043	CG	PRO	422	30.947	62.623	21.606	1.00	43.01	AAAA C
ATOM	4044	C	PRO	422	30.577	65.284	23.735	1.00	51.16	AAAA C
ATOM	4045	O	PRO	422	30.223	66.486	23.744	1.00	48.54	AAAA O
ATOM	4046	N	LYS	423	30.320	64.487	24.774	1.00	52.90	AAAA N
ATOM	4048	CA	LYS	423	29.431	64.908	25.865	1.00	58.82	AAAA C
ATOM	4049	CB	LYS	423	28.556	63.721	26.360	1.00	52.93	AAAA C
ATOM	4050	CG	LYS	423	28.209	62.810	25.196	1.00	70.55	AAAA C
ATOM	4051	CD	LYS	423	26.743	62.448	24.996	1.00	73.79	AAAA C
ATOM	4052	CE	LYS	423	26.030	63.374	24.021	1.00	77.06	AAAA C
ATOM	4053	NZ	LYS	423	25.949	64.748	24.614	1.00	64.99	AAAA N
ATOM	4057	C	LYS	423	30.158	65.482	27.071	1.00	57.43	AAAA C
ATOM	4058	O	LYS	423	29.582	65.478	28.152	1.00	55.22	AAAA O
ATOM	4059	N	LEU	424	31.425	65.859	26.862	1.00	55.95	AAAA N
ATOM	4061	CA	LEU	424	32.261	66.162	28.017	1.00	57.07	AAAA C
ATOM	4062	CB	LEU	424	33.463	65.250	28.237	1.00	49.16	AAAA C
ATOM	4063	CG	LEU	424	34.390	65.748	29.370	1.00	68.27	AAAA C
ATOM	4064	CD1	LEU	424	33.821	65.362	30.734	1.00	60.66	AAAA C
ATOM	4065	CD2	LEU	424	35.825	65.276	29.123	1.00	60.35	AAAA C
ATOM	4066	C	LEU	424	32.709	67.585	27.878	1.00	56.29	AAAA C
ATOM	4067	O	LEU	424	33.696	67.861	27.201	1.00	59.98	AAAA O
ATOM	4068	N	CYS	425	31.995	68.488	28.492	1.00	58.76	AAAA N
ATOM	4070	CA	CYS	425	32.342	69.916	28.406	1.00	60.39	AAAA C
ATOM	4071	C	CYS	425	33.771	70.119	28.810	1.00	62.59	AAAA C
ATOM	4072	O	CYS	425	34.288	69.665	29.831	1.00	64.45	AAAA O
ATOM	4073	CB	CYS	425	31.249	70.644	29.214	1.00	68.23	AAAA C
ATOM	4074	SG	CYS	425	29.916	71.303	28.086	1.00	81.03	AAAA S
ATOM	4075	N	VAL	426	34.529	70.953	28.102	1.00	65.31	AAAA N
ATOM	4077	CA	VAL	426	35.943	71.149	28.358	1.00	65.49	AAAA C
ATOM	4078	CB	VAL	426	36.644	72.022	27.310	1.00	66.66	AAAA C
ATOM	4079	CG1	VAL	426	36.715	71.413	25.925	1.00	62.49	AAAA C
ATOM	4080	CG2	VAL	426	35.962	73.365	27.239	1.00	60.92	AAAA C
ATOM	4081	C	VAL	426	36.105	71.711	29.757	1.00	65.99	AAAA C
ATOM	4082	O	VAL	426	37.180	71.724	30.388	1.00	64.51	AAAA O
ATOM	4083	N	SER	427	35.090	72.361	30.267	1.00	67.67	AAAA N
ATOM	4085	CA	SER	427	35.091	72.927	31.599	1.00	66.85	AAAA C
ATOM	4086	CB	SER	427	33.685	73.499	31.864	1.00	61.16	AAAA C
ATOM	4087	OG	SER	427	34.088	74.860	32.098	1.00	67.05	AAAA O
ATOM	4089	C	SER	427	35.515	71.972	32.701	1.00	64.24	AAAA C
ATOM	4090	O	SER	427	36.332	72.328	33.573	1.00	63.66	AAAA O
ATOM	4091	N	GLU	428	34.965	70.771	32.618	1.00	58.75	AAAA N
ATOM	4093	CA	GLU	428	35.384	69.753	33.585	1.00	63.39	AAAA C
ATOM	4094	CB	GLU	428	34.594	68.485	33.240	1.00	68.67	AAAA C
ATOM	4095	CG	GLU	428	33.115	68.560	33.537	1.00	66.59	AAAA C
ATOM	4096	CD	GLU	428	32.785	68.560	35.023	1.00	72.33	AAAA C
ATOM	4097	OE1	GLU	428	32.729	67.522	35.722	1.00	81.62	AAAA O
ATOM	4098	OE2	GLU	428	32.581	69.638	35.517	1.00	70.97	AAAA O
ATOM	4099	C	GLU	428	36.970	69.485	33.429	1.00	61.63	AAAA C
ATOM	4100	O	GLU	428	37.671	69.696	34.307	1.00	62.03	AAAA O
ATOM	4101	N	ILE	429	37.265	69.262	32.165	1.00	61.26	AAAA N
ATOM	4103	CA	ILE	429	38.631	69.038	31.789	1.00	61.09	AAAA C
ATOM	4104	CB	ILE	429	38.759	68.933	30.263	1.00	59.32	AAAA C
ATOM	4105	CG2	ILE	429	40.257	68.915	29.895	1.00	45.93	AAAA C
ATOM	4106	CG1	ILE	429	37.968	67.719	29.794	1.00	57.66	AAAA C
ATOM	4107	CD1	ILE	429	38.038	67.555	28.285	1.00	53.49	AAAA C
ATOM	4108	C	ILE	429	39.498	70.166	32.323	1.00	61.90	AAAA C
ATOM	4109	O	ILE	429	40.592	70.017	32.867	1.00	61.28	AAAA O
ATOM	4110	N	TYR	430	38.987	71.384	32.200	1.00	65.34	AAAA N
ATOM	4112	CA	TYR	430	39.729	72.543	32.719	1.00	68.10	AAAA C
ATOM	4113	CB	TYR	430	39.180	73.822	32.099	1.00	71.02	AAAA C
ATOM	4114	CG	TYR	430	39.538	74.006	30.639	1.00	75.98	AAAA C
ATOM	4115	CD1	TYR	430	38.653	73.821	29.599	1.00	77.60	AAAA C
ATOM	4116	CE1	TYR	430	38.953	73.977	28.270	1.00	75.72	AAAA C
ATOM	4117	CD2	TYR	430	40.810	74.401	30.260	1.00	75.95	AAAA C
ATOM	4118	CE2	TYR	430	41.155	74.575	28.937	1.00	74.81	AAAA C
ATOM	4119	CZ	TYR	430	40.221	74.359	27.952	1.00	78.51	AAAA C
ATOM	4120	OH	TYR	430	40.564	74.542	26.616	1.00	85.40	AAAA O
ATOM	4122	C	TYR	430	39.779	72.634	34.241	1.00	63.72	AAAA C
ATOM	4123	O	TYR	430	40.654	73.321	34.758	1.00	58.26	AAAA O
ATOM	4124	N	ARG	431	38.819	72.017	34.907	1.00	65.53	AAAA N
ATOM	4126	CA	ARG	431	38.747	72.043	36.356	1.00	68.15	AAAA C
ATOM	4127	CB	ARG	431	37.348	71.748	36.898	1.00	73.32	AAAA C
ATOM	4128	CG	ARG	431	37.345	71.815	38.430	1.00	82.99	AAAA C
ATOM	4129	CD	ARG	431	37.270	73.279	38.860	1.00	88.39	AAAA C
ATOM	4130	NE	ARG	431	37.698	73.472	40.258	1.00	92.48	AAAA N
ATOM	4132	CZ	ARG	431	36.835	73.258	41.259	1.00	94.93	AAAA C
ATOM	4133	NH1	ARG	431	35.610	72.872	40.872	1.00	87.40	AAAA N
ATOM	4136	NH2	ARG	431	37.021	73.371	42.567	1.00	95.17	AAAA N
ATOM	4139	C	ARG	431	39.718	70.986	36.877	1.00	67.75	AAAA C
ATOM	4140	O	ARG	431	40.637	71.292	37.629	1.00	66.74	AAAA O
ATOM	4141	N	MET	432	39.541	69.791	36.305	1.00	63.87	AAAA N
ATOM	4143	CA	MET	432	40.437	68.703	36.652	1.00	64.40	AAAA C

ATOM	4144	CB	MET	432	40.237	67.522	35.719	1.00	54.25	AAAA C
ATOM	4145	CG	MET	432	41.254	66.426	35.971	1.00	40.18	AAAA C
ATOM	4146	SD	MET	432	40.829	64.925	35.112	1.00	52.21	AAAA S
ATOM	4147	CE	MET	432	41.582	63.681	36.137	1.00	54.89	AAAA C
ATOM	4148	C	MET	432	41.891	69.170	36.626	1.00	64.65	AAAA C
ATOM	4149	O	MET	432	42.530	68.992	37.653	1.00	65.88	AAAA O
ATOM	4150	N	GLU	433	42.331	69.811	35.556	1.00	65.78	AAAA N
ATOM	4152	CA	GLU	433	43.622	70.469	35.510	1.00	69.16	AAAA C
ATOM	4153	CB	GLU	433	43.704	71.506	34.401	1.00	69.58	AAAA C
ATOM	4154	CG	GLU	433	44.121	70.967	33.048	1.00	76.91	AAAA C
ATOM	4155	CD	GLU	433	44.623	72.149	32.242	1.00	82.02	AAAA C
ATOM	4156	OE1	GLU	433	44.718	73.224	32.874	1.00	86.82	AAAA O
ATOM	4157	OE2	GLU	433	44.905	72.050	31.042	1.00	88.26	AAAA O
ATOM	4158	C	GLU	433	44.016	71.219	36.781	1.00	71.29	AAAA C
ATOM	4159	O	GLU	433	45.133	71.083	37.294	1.00	74.29	AAAA O
ATOM	4160	N	GLU	434	43.178	72.120	37.280	1.00	72.93	AAAA N
ATOM	4162	CA	GLU	434	43.505	72.873	38.485	1.00	72.88	AAAA C
ATOM	4163	CB	GLU	434	42.458	73.916	38.840	1.00	81.36	AAAA C
ATOM	4164	CG	GLU	434	41.191	73.956	38.032	1.00	83.34	AAAA C
ATOM	4165	CD	GLU	434	40.181	75.004	38.432	1.00	97.32	AAAA C
ATOM	4166	OE1	GLU	434	39.521	74.928	39.505	1.00	97.34	AAAA O
ATOM	4167	OE2	GLU	434	40.080	75.941	37.583	1.00	99.95	AAAA O
ATOM	4168	C	GLU	434	43.675	71.886	39.632	1.00	71.46	AAAA C
ATOM	4169	O	GLU	434	44.728	71.858	40.251	1.00	78.49	AAAA O
ATOM	4170	N	VAL	435	42.670	71.095	39.926	1.00	66.34	AAAA N
ATOM	4172	CA	VAL	435	42.711	70.129	41.001	1.00	62.49	AAAA C
ATOM	4173	CB	VAL	435	41.451	69.217	40.972	1.00	60.38	AAAA C
ATOM	4174	CG1	VAL	435	41.547	68.214	42.104	1.00	52.32	AAAA C
ATOM	4175	CG2	VAL	435	40.203	70.073	41.029	1.00	50.79	AAAA C
ATOM	4176	C	VAL	435	43.939	69.253	41.018	1.00	60.74	AAAA C
ATOM	4177	O	VAL	435	44.607	69.165	42.034	1.00	62.37	AAAA O
ATOM	4178	N	THR	436	44.282	68.506	39.988	1.00	60.67	AAAA N
ATOM	4180	CA	THR	436	45.335	67.516	39.936	1.00	56.36	AAAA C
ATOM	4181	CB	THR	436	45.199	66.565	38.736	1.00	50.92	AAAA C
ATOM	4182	OG1	THR	436	44.913	67.283	37.503	1.00	47.03	AAAA O
ATOM	4184	CG2	THR	436	44.108	65.526	38.901	1.00	54.38	AAAA C
ATOM	4185	C	THR	436	46.701	68.184	39.930	1.00	60.55	AAAA C
ATOM	4186	O	THR	436	47.714	67.490	40.024	1.00	60.61	AAAA O
ATOM	4187	N	GLY	437	46.836	69.496	39.835	1.00	60.65	AAAA N
ATOM	4189	CA	GLY	437	48.102	70.164	39.749	1.00	59.47	AAAA C
ATOM	4190	C	GLY	437	48.800	69.964	38.424	1.00	64.78	AAAA C
ATOM	4191	O	GLY	437	49.923	70.254	38.245	1.00	62.70	AAAA O
ATOM	4192	N	THR	438	48.112	69.387	37.390	1.00	63.79	AAAA N
ATOM	4194	CA	THR	438	48.731	69.169	36.076	1.00	65.09	AAAA C
ATOM	4195	CB	THR	438	47.967	68.027	35.411	1.00	66.87	AAAA C
ATOM	4196	OG1	THR	438	46.600	68.385	35.731	1.00	62.22	AAAA O
ATOM	4198	CG2	THR	438	48.209	66.659	36.019	1.00	68.74	AAAA C
ATOM	4199	C	THR	438	48.590	70.415	35.220	1.00	66.14	AAAA C
ATOM	4200	O	THR	438	49.003	70.543	34.070	1.00	69.06	AAAA O
ATOM	4201	N	LYS	439	48.089	71.481	35.822	1.00	67.37	AAAA N
ATOM	4203	CA	LYS	439	47.927	72.757	35.154	1.00	71.08	AAAA C
ATOM	4204	CB	LYS	439	47.114	73.708	36.034	1.00	69.23	AAAA C
ATOM	4205	CG	LYS	439	46.677	74.938	35.265	1.00	77.26	AAAA C
ATOM	4206	CD	LYS	439	45.832	75.942	36.014	1.00	81.65	AAAA C
ATOM	4207	CE	LYS	439	44.385	75.475	36.182	1.00	87.39	AAAA C
ATOM	4208	NZ	LYS	439	43.667	76.431	37.100	1.00	93.85	AAAA N
ATOM	4212	C	LYS	439	49.249	73.396	34.752	1.00	73.01	AAAA C
ATOM	4213	O	LYS	439	49.996	73.986	35.541	1.00	74.60	AAAA O
ATOM	4214	N	GLY	440	49.517	73.453	33.441	1.00	73.33	AAAA N
ATOM	4216	CA	GLY	440	50.733	74.167	33.014	1.00	71.39	AAAA C
ATOM	4217	C	GLY	440	51.716	73.204	32.389	1.00	71.20	AAAA C
ATOM	4218	O	GLY	440	52.684	73.650	31.822	1.00	72.70	AAAA O
ATOM	4219	N	ARG	441	51.445	71.908	32.436	1.00	72.99	AAAA N
ATOM	4221	CA	ARG	441	52.343	70.945	31.831	1.00	74.12	AAAA C
ATOM	4222	CB	ARG	441	52.617	69.740	32.716	1.00	69.44	AAAA C
ATOM	4223	CG	ARG	441	51.847	69.695	34.003	1.00	63.34	AAAA C
ATOM	4224	CD	ARG	441	52.060	68.314	34.595	1.00	67.64	AAAA C
ATOM	4225	NE	ARG	441	52.244	68.395	36.030	1.00	61.00	AAAA N
ATOM	4227	CZ	ARG	441	52.326	67.357	36.831	1.00	59.21	AAAA C
ATOM	4228	NH1	ARG	441	52.258	66.117	36.395	1.00	60.57	AAAA N
ATOM	4231	NH2	ARG	441	52.468	67.596	38.128	1.00	72.94	AAAA N
ATOM	4234	C	ARG	441	51.760	70.446	30.511	1.00	73.50	AAAA C
ATOM	4235	O	ARG	441	52.195	69.424	30.012	1.00	74.73	AAAA O
ATOM	4236	N	GLN	442	50.732	71.114	30.043	1.00	74.69	AAAA N
ATOM	4239	CA	GLN	442	49.959	70.646	28.914	1.00	75.13	AAAA C
ATOM	4239	CB	GLN	442	48.457	70.875	29.126	1.00	68.73	AAAA C
ATOM	4240	CG	GLN	442	47.669	69.576	29.195	1.00	71.20	AAAA C
ATOM	4241	CD	GLN	442	47.623	69.028	30.607	1.00	70.98	AAAA C
ATOM	4242	OE1	GLN	442	47.714	67.822	30.868	1.00	78.66	AAAA O
ATOM	4243	NE2	GLN	442	47.477	69.907	31.584	1.00	66.86	AAAA N
ATOM	4246	C	GLN	442	50.326	71.359	27.627	1.00	77.69	AAAA C
ATOM	4247	O	GLN	442	50.227	72.569	27.530	1.00	75.57	AAAA O
ATOM	4248	N	ALA	443	50.474	70.554	26.575	1.00	81.54	AAAA N
ATOM	4250	CA	ALA	443	50.643	71.148	25.236	1.00	82.95	AAAA C
ATOM	4251	CB	ALA	443	51.104	70.118	24.220	1.00	81.69	AAAA C

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ATOM   4252  C   ALA   443      49.259  71.706  24.952  1.00 83.73      AAAA C
ATOM   4253  O   ALA   443      48.398  71.744  25.830  1.00 83.87      AAAA O
ATOM   4254  N   LYS   444      48.914  72.052  23.713  1.00 86.20      AAAA N
ATOM   4256  CA  LYS   444      47.559  72.524  23.482  1.00 85.88      AAAA C
ATOM   4257  CB  LYS   444      47.426  73.997  23.128  1.00 83.99      AAAA C
ATOM   4258  CG  LYS   444      46.673  74.734  24.241  1.00 93.60      AAAA C
ATOM   4259  CD  LYS   444      45.883  73.841  25.186  1.00 95.14      AAAA C
ATOM   4260  CE  LYS   444      46.390  73.786  26.614  1.00 97.04      AAAA C
ATOM   4261  NZ  LYS   444      45.368  73.090  27.473  1.00 97.22      AAAA N
ATOM   4265  C   LYS   444      46.659  71.779  22.508  1.00 84.20      AAAA C
ATOM   4266  O   LYS   444      45.428  71.901  22.635  1.00 85.63      AAAA O
ATOM   4267  N   GLY   445      47.214  70.734  21.916  1.00 78.85      AAAA N
ATOM   4269  CA  GLY   445      46.368  69.786  21.208  1.00 75.06      AAAA C
ATOM   4270  C   GLY   445      45.803  68.844  22.260  1.00 72.30      AAAA C
ATOM   4271  O   GLY   445      44.963  67.993  21.940  1.00 74.90      AAAA O
ATOM   4272  N   ASP   446      46.300  68.981  23.492  1.00 67.97      AAAA N
ATOM   4274  CA  ASP   446      45.914  68.174  24.642  1.00 62.81      AAAA C
ATOM   4275  CB  ASP   446      46.754  68.552  25.873  1.00 55.24      AAAA C
ATOM   4276  CG  ASP   446      48.213  68.169  25.801  1.00 54.07      AAAA C
ATOM   4277  OD1 ASP   446      48.693  67.385  24.946  1.00 45.08      AAAA O
ATOM   4278  OD2 ASP   446      49.091  68.595  26.593  1.00 50.12      AAAA O
ATOM   4279  C   ASP   446      44.438  68.274  25.016  1.00 58.07      AAAA C
ATOM   4280  O   ASP   446      43.610  67.369  25.127  1.00 55.59      AAAA O
ATOM   4281  N   ILE   447      44.043  69.527  25.226  1.00 54.13      AAAA N
ATOM   4283  CA  ILE   447      42.652  69.822  25.510  1.00 54.09      AAAA C
ATOM   4284  CB  ILE   447      42.505  70.502  26.877  1.00 48.92      AAAA C
ATOM   4285  CG2 ILE   447      41.030  70.663  27.182  1.00 41.02      AAAA C
ATOM   4286  CG1 ILE   447      43.211  69.621  27.932  1.00 52.36      AAAA C
ATOM   4287  CD1 ILE   447      43.468  70.329  29.237  1.00 48.47      AAAA C
ATOM   4288  C   ILE   447      42.027  70.591  24.364  1.00 53.06      AAAA C
ATOM   4289  O   ILE   447      41.718  71.772  24.423  1.00 56.08      AAAA O
ATOM   4290  N   ASN   448      41.625  69.915  23.307  1.00 53.17      AAAA N
ATOM   4292  CA  ASN   448      41.013  70.642  22.202  1.00 54.61      AAAA C
ATOM   4293  CB  ASN   448      41.283  69.982  20.863  1.00 49.17      AAAA C
ATOM   4294  CG  ASN   448      40.415  68.786  20.577  1.00 49.40      AAAA C
ATOM   4295  OD1 ASN   448      39.287  68.977  20.113  1.00 52.34      AAAA O
ATOM   4296  ND2 ASN   448      40.990  67.622  20.871  1.00 52.49      AAAA N
ATOM   4299  C   ASN   448      39.518  70.824  22.402  1.00 56.44      AAAA C
ATOM   4300  O   ASN   448      38.916  69.974  22.939  1.00 55.83      AAAA O
ATOM   4301  N   THR   449      39.071  71.917  21.764  1.00 58.52      AAAA N
ATOM   4303  CA  THR   449      37.682  72.351  21.901  1.00 58.62      AAAA C
ATOM   4304  CB  THR   449      37.497  73.945  22.169  1.00 55.90      AAAA C
ATOM   4305  OG1 THR   449      37.913  74.485  20.943  1.00 68.89      AAAA O
ATOM   4307  CG2 THR   449      38.354  74.352  23.310  1.00 59.06      AAAA C
ATOM   4308  C   THR   449      36.920  72.053  20.628  1.00 56.82      AAAA C
ATOM   4309  O   THR   449      35.750  72.381  20.473  1.00 60.87      AAAA O
ATOM   4310  N   ARG   450      37.539  71.304  19.757  1.00 55.76      AAAA N
ATOM   4312  CA  ARG   450      36.887  70.935  18.507  1.00 54.66      AAAA C
ATOM   4313  CB  ARG   450      37.945  71.179  17.377  1.00 48.33      AAAA C
ATOM   4314  CG  ARG   450      38.395  69.975  16.645  1.00 54.81      AAAA C
ATOM   4315  CD  ARG   450      39.487  70.561  15.696  1.00 44.92      AAAA C
ATOM   4316  NE  ARG   450      40.706  70.719  16.488  1.00 52.49      AAAA N
ATOM   4318  CZ  ARG   450      41.544  69.757  16.882  1.00 39.09      AAAA C
ATOM   4319  NH1 ARG   450      41.176  68.572  16.466  1.00 41.07      AAAA N
ATOM   4322  NH2 ARG   450      42.601  70.001  17.610  1.00 45.18      AAAA N
ATOM   4325  C   ARG   450      36.267  69.553  18.557  1.00 56.82      AAAA C
ATOM   4326  O   ARG   450      35.186  69.303  17.992  1.00 58.15      AAAA O
ATOM   4327  N   ASN   451      36.800  68.583  19.324  1.00 56.66      AAAA N
ATOM   4329  CA  ASN   451      36.107  67.311  19.434  1.00 50.27      AAAA C
ATOM   4330  CB  ASN   451      36.725  66.127  18.760  1.00 48.54      AAAA C
ATOM   4331  CG  ASN   451      38.243  66.143  18.764  1.00 60.51      AAAA C
ATOM   4332  OD1 ASN   451      38.779  66.279  19.855  1.00 53.45      AAAA O
ATOM   4333  ND2 ASN   451      38.707  65.976  17.506  1.00 54.88      AAAA N
ATOM   4336  C   ASN   451      35.849  66.854  20.869  1.00 52.97      AAAA C
ATOM   4337  O   ASN   451      35.330  65.750  21.096  1.00 49.71      AAAA O
ATOM   4338  N   ASN   452      36.126  67.668  21.851  1.00 51.98      AAAA N
ATOM   4340  CA  ASN   452      35.769  67.485  23.229  1.00 55.88      AAAA C
ATOM   4341  CB  ASN   452      36.947  67.873  24.136  1.00 54.62      AAAA C
ATOM   4342  CG  ASN   452      37.936  66.736  24.285  1.00 60.96      AAAA C
ATOM   4343  OD1 ASN   452      37.646  65.633  24.735  1.00 51.30      AAAA O
ATOM   4344  ND2 ASN   452      39.153  67.098  23.855  1.00 56.75      AAAA N
ATOM   4347  C   ASN   452      34.603  68.385  23.688  1.00 58.11      AAAA C
ATOM   4348  O   ASN   452      34.785  69.629  23.657  1.00 55.07      AAAA O
ATOM   4349  N   GLY   453      33.444  67.813  23.985  1.00 55.08      AAAA N
ATOM   4351  CA  GLY   453      32.313  68.658  24.296  1.00 59.47      AAAA C
ATOM   4352  C   GLY   453      31.500  69.269  23.174  1.00 64.95      AAAA C
ATOM   4353  O   GLY   453      30.302  69.603  23.276  1.00 65.71      AAAA O
ATOM   4354  N   GLU   454      31.910  69.109  21.910  1.00 67.44      AAAA N
ATOM   4356  CA  GLU   454      31.266  69.543  20.690  1.00 63.63      AAAA C
ATOM   4357  CB  GLU   454      31.739  68.818  19.401  1.00 53.71      AAAA C
ATOM   4358  CG  GLU   454      32.348  67.430  19.738  1.00 49.50      AAAA C
ATOM   4359  CD  GLU   454      32.368  66.620  18.454  1.00 54.61      AAAA C
ATOM   4360  OE1 GLU   454      31.368  66.637  17.702  0.01 54.10      AAAA O
ATOM   4361  OE2 GLU   454      33.417  66.003  18.160  0.01 54.17      AAAA O
ATOM   4362  C   GLU   454      29.762  69.301  20.767  1.00 65.41      AAAA C
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ATOM	4363	O	GLU	454	29.022	70.089	20.169	1.00	67.86	AAAA O
ATOM	4364	N	ARG	455	29.288	68.187	21.333	1.00	66.45	AAAA N
ATOM	4366	CA	ARG	455	27.943	67.997	21.371	1.00	69.33	AAAA C
ATOM	4367	CB	ARG	455	27.448	66.733	20.652	1.00	73.38	AAAA C
ATOM	4368	CG	ARG	455	28.467	65.912	19.924	1.00	74.27	AAAA C
ATOM	4369	CD	ARG	455	27.775	64.740	19.240	1.00	79.54	AAAA C
ATOM	4370	NE	ARG	455	27.301	63.638	20.052	1.00	86.31	AAAA N
ATOM	4372	CZ	ARG	455	27.802	62.412	20.189	1.00	88.60	AAAA C
ATOM	4373	NH1	ARG	455	28.890	61.997	19.538	1.00	84.51	AAAA N
ATOM	4376	NH2	ARG	455	27.225	61.523	21.003	1.00	87.36	AAAA N
ATOM	4379	C	ARG	455	27.213	67.934	22.756	1.00	67.35	AAAA C
ATOM	4380	O	ARG	455	26.423	67.025	22.961	1.00	66.26	AAAA O
ATOM	4381	N	ALA	456	27.499	68.879	23.623	1.00	66.52	AAAA N
ATOM	4383	CA	ALA	456	26.947	68.906	24.964	1.00	72.01	AAAA C
ATOM	4384	CB	ALA	456	27.832	68.147	25.939	1.00	61.84	AAAA C
ATOM	4385	C	ALA	456	26.802	70.379	25.371	1.00	75.25	AAAA C
ATOM	4386	O	ALA	456	27.706	71.219	25.202	1.00	81.30	AAAA O
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ATOM	4389	CA	SER	457	25.431	72.095	26.358	0.50	69.64	AAAA C
ATOM	4390	CB	SER	457	23.991	72.247	26.836	0.50	73.30	AAAA C
ATOM	4391	OG	SER	457	23.422	73.294	26.060	0.50	73.31	AAAA O
ATOM	4393	C	SER	457	26.418	72.510	27.437	0.50	69.27	AAAA C
ATOM	4394	O	SER	457	26.458	71.957	28.530	0.50	67.32	AAAA O
ATOM	4395	N	CYS	458	27.197	73.531	27.117	0.50	70.44	AAAA N
ATOM	4397	CA	CYS	458	28.287	73.960	27.972	0.50	72.57	AAAA C
ATOM	4398	C	CYS	458	27.949	75.205	28.757	0.50	72.54	AAAA C
ATOM	4399	O	CYS	458	27.065	75.128	29.606	0.50	76.63	AAAA O
ATOM	4400	CB	CYS	458	29.527	74.171	27.089	0.50	75.38	AAAA C
ATOM	4401	SG	CYS	458	30.844	73.032	27.490	0.50	72.18	AAAA S
ATOM	4402	N	ALA	459	28.607	76.306	28.441	0.50	70.13	AAAA N
ATOM	4404	CA	ALA	459	28.445	77.572	29.116	0.50	70.05	AAAA C
ATOM	4405	CB	ALA	459	27.046	78.149	28.996	0.50	70.57	AAAA C
ATOM	4406	C	ALA	459	28.826	77.461	30.601	0.50	70.13	AAAA C
ATOM	4407	O	ALA	459	29.080	78.556	31.154	0.50	69.96	AAAA O
ATOM	4407	OT	ALA	459	28.856	76.301	31.054	0.50	68.22	AAAA O
ATOM	4522	C1	NAG	461	59.591	7.102	61.119	1.00	88.13	AAAA C
ATOM	4524	C2	NAG	461	59.964	7.338	59.697	1.00	91.94	AAAA C
ATOM	4526	N2	NAG	461	58.739	7.699	58.920	1.00	92.72	AAAA N
ATOM	4527	C7	NAG	461	58.400	9.020	58.999	1.00	96.97	AAAA C
ATOM	4529	O7	NAG	461	59.879	9.774	59.726	1.00	98.62	AAAA O
ATOM	4530	C8	NAG	461	57.323	9.390	58.043	1.00	100.60	AAAA C
ATOM	4534	C3	NAG	461	60.725	6.225	59.085	1.00	94.77	AAAA C
ATOM	4536	O3	NAG	461	61.417	6.725	57.930	1.00	98.51	AAAA O
ATOM	4539	C4	NAG	461	61.873	5.869	60.064	1.00	96.01	AAAA C
ATOM	4540	O4	NAG	461	62.661	4.921	59.484	1.00	99.20	AAAA O
ATOM	4542	C5	NAG	461	61.359	5.529	61.474	1.00	95.13	AAAA C
ATOM	4545	C6	NAG	461	62.465	5.321	62.495	1.00	93.66	AAAA C
ATOM	4548	O6	NAG	461	62.745	6.364	63.354	1.00	92.13	AAAA O
ATOM	4544	O5	NAG	461	60.625	6.648	61.949	1.00	91.92	AAAA O
ATOM	4550	C1	NAG	463	33.054	15.249	72.938	1.00	43.58	AAAA C
ATOM	4552	C2	NAG	463	31.644	15.292	73.412	1.00	43.62	AAAA C
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ATOM	4556	C7	NAG	463	29.912	13.584	73.099	1.00	40.84	AAAA C
ATOM	4557	O7	NAG	463	29.928	13.406	74.222	1.00	40.10	AAAA O
ATOM	4558	C8	NAG	463	28.975	12.694	72.394	1.00	35.47	AAAA C
ATOM	4562	C3	NAG	463	31.150	16.675	73.448	1.00	45.40	AAAA C
ATOM	4564	O3	NAG	463	29.979	16.555	74.196	1.00	45.99	AAAA O
ATOM	4566	C4	NAG	463	32.117	17.617	74.171	1.00	50.36	AAAA C
ATOM	4568	O4	NAG	463	31.596	18.919	73.891	1.00	53.97	AAAA O
ATOM	4569	C5	NAG	463	33.589	17.477	73.725	1.00	48.50	AAAA C
ATOM	4572	C6	NAG	463	34.490	17.996	74.742	1.00	49.34	AAAA C
ATOM	4575	O6	NAG	463	34.906	18.739	75.671	1.00	57.11	AAAA O
ATOM	4571	O5	NAG	463	33.942	16.120	73.583	1.00	48.58	AAAA O
ATOM	4576	C1	FUC	464	34.544	19.954	76.083	1.00	81.45	AAAA C
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ATOM	4584	O3	FUC	464	34.691	23.613	75.596	1.00	87.83	AAAA O
ATOM	4586	C4	FUC	464	33.871	22.274	77.412	1.00	86.67	AAAA C
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ATOM	4590	C5	FUC	464	33.921	20.894	78.040	1.00	85.85	AAAA C
ATOM	4593	C6	FUC	464	34.279	20.768	79.512	1.00	83.37	AAAA C
ATOM	4592	O5	FUC	464	35.042	20.150	77.425	1.00	82.43	AAAA O
ATOM	4597	C1	NAG	465	31.575	19.813	74.940	1.00	64.68	AAAA C
ATOM	4599	C2	NAG	465	31.267	21.207	74.437	1.00	69.57	AAAA C
ATOM	4601	N2	NAG	465	32.480	21.642	73.690	1.00	71.25	AAAA N
ATOM	4603	C7	NAG	465	32.401	21.953	72.381	1.00	73.86	AAAA C
ATOM	4604	O7	NAG	465	31.373	21.835	71.881	1.00	74.80	AAAA O
ATOM	4605	C8	NAG	465	33.679	22.401	71.787	1.00	76.00	AAAA C
ATOM	4609	C3	NAG	465	31.050	22.214	75.546	1.00	72.71	AAAA C
ATOM	4611	O3	NAG	465	30.713	23.517	75.108	1.00	71.03	AAAA O
ATOM	4613	C4	NAG	465	30.035	21.654	76.560	1.00	75.71	AAAA C
ATOM	4615	O4	NAG	465	29.993	22.409	77.793	1.00	76.79	AAAA O
ATOM	4617	C5	NAG	465	30.498	20.238	76.977	1.00	75.45	AAAA C
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ATOM	4620	O6	NAG	465	28.385	19.238	77.142	1.00	76.25	AAAA O
ATOM	4619	O5	NAG	465	30.514	19.425	75.807	1.00	71.44	AAAA O
ATOM	4625	C1	NAG	467	49.927	11.058	87.926	1.00	96.51	AAAA C
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ATOM	4629	N2	NAG	467	49.662	12.898	89.458	1.00	101.79	AAAA N
ATOM	4631	C7	NAG	467	49.299	13.021	90.759	1.00	103.63	AAAA C
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ATOM	4633	C8	NAG	467	48.526	14.239	91.102	1.00	105.02	AAAA C
ATOM	4637	C3	NAG	467	51.967	12.134	88.802	1.00	101.03	AAAA C
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ATOM	4685	C3	FUC	470	53.421	48.429	71.757	1.00	58.39	AAAA C
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ATOM	4707	O7	NAG	471	56.892	44.744	72.885	1.00	51.50	AAAA O
ATOM	4708	C8	NAG	471	58.202	42.814	73.323	1.00	46.02	AAAA C
ATOM	4712	C3	NAG	471	58.901	47.250	73.291	1.00	34.50	AAAA C
ATOM	4714	O3	NAG	471	59.698	46.917	74.385	1.00	35.84	AAAA O
ATOM	4716	C4	NAG	471	59.645	48.488	72.694	1.00	38.52	AAAA C
ATOM	4718	O4	NAG	471	59.754	49.464	73.694	1.00	37.44	AAAA O
ATOM	4719	C5	NAG	471	59.056	48.958	71.332	1.00	36.94	AAAA C
ATOM	4722	C6	NAG	471	60.116	49.692	70.525	1.00	36.14	AAAA C
ATOM	4726	O6	NAG	471	61.106	50.390	71.080	1.00	43.49	AAAA O
ATOM	4721	O5	NAG	471	58.853	47.785	70.530	1.00	34.98	AAAA O
ATOM	4727	C1	MAN	472	61.035	49.984	73.959	1.00	53.37	AAAA C
ATOM	4729	C2	MAN	472	60.920	51.497	74.260	1.00	56.72	AAAA C
ATOM	4730	O2	MAN	472	59.924	51.584	75.272	1.00	62.11	AAAA O
ATOM	4733	C3	MAN	472	62.216	52.031	74.840	1.00	60.70	AAAA C
ATOM	4735	O3	MAN	472	62.028	53.337	75.383	1.00	60.70	AAAA O
ATOM	4736	C4	MAN	472	62.787	51.161	75.932	1.00	55.46	AAAA C
ATOM	4738	O4	MAN	472	64.085	51.595	76.171	1.00	57.16	AAAA O
ATOM	4740	C5	MAN	472	62.797	49.685	75.511	1.00	52.10	AAAA C
ATOM	4743	C6	MAN	472	63.458	48.905	76.595	1.00	50.32	AAAA C
ATOM	4746	O6	MAN	472	62.990	48.969	77.885	1.00	51.02	AAAA O
ATOM	4742	O5	MAN	472	61.443	49.407	75.200	1.00	53.33	AAAA O
ATOM	4748	C1	MAN	473	62.594	54.401	74.672	1.00	72.61	AAAA C
ATOM	4750	C2	MAN	473	62.417	55.679	75.569	1.00	75.28	AAAA C
ATOM	4751	O2	MAN	473	63.378	56.709	75.348	1.00	74.98	AAAA O
ATOM	4754	C3	MAN	473	60.977	56.163	75.493	1.00	78.65	AAAA C
ATOM	4756	O3	MAN	473	60.841	57.447	76.148	1.00	79.16	AAAA O
ATOM	4758	C4	MAN	473	60.344	56.204	74.114	1.00	78.70	AAAA C
ATOM	4760	O4	MAN	473	58.983	56.571	74.178	1.00	78.93	AAAA O
ATOM	4762	C5	MAN	473	60.499	54.802	73.474	1.00	76.89	AAAA C
ATOM	4765	C6	MAN	473	59.968	54.490	72.091	1.00	74.73	AAAA C
ATOM	4768	O6	MAN	473	60.239	55.469	71.138	1.00	71.39	AAAA O
ATOM	4764	O5	MAN	473	61.916	54.562	73.463	1.00	74.97	AAAA O
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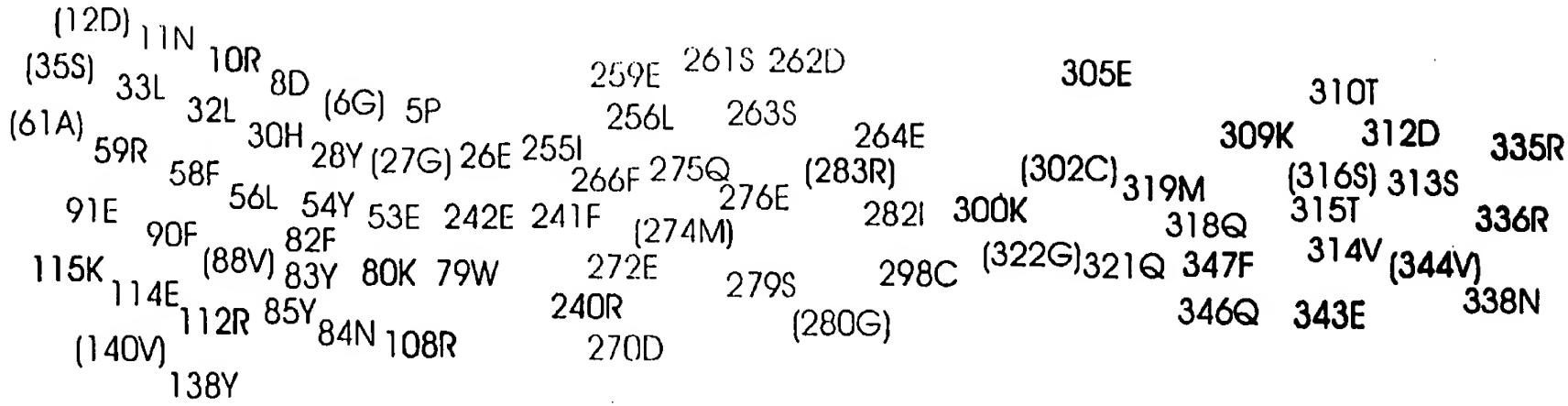
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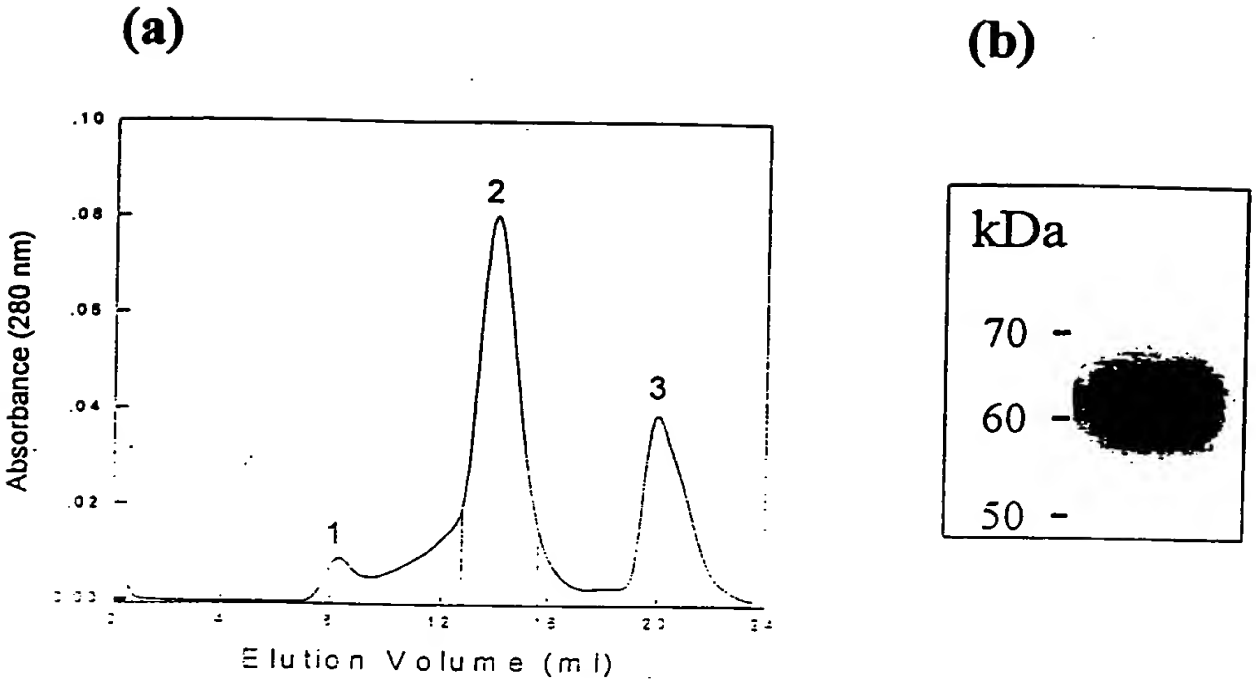
Figure 2


(a)
(b)
Absorbance (280 nm)
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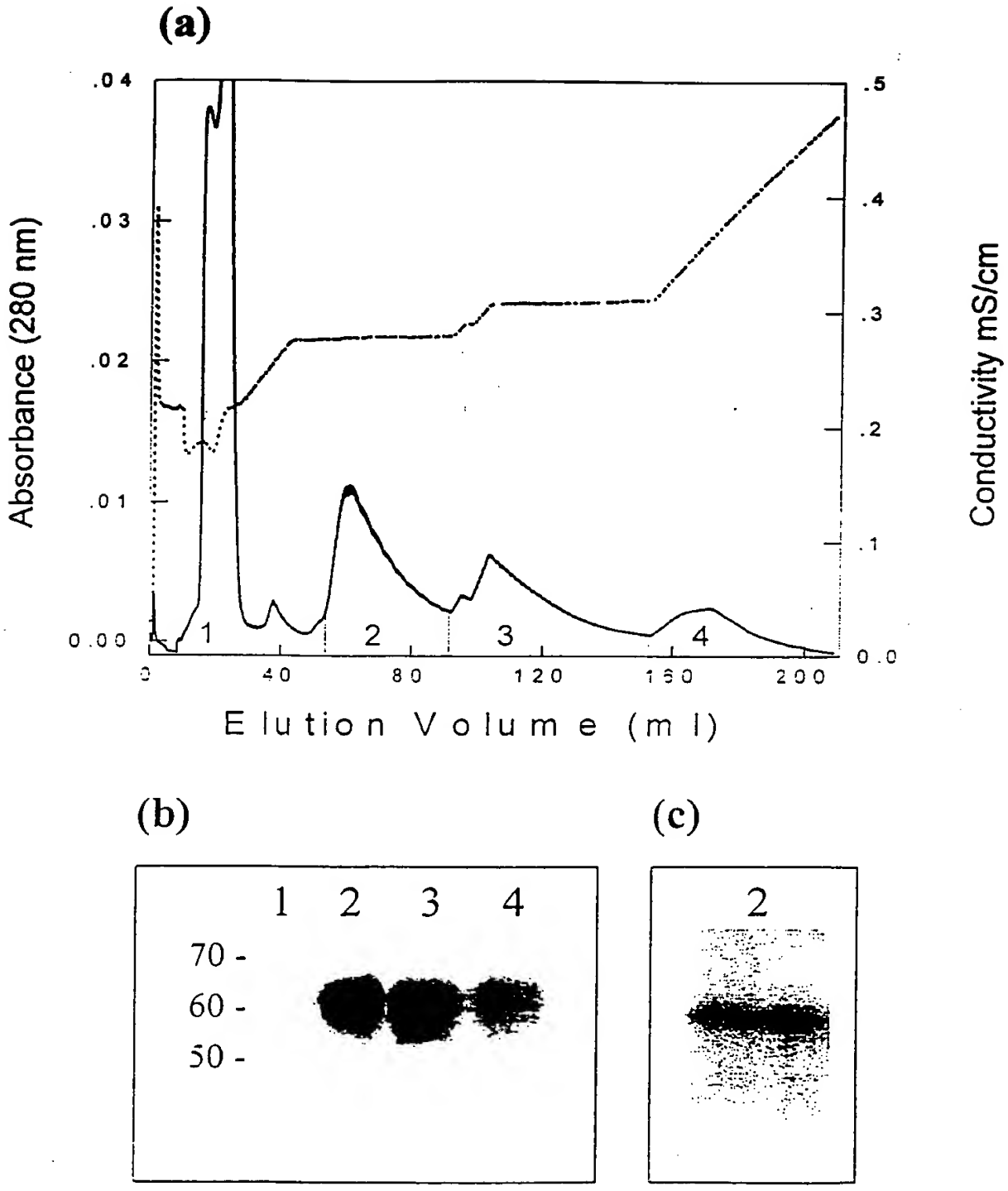
.08
.06
.04
.02
1
2
3
Elution Volume (ml)
kDa
70
60
50

Figure 3


(a)
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.03
.02
.01
0.00
Absorbance (280 nm)
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.4
.3
.2
.1
0.0
Conductivity mS/cm
1
2
3
4
0
40
80
120
160
200
Elution Volume (ml)
(b)
1 2 3 4
70 -
60 -
50 -
(c)
2

Figure 4

Figure 5

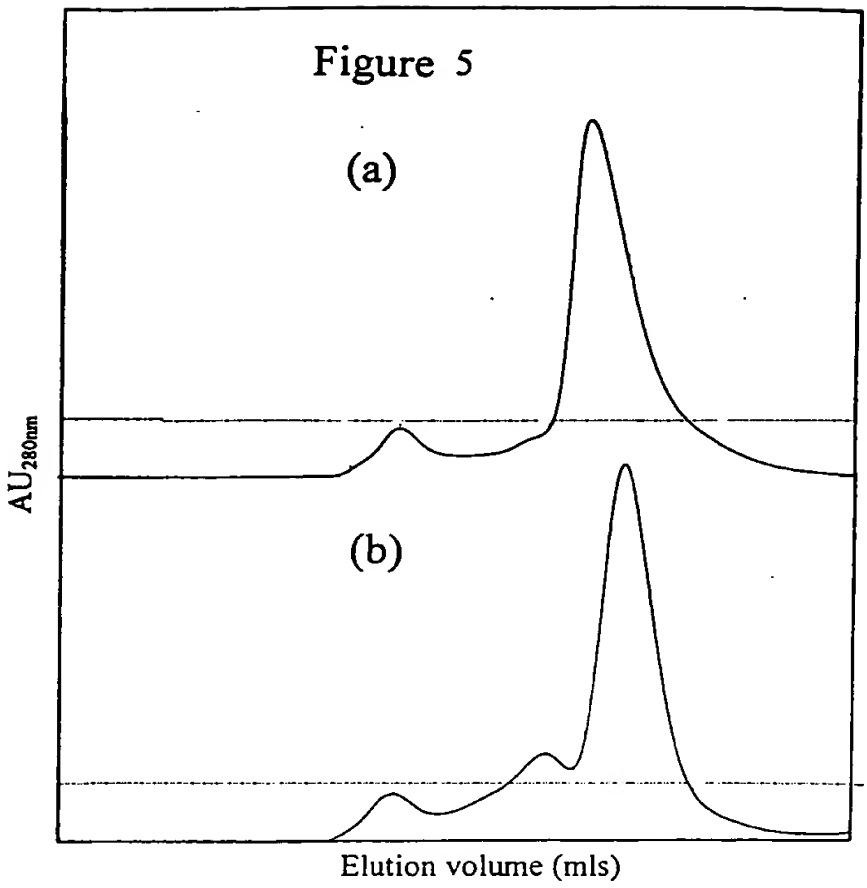
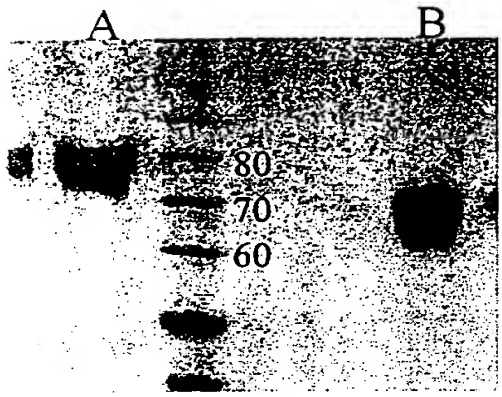
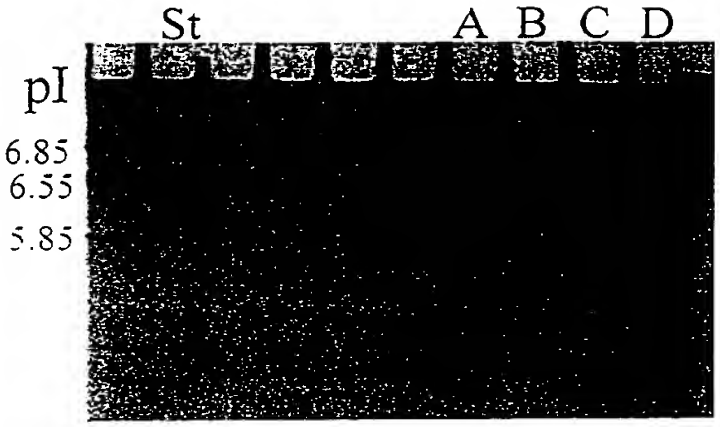


Figure 6

(a) SDS PAGE



(b) IEF pH3-7



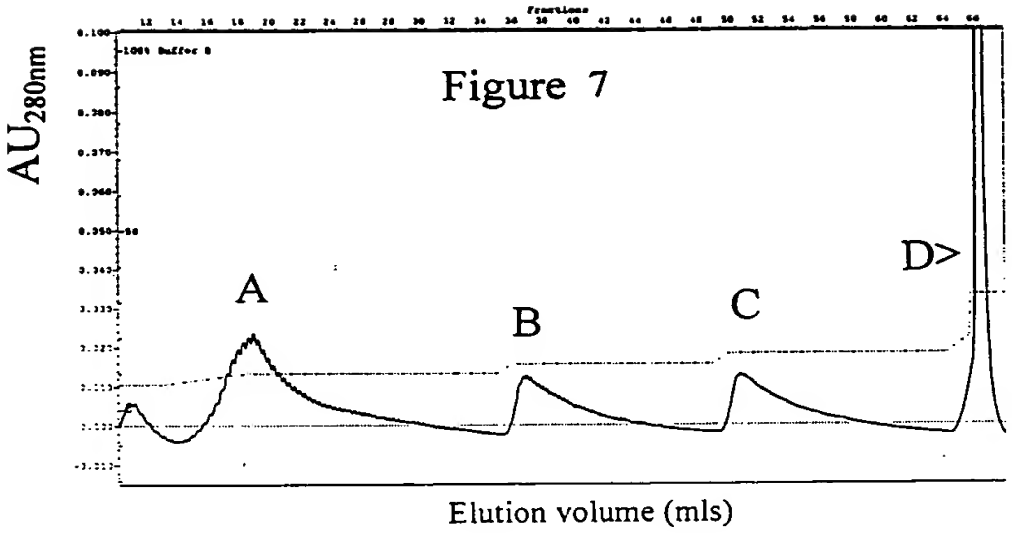
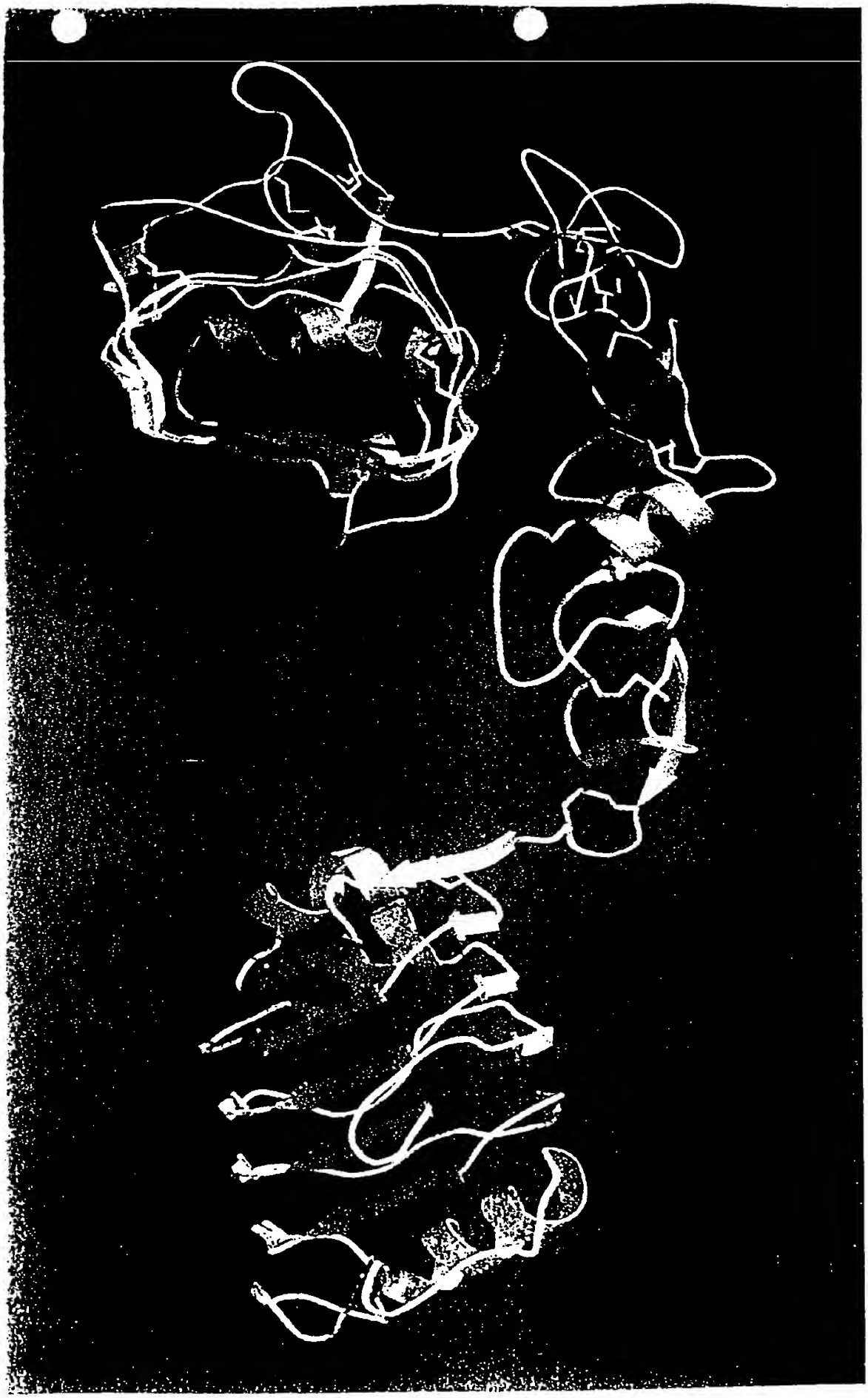
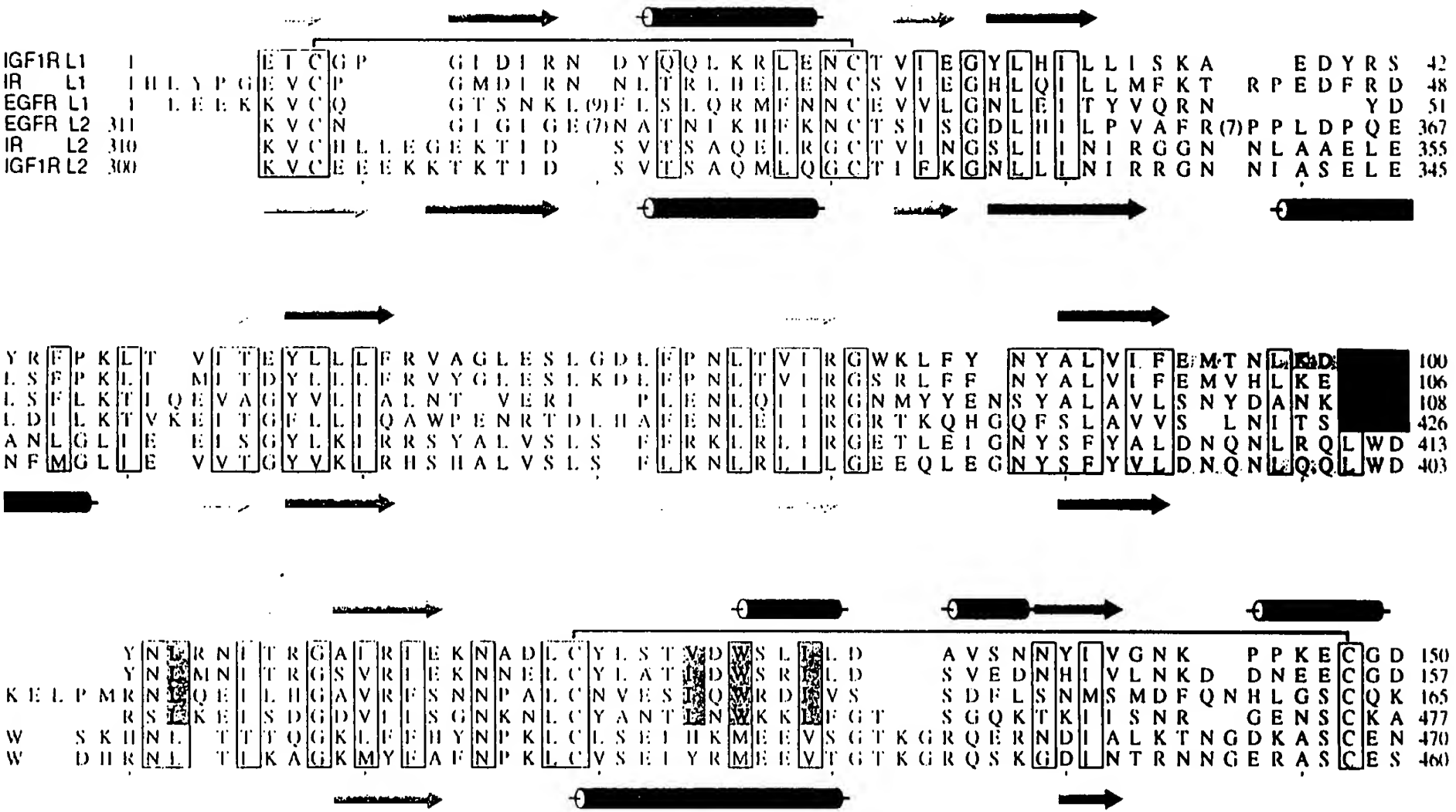
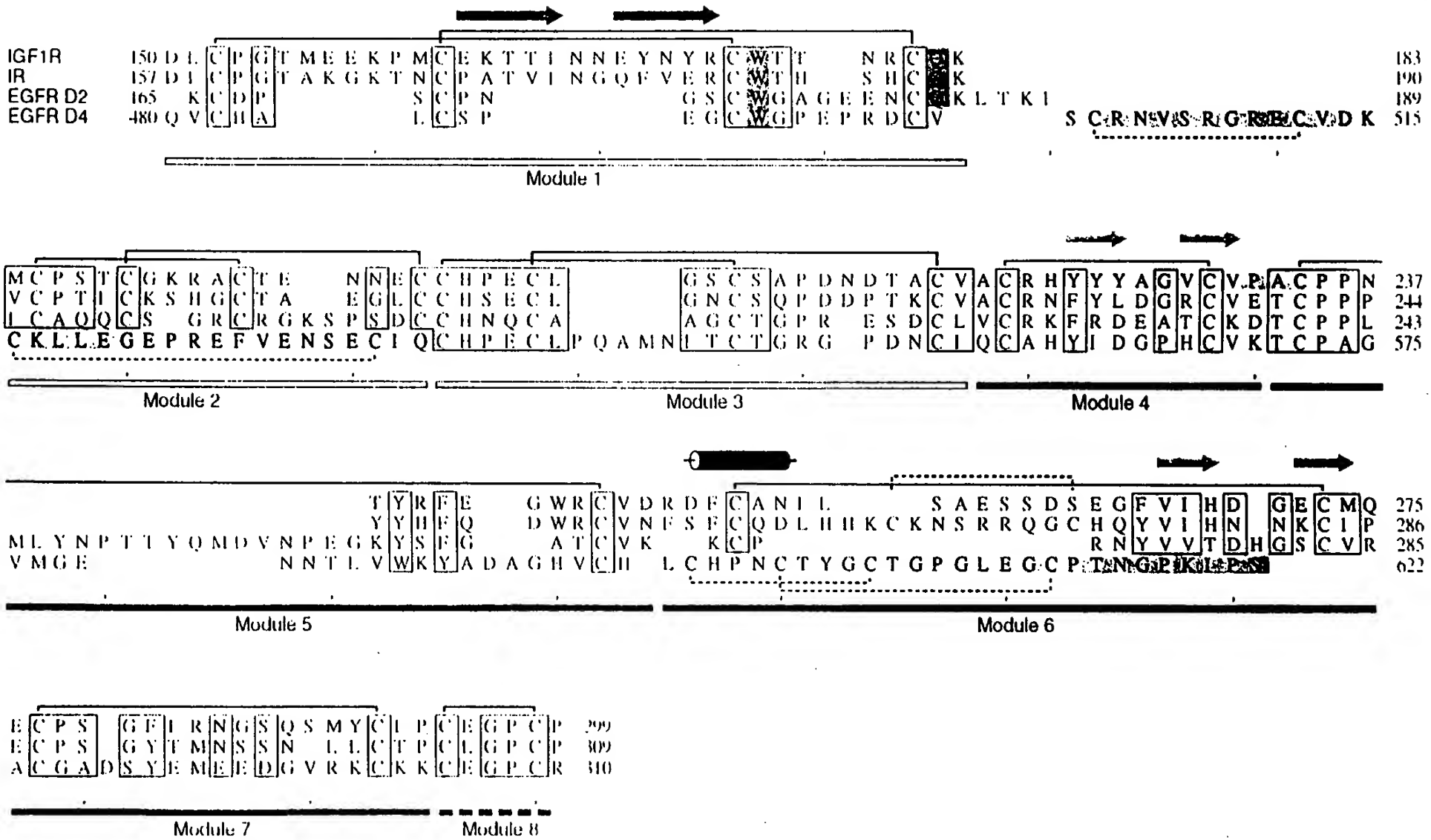


Figure 7




IGF1R L1
IR L1
EGFR L1
EGFR L2
IR L2
IGF1R L2


IGF1R
IR
EGFR D2
EGFR D4
Module 1
Module 2
Module 3
Module 4
Module 5
Module 6
Module 7
Module 8

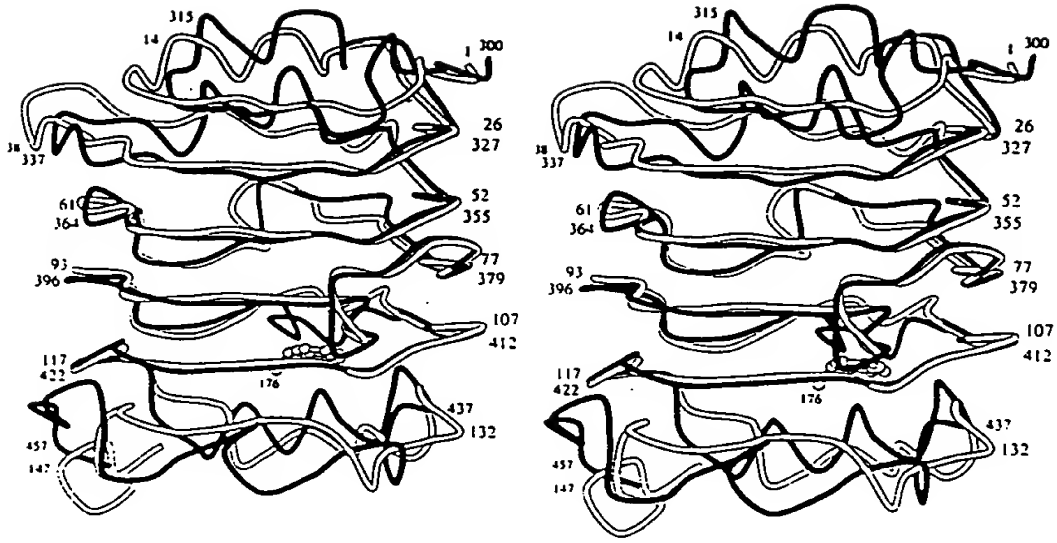

315
14
1
300
26
327
38
337
61
364
52
355
93
396
77
379
107
412
117
422
176
437
132
457
147

Figure 10

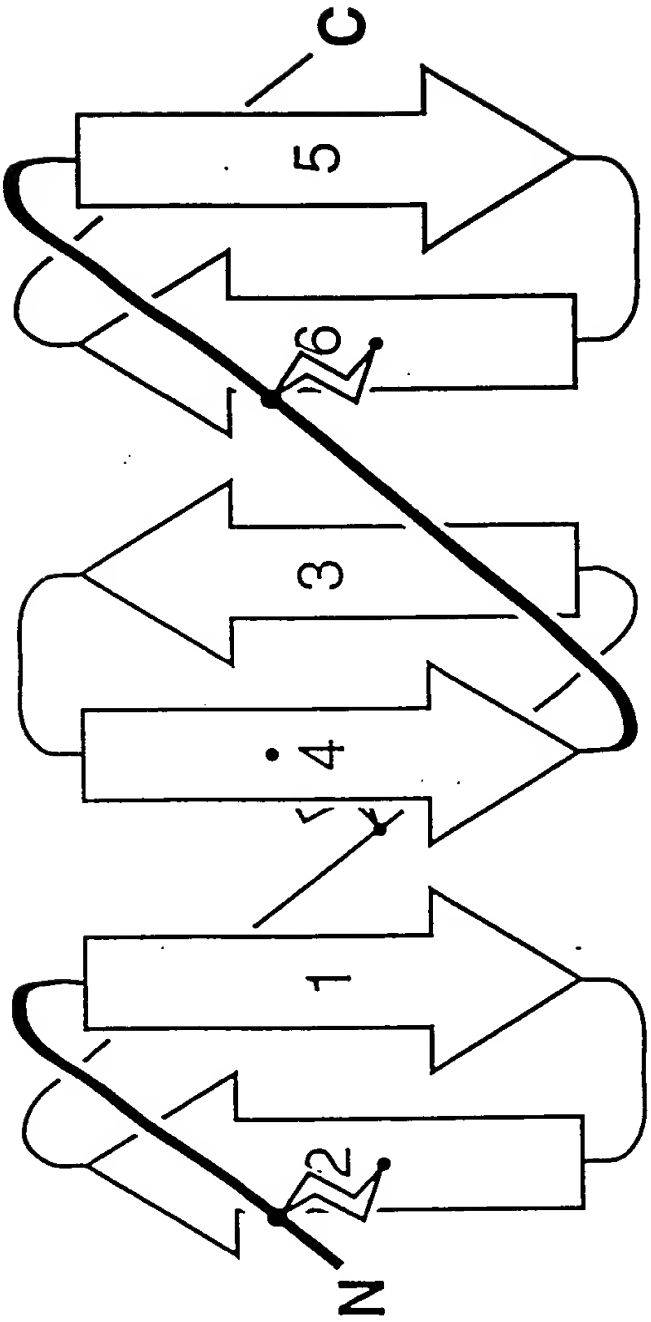


Figure 11

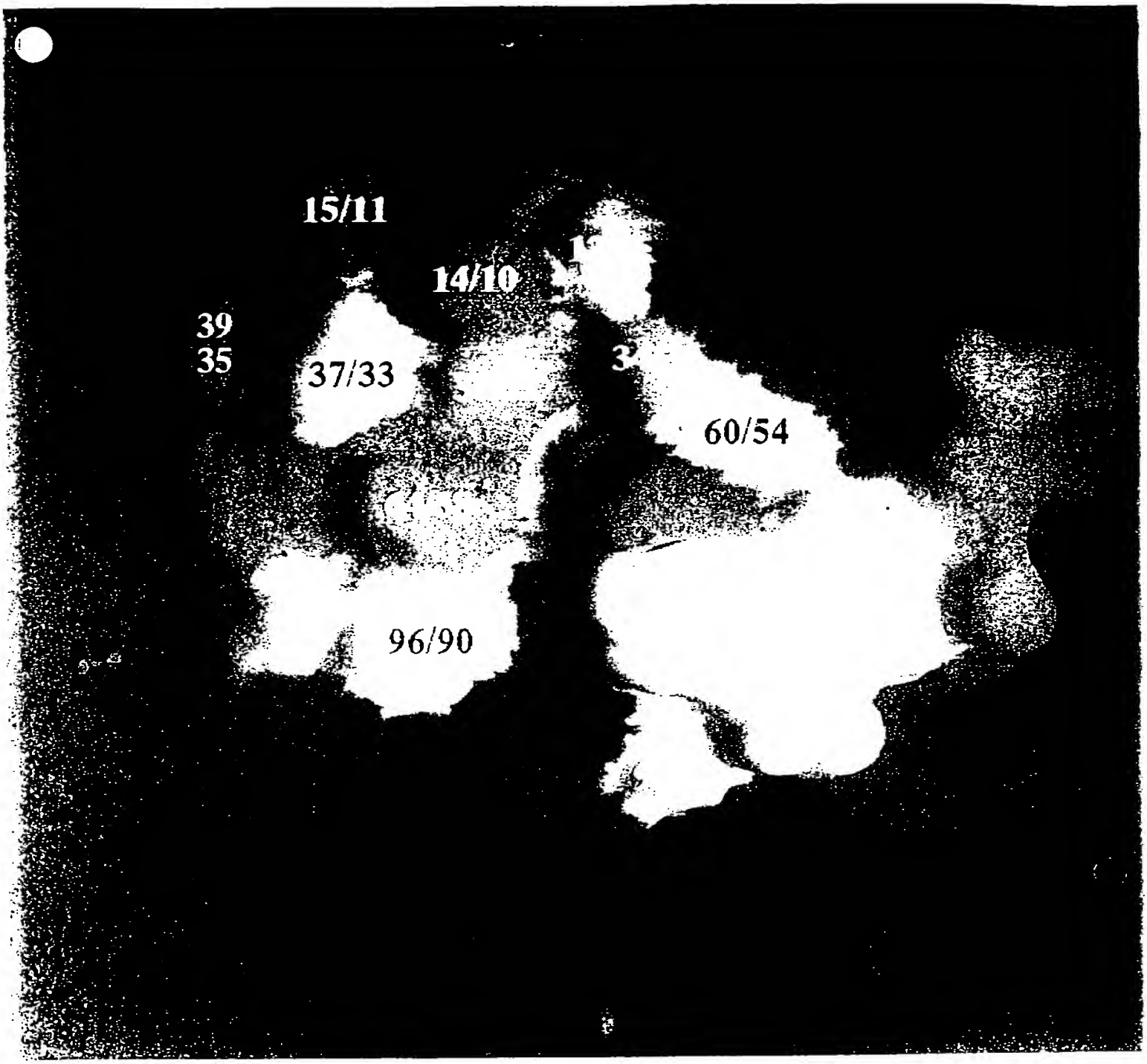


Figure 12

Figure 13: Sequence Alignment of hIGF-1R, hIR and hIRR ectodomains.

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

```
Symbol Comparison table: GenRunData:PileUpPep.Cmp  CompCheck: 1254

                 GapWeight: 3.0
           GapLengthWeight: 0.1

 Name: Higf1r          Len:   972  Check: 1781  Weight:  1.00
 Name: Hir             Len:   972  Check: 2986  Weight:  1.00
 Name: Hirr            Len:   972  Check: 9819  Weight:  1.00

            *                       *
Higf1r  .....EICGP GIDIRNDYQQ LKRLENCTVI EGYLHILLIS K..AEDYRSY 43
  Hir   HLYPGEVC.P GMDIRNNLTR LHELENCSVI EGHLQILLMF KTRPEDFRDL 49
  Hirr  ....MNVC.P SLDIRSEVAE LRQLENCSVV EGHLQILLMF TATGEDFRGL 45

Higf1r  RFPKLTVITE YLLLFRVAGL ESLGDLFPNL TVIRGWKLFY NYALVIFEMT 93
  Hir   SFPKLIMITD YLLLFRVYGL ESLKDLFPNL TVIRGSRLFF NYALVIFEMV 99
  Hirr  SFPRLTQVTD YLLLFRVYGL ESLRDLFPNL AVIRGTRLFL GYALVIFEMP 95

                                      *
Higf1r  NLKDIGLYNL RNITRGAIRI EKNADLCYLS TVDWSLILDA VSNNYIVGNK 143
  Hir   HLKELGLYNL MNITRGSVRI EKNNELCYLA TIDWSRILDS VEDNYIVLNK 149
  Hirr  HLRDVALPAL GAVLRGAVRV EKNQELCHLS TIDWGLLQPA PGANHIVGNK 145

          *   *               *                *     *    *
Higf1r  PPK.ECGDLC PGTMEEKPM. CEKTTINNEY NYRCWTTNRC QKMCPSTCGK 191
  Hir   DDNEECGDIC PGTAKGKTN. CPATVINGQF VERCWTHSHC QKVCPTICKS 198
  Hirr  LG.EECADVC PGVLGAAGEP CAKTTFSGHT DYRCWTSSHC QRVCPCPHG. 193

        *     **    *   *          *  *          *    *
Higf1r  RACTENNECC HPECLGSCSA PDNDTACVAC RHYYYAGVCV PACPPNTYRF 241
  Hir   HGCTAEGLCC HSECLGNCSQ PDDPTKCVAC RNFYLDGRCV ETCPPPYYHF 248
  Hirr  MACTARGECC HTECLGGCSQ PEDPRACVAC RHLYFQGACL WACPPGTYQY 243

          *       *      *---------*          *   *
Higf1r  EGWRCVDRDF CANILSAES. ...SDSEGFV IHDGECMQEC PSGFIRNGSQ 287
  Hir   QDWRCVNFSF CQDLHHKCKN SRRQGCHQYV IHNNKCIPEC PSGYTMNSSN 298
  Hirr  ESWRCVTAER CASLHSVPG. ....RASTFG IHQGSCLAQC PSGFTRNSS. 287

        *  *    *   *                        *
Higf1r  SMYCIPCEGP CPKVCEEEKK TKTIDSVTSA QMLQGCTIFK GNLLINIRRG 337
  Hir   .LLCTPCLGP CPKVCHLLEG EKTIDSVTSA QELRGCTVIN GSLIINIRGG 347
  Hirr  SIFCHKCEGL CPKECKV..G TKTIDSIQAA QDLVGCTHVE GSLILNLRQG 335

Higf1r  NNIASELENF MGLIEVVTGY VKIRHSHALV SLSFLKNLRL ILGEEQLEGN  387
  Hir   NNLAAELEAN LGLIEEISGY LKIRRSYALV SLSFFRKLRL IRGETLEIGN  397
  Hirr  YNLEPQLQHS LGLVETITGF LKIKHSFALV SLGFFKNLKL IRGDAMVDGN  385

                                                  *
Higf1r  YSFYVLDNQN LQQLWDWDHR NLTIKAGKMY FAFNPKLCVS EIYRMEEVTG  437
  Hir   YSFYALDNQN LRQLWDWSKH NLTITQGKLF FHYNPKLCLS EIHKMEEVSG  447
  Hirr  YTLYVLDNQN LQQLGSWVAA GLTIPVGKIY FAFNPRLCLE HIYRLEEVTG  435

                                  *    !End of 1-462 fragment
Higf1r  TKGRQSKGDI NTRNNGERAS CESDV  LHFTS TTTSKNRIII TWHRYRPPDY  487
  Hir   TKGRQERNDI ALKTNGDQAS CENEL  LKFSY IRTSFDKILL RWEPYWPPDF  497
  Hirr  TRGRQNKAEI NPRTNGDRAA CQTRT  LRFVS NVTEADRILL RWERYEPLEA  485
```

```
                                        *
Higf1r  RDLISFTVYY KEAPFKNVTE YDGQDACGSN SWNMVDVDLP .....PNKDV  532
  Hir   RDLLGFMLFY KEAPYQNVTE FDGQDACGSN SWTVVDIDPP LRSNDPKSQN  547
 Hirr   RDLLSFIVYY KESPFQNATE HVGPDACGTQ SWNLLDVELP L.....SRTQ  530

Higf1r  EPGILLHGLK PWTQYAVYVK AVTLTMVEND HIRGAKSEIL YIRTNASVPS  582
  Hir   HPGWLMRGLK PWTQYAIFVK TL.VTFSDER RTYGAKSDII YVQTDATNPS  596
 Hirr   EPGVTLASLK PWTQYAVFVR AITLTTEEDS PHQGAQSPIV YLRTLPAAPT  580

Higf1r  IPLDVLSASN SSSQLIVKWN PPSLPNGNLS YYIVRWQRQP QDGYLYRHNY  632
  Hir   VPLDPISVSN SSSQIILKWK PPSDPNGNIT HYLVFWERQA EDSELFELDY  646
 Hirr   VPQDVISTSN SSSHLLVRWK PPTQRNGNLT YYLVLWQRLA EDGDLYLNDY  630

        *                                 *   ** **  *
Higf1r  CSKD.KIPIR KYADGTIDIE EVTENPKTEV CGGEKGPCCA C...PKTEAE  678
  Hir   CLKGLKLPSR TWS.PPFESE DSQKHNQSE. YEDSAGECCS C...PKTDSQ  691
 Hirr   CHRGLRLPTS N.NDPRFDGE DGDPEAEME. .....SDCCP CQHPPPGQVL  673

                                    α------->><------β
Higf1r  KQAEKEEAEY RKVFENFLHN SIFVPRPERK RRDVMQVANT TMSSRSRNTT  728
  Hir   ILKELEESSF RKTFEDYLHN VVFVPRPSRK RRSLGDVGNV TVAVP...TV  738
 Hirr   PPLEAQEASF QKKFENFLHN AITIPISPWK VTSINKSPQR D.SGRHRRAA  722
                                                              *
Higf1r  AA..DTYNIT DPEELETEYP FFESRVDNKE RTVISNLRPF TLYRIDIHSC 776
  Hir   AAFPNTSSTS VPTSPEEHRP F..EKVVNKE SLVISGLRHF TGYRIELQAC 786
 Hirr   GPLRLGGNSS DFEIQEDKVP ........RE RAVLSGLRHF TEYRIDIHAC 764

               *
Higf1r  NHEAEKLGCS ASNFVFARTM PAEGADDIPG PVTWEPRPEN SIFLKWPEPE 826
  Hir   NQDTPEERCS VAAYVSARTM PEAKADDIVG PVTHEIFENN VVHLMWQEPK 836
 Hirr   NHAAHTVGCS AATFVFARTM PHREADGIPG KVAWEASSKN SVLLRWLEPP 814

                                       *               *
Higf1r  NPNGLILMYE IKYGS.QVED QRECVSRQEY RKYGGAKLNR LNPGNYTARI 875
  Hir   EPNGLIVLYE VSYRRYGDEE LHLCVSRKHF ALERGCRLRG LSPGNYSVRI 886
 Hirr   DPNGLILKYE IKYRRLGEEA TVLCVSRLRY AKFGGVHLAL LPPGNYSARV 864

Higf1r  QATSLSGNGS WTDPVFFYVQ AKTGYENFIH L                     906
  Hir   RATSLAGNGS WTEPTYFYVT DYLDVPSNIA K                     917
 Hirr   RATSLAGNGS WTDSVAFYIL GPEEEDAGGL H                     895
```

Figure 14: Sequence Alignment of EGFR, ErbB2, ErbB3 and ErbB4 Ectodomains.

[For alignment on the IGF-1R fragment see Fig. 9]

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

```
Symbol comparison table: GenRunData:Pileuppep.Cmp  CompCheck: 1254

                 GapWeight: 3.000
           GapLengthWeight: 0.100

Name: Erb3             Len:   649  Check: 4625  Weight:  1.00
Name: Erb4             Len:   649  Check:  790  Weight:  1.00
Name: Egfr             Len:   649  Check: 2381  Weight:  1.00
Name: Erb2             Len:   649  Check: 8174  Weight:  1.00

     1                                                    50
Erb3  SEVGNSQAVC PGTLNGLSVT GDAENQYQTL YKLYERCEVV MGNLEIVLTG
Erb4  ...SDSQSVC AGTENKLSSL SDLEQQYRAL RKYYENCEVV MGNLEITSIE
Egfr  ...LEEKKVC QGTSNKLTQL GTFEDHFLSL QRMFNNCEVV LGNLEITYVQ
Erb2  .....STQVC TGTDMKLRLP ASPETHLDML RHLYQGCQVV QGNLELTYLP

     51                                                   100
Erb3  HNADLSFLQW IREVTGYVLV AMNEFSTLPL PNLRVVRGTQ VYDGKFAIFV
Erb4  HNRDLSFLRS VREVTGYVLV ALNQFRYLPL ENLRIIRGTK LYEDRYALAI
Egfr  RNYDLSFLKT IQEVAGYVLI ALNTVERIPL ENLQIIRGNM YYENSYALAV
Erb2  TNASLSFLQD IQEVQGYVLI AHNQVRQVPL QRLRIVRGTQ LFEDNYALAV

     101                                                  150
Erb3  MLNYN..... ....TNSSHA LRQLRLTQLT EILSGGVYIE KNDKLCHMDT
Erb4  FLNYR..... ....KDGNFG LQELGLKNLT EILNGGVYVD QNKFLCYADT
Egfr  LSNYD..... ....ANKT.G LKELPMRNLQ EILHGAVRFS NNPALCNVES
Erb2  LDNGDPLNNT TPVTGASPGG LRELQLRSLT EILKGGVLIQ RNPQLCYQDT

     151                                                  200
Erb3  IDWRDIVRDR ...DAEIVVK DNGRSCPPCH EVC.KGRCWG PGSEDCQTLT
Erb4  IHWQDIVRNP WPSNLTLVST NGSSGCGRCH KSC.TGRCWG PTENHCQTLT
Egfr  IQWRDIVSSD FLSNMSMDFQ NHLGSCQKCD PSCPNGSCWG AGEENCQKLT
Erb2  ILWKDIFHKN NQLALTLIDT NRSRACHPCS PMCKGSRCWG ESSEDCQSLT

     201                                                  250
Erb3  KTICAPQCNG HCFGPNPNQC CHDECAGGCS GPQDTDCFAC RHFNDSGACV
Erb4  RTVCAEQCDG RCYGPYVSDC CHRECAGGCS GPKDTDCFAC MNFNDSGACV
Egfr  KIICAQQCSG RCRGKSPSDC CHNQCAAGCT GPRESDCLVC RKFRDEATCK
Erb2  RTVCAGGC.A RCKGPLPTDC CHEQCAAGCT GPKHSDCLAC LHFNHSGICE

     251                                                  300
Erb3  PRCPQPLVYN KLTFQLEPNP HTKYQYGGVC VASCPHNFVV .DQTSCVRAC
Erb4  TQCPQTFVYN PTTFQLEHNF NAKYTYGAFC VKKCPHNFVV .DSSSCVRAC
Egfr  DTCPPLMLYN PTTYQMDVNP EGKYSFGATC VKKCPRNYVV TDHGSCVRAC
Erb2  LHCPALVTYN TDTFESMPNP EGRYTFGASC VTACPYNYLS TDVGSCTLVC

     301                                                  350
Erb3  PPDKMEV.DK NGLKMCEPCG GLCPKACEGT GSGSRF..QT VDSSNIDGFV
Erb4  PSSKMEV.EE NGIKMCKPCT DICPKACDGI GTGSLMSAQT VDSSNIDKFI
Egfr  GADSYEM.EE DGVRKCKKCE GPCRKVCNGI GIGEFKDSLS INATNIKHFK
Erb2  PLHNQEVTAE DGTQRCEKCS KPCARVCYGL GMEHLREVRA VTSANIQEFA

     351                                                  400
Erb3  NCTKILGNLD FLITGLNGDP WHKIPALDPE KLNVFRTVRE ITGYLNIQSW
Erb4  NCTKINGNLI FLVTGIHGDP YNAIEAIDPE KLNVFRTVRE ITGFLNIQSW
Egfr  NCTSISGDLH ILPVAFRGDS FTHTPPLDPQ ELDILKTVKE ITGFLLIQAW
Erb2  GCKKIFGSLA FLPESFDGDP ASNTAPLQPE QLQVFETLEE ITGYLYISAW

     401                                                  450
Erb3  PPHMHNFSVF SNLTTIGGRS LYNRGFSLLI MKNLNVTSLG FRSLKEISAG
Erb4  PPNMTDFSVF SNLVTIGGRV LYS.GLSLLI LKQQGITSLQ FQSLKEISAG
```

```
Egfr   PENRTDLHAF ENLEIIRGRT KQHGQFSLAV VS.LNITSLG LRSLKEISDG
Erb2   PDSLPDLSVF QNLQVIRGRI LHNGAYSL.T LQGLGISWLG LRSLRELGSG

       451                                End L2 domain>       500
Erb3   RIYISANRQL CYHHSLNWTK VLRGPTEERL DIKHNRPRRD CVA   EGKVCDP
Erb4   NIYITDNSNL CYYHTINWTT LF.STINQRI VIRDNRKAEN CTA   EGMVCNH
Egfr   DVIISGNKNL CYANTINWKK LF.GTSGQKT KIISNRGENS CKA   TGQVCHA
Erb2   LALIHHNTHL CFVHTVPWDQ LFRNP.HQAL LHTANRPEDE CVG   EGLACHQ

       501                                              550
Erb3   LCSSGGCWGP GPGQCLSCRN YSRGGVCVTH CNFLNGEPRE FAHEAECFSC
Erb4   LCSSDGCWGP GPDQCLSCRR FSRGRICIES CNLYDGEFRE FENGSICVEC
Egfr   LCSPEGCWGP EPRDCVSCRN VSRGRECVDK CKLLEGEPRE FVENSECIQC
Erb2   LCARGHCWGP GPTQCVNCSQ FLRGQECVEE CRVLQGLPRE YVNARHCLPC

       551                                              600
Erb3   HPECQPME.G TATCNGSGSD TCAQCAHFRD GPHCVSSCPH GVLGA.KGP.
Erb4   DPQCEKMEDG LLTCHGPGPD NCTKCSHFKD GPNCVEKCPD GLQGA.NSF.
Egfr   HPECLPQAMN I.TCTGRGPD NCIQCAHYID GPHCVKTCPA GVMGENNTL.
Erb2   HPECQPQN.G SVTCFGPEAD QCVACAHYKD PPFCVARCPS GVKPDLSYMP

       601                                              649
Erb3   IYKYPDVQNE CRPCHENCTQ GCKGPELQDC L.....GQT. .........
Erb4   IFKYADPDRE CHPCHPNCTQ GCNGPTSHDC IYYPWTGHST LPQHARTPL
Egfr   VWKYADAGHV CHLCHPNCTY GCTGPGLEGC PTNGPKIPS. .........
Erb2   IWKFPDEEGA CQPCPINCTH SCVDLDDKGC PAEQRASPLT S.........
```

Figure 15. Classification of Cys-rich modules

C2-4 denote modules with the 1-3/2-4 double disulphide bond connections.
C1-2 for the single disulphide bonded modules and
C1-2t for stabilised beta turn.

First Cys-rich region

C2-4 modules

		1 2 3 4		
Higf1r	152	CPGTMEEKPM-CEKTTINNEYNYRCWTTNRC QKM	184	(1st)
Hir	159	CPGTAKGKTN-CPATVINGQFVERCWTHSHC QKV	191	(1st)
Hirr	154	CPGVLGAAGEPCAKTTFSGHTDYRCWTSSHC QRV	187	(1st)
Egfr	166	CDPSCPNG-SCWGAG-EENC QKLTKII	190	(1st)
hErb2	174	CSPMCKGS-RCWGES-SEDC QSLTRTV	198	(1st)
hErb3	167	CHEVCKG--RCWGPG-SEDC QTLTKTI	190	(1st)
hErb4	167	CHKSCTG--RCWGPT-ENHC QTLTRTV	190	(1st)
Higf1r	195	CPSTCGK-RACTEN---NEC	200	(2nd)
Hir	192	CPTICKS-HGCTAE---GLC	207	(2nd)
Hirr	188	CP--CPHGMACTAR---GEC	202	(2nd)
Egfr	191	CAQQCSG--RCRGKS-PSDC	207	(2nd)
hErb2	199	CAGGCA---RCKGPL-PTDC	214	(2nd)
hErb3	191	CAPQCNG--HCFGPN-PNQC	207	(2nd)
hErb4	191	CAEQCDG--RCYGPY-VSDC	207	(2nd)
Higf1r	201	CHPECLG--SCSAPDNDTAC VA	220	(3rd)
Hir	208	CHSECLG--NCSQPDDPTKC VA	227	(3rd)
Hirr	203	CHTECLG--GCSQPEDPRAC VA	222	(3rd)
Egfr	208	CHNQCAA--GCTGPR-ESDC LV	226	(3rd)
Erb2	215	CHEQCAA--GCTGPK-HSDC LA	233	(3rd)
hErb3	208	CHDECAG--GCSGPQ-DTDC FA	226	(3rd)
hErb4	208	CHRECAG--GCSGPK-DTDC FA	226	(3rd)

C1-2 modules

Higf1r	221	CRHYY---YAGVC VPA	233	(4th)
Hir	228	CRNFY---LDGRC VET	240	(4th)
Hirr	223	CRHLY---FQGAC LMA	235	(4th)
Egfr-I	227	CRKFR---DEATC KDT	239	(4th)
hErb2	234	CLHFN---HSGIC ELH	246	(4th)
hErb3	227	CFHFN---DSGAC VPR	239	(4th)
hErb4	227	CMNFN---DSGAC VTQ	239	(4th)
Higf1r	234	CPPNTYRFEGWRC VDRDF	251	(5th)
Hir	241	CPPPYYHFQDWRC VNFSF	258	(5th)
Hirr	236	CPPGTYQYESWRC VTAER	253	(5th)
Egfr	240	CPPLMLYNPTTYQMDVNPEGKYSFGATC VKK	270	(5th)
hErb2	247	CPALVTYNTDTFESMPNPEGRYTFGASC VTA	277	(5th)
hErb3	240	CPQPLVYNKLTFQLEPNPHTKYQYGGVC VAS	270	(5th)
hErb4	240	CPQTFVYNPTTFQLEHNFNAKYTYGAFC VKK	270	(5th)
Higf1r	252	CANILSAESSDSEG.....FVIHD.GEC MQE	276	(6th)
Hir	259	CQD.LHHKCKNSRRQGCHQYVIHN.NKC IPE	287	(6th)
Hirr	254	CAS.LHSVPGRAST.....FGIHQ.GSC LAQ	276	(6th)
Egfr	271	CPRNYVVTDHGSC VRA	286	(6th)
hErb2	278	CPYNYLSTDVGSC TLV	293	(6th)
hErb3	271	CPHNFVV.DQTSC VRA	285	(6th)
hErb4	271	CPHNFVV.DSSSC VRA	285	(6th)
Higf1r	277	CPSG.FIRNGSQ-SMYC IP	293	(7th)
Hir	288	CPSG.YTMNSSN--LLC TP	303	(7th)
Hirr	278	CPSG.FTRNSS--GIFC HK	293	(7th)
Egfr	287	CGADSYEME-EDGVRKC KK	304	(7th)
hErb2	294	CPLHNQEVTAEDGTQRC EK	312	(7th)
hErb3	286	CPPDKMEVDKN-GLKMC EP	303	(7th)
hErb4	286	CPSGKMEVEEN-GIKMC KP	303	(7th)

C1-2t module

Higf1r	294	CEGPC	298	(8th)
Hir	304	CLGPC	308	(8th)
Hirr	294	CEGLC	298	(8th)
hEgfr	305	CEGPC	309	(8th)
hErb2	313	CSKPC	317	(8th)
hErb3	304	CGGLC	308	(8th)
hErb4	304	CTDIC	308	(8th)

Second Cys-rich region.

C2-4 modules

hEgfr	482	CHALCSP-----EGCWGPEPRDCVS	501	(1st)
hErb2	490	CHQLCAR-----GHCWGPGPTQCVN	509	(1st)
hErb3	481	CDPLCSS-----GGCWGPGPGQCLS	500	(1st)
hErb4	481	CNHLCSS-----DGCWGPGPDQCLS	500	(1st)
Egfr	534	CHPECLPQAM-NITCTGRGPDNC IQ	557	(4th)
hErb2	542	CHPECQPQNG-SVTCFGPEADQC VA	565	(4th)
hErb3	533	CHPECQPMEG-TATCNGSGSDTC AQ	556	(4th)
hErb4	533	CDPQCEKMEDGLLTCHGPGPDNC TK	557	(4th)
hEgfr	596	CHPNCTY------GCTGPGLEGC PTNGPKIPS/	621	(7th)
hErb2	605	CPINCTH------SCVDLDDKGC PAEQRAQRASPLTS/	632	(7th)
hErb3	594	CHENCTQ------GCKGPELQDC LGQT/	614	(7th)
hErb4	595	CHPNCTQ------GCNGPTSHDC IYYPWTGHSTLPQHARTPL	630	(7th)

C1-2 modules

hEgfr	502	CRNVS---RGREC VDK	514	(2nd)
hErb2	510	CSQFL---RGQEC VEE	522	(2nd)
hErb3	501	CRNVS---RGGVC VTH	513	(2nd)
hErb4	501	CRRFS---RGRIC IES	513	(2nd)
hEgfr	515	CKLLEGEPREFVENSEC IQ	533	(3rd)
hErb2	523	CRVLQGLPREYVNARHC LP	541	(3rd)
hErb3	514	CNFLNGEPREFAHEAEC FS	532	(3rd)
hErb4	514	CNLYDGEFREFENGSIC VE	532	(3rd)
hEgfr	553	CAHYI---DGPHC VKT	570	(5th)
hErb2	566	CAHYK---DPPFC V-A	578	(5th)
hErb3	557	CAHFR---DGPHC V-S	569	(5th)
hErb4	553	CSHFK---DGPNC VEK	570	(5th)
hEgfr	571	CPAGVMGENNTL-VWKYADAGHVC HL	595	(6th)
hErb2	579	CPSGVKPDLSYMPIWKFPDEEGAC QP	604	(6th)
hErb3	570	CPHGVLGAKG--PIYKYPDVQNEC RP	593	(6th)
hErb4	571	CPDGLQGANS--FIFKYADPDREC HP	594	(6th)

See Pattern is:

IR family: C2-4, C2-4, C2-4, C1-2, C1-2, C1-2, C1-2, C1-2t

EGFR family: 1st C2-4, C2-4, C2-4, C1-2, C1-2, C1-2, C1-2, C1-2t

2nd C2-4, C1-2, C1-2,
C2-4, C1-2, C1-2,
C2-4

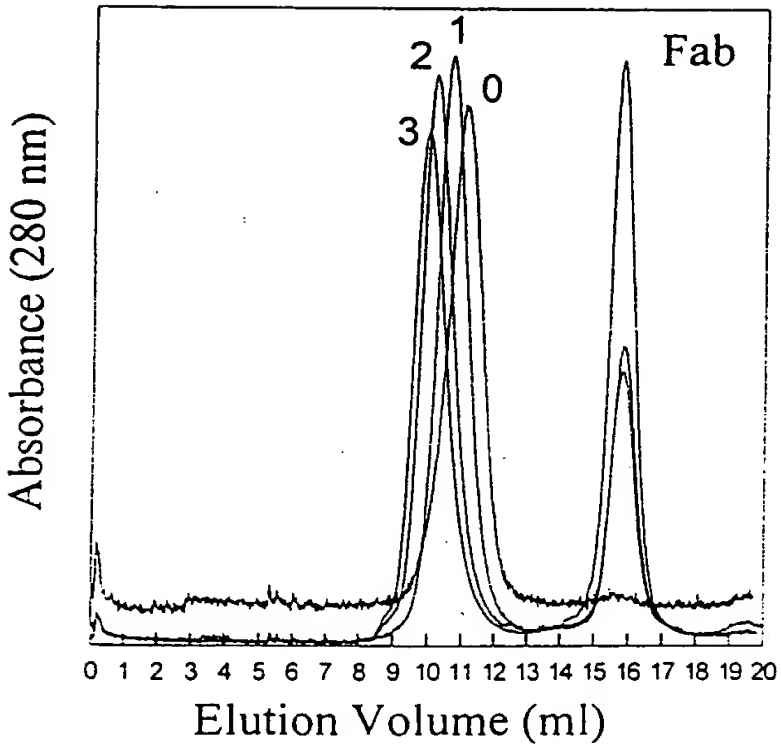

Absorbance (280 nm)
1
2
0
3
Fab
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Elution Volume (ml)

Figure 16

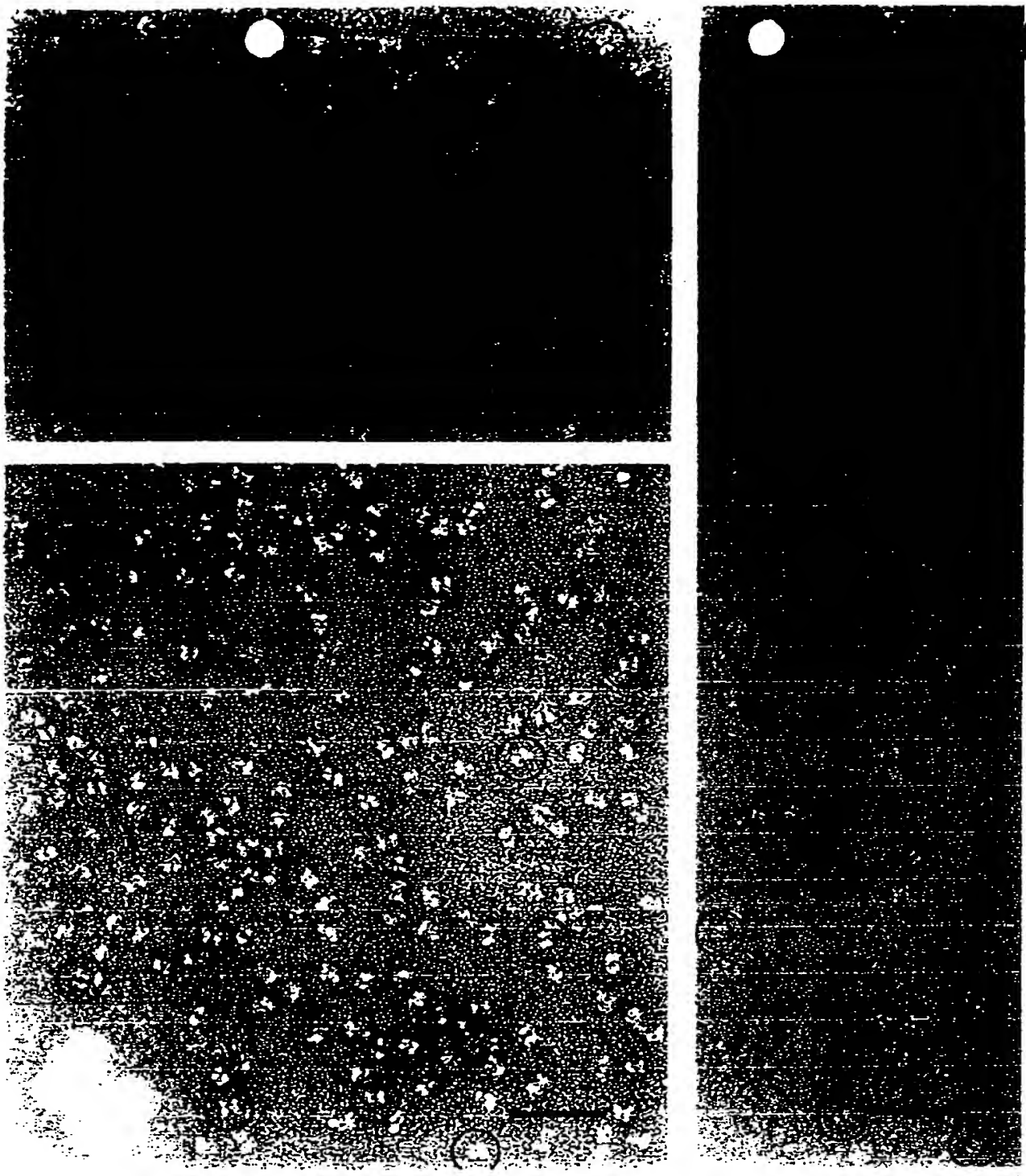


Figure 17

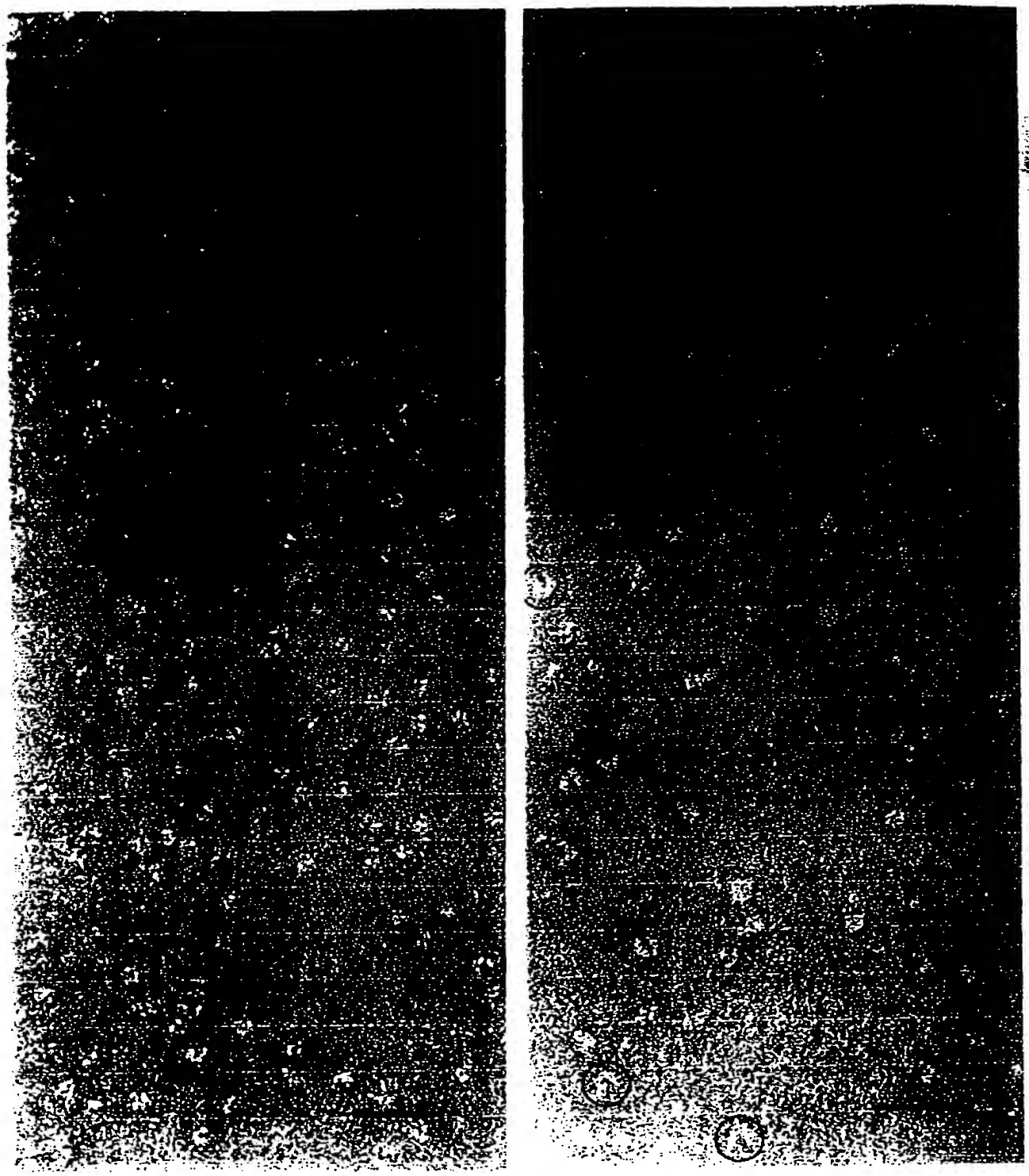


Figure 1.

Figure 19

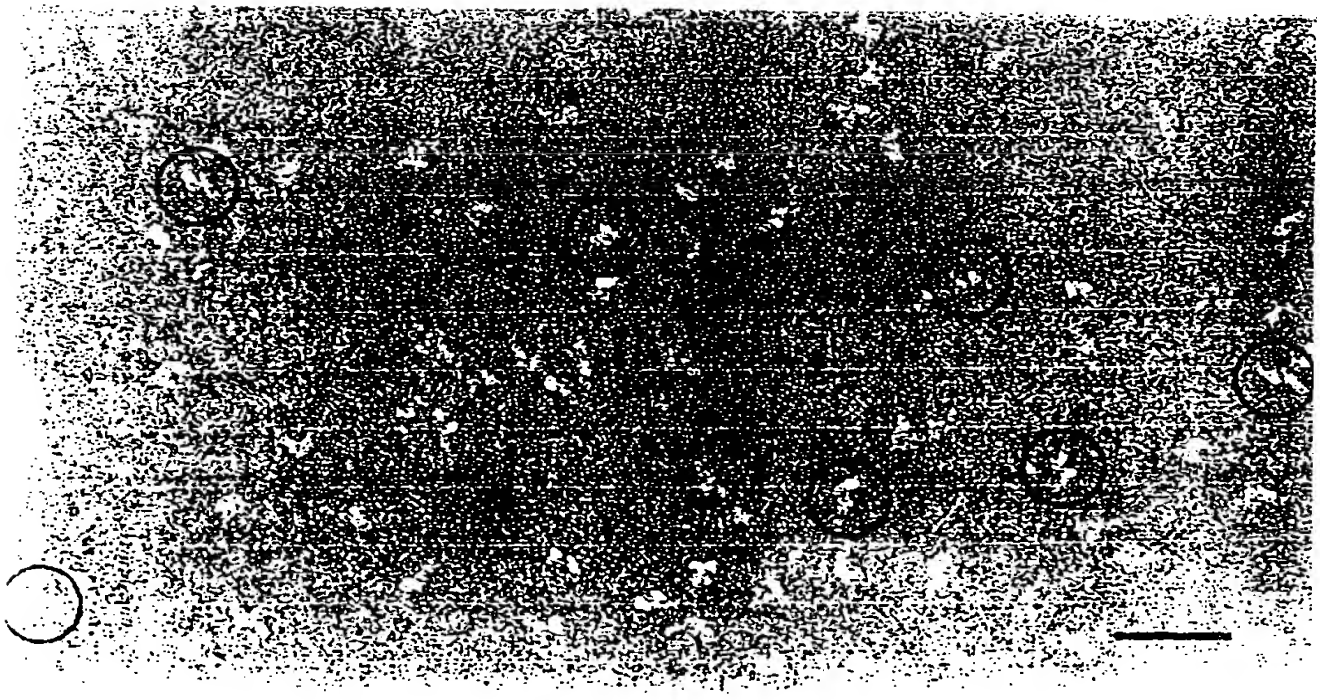


Figure 20

(a)

(b)

Figure 21

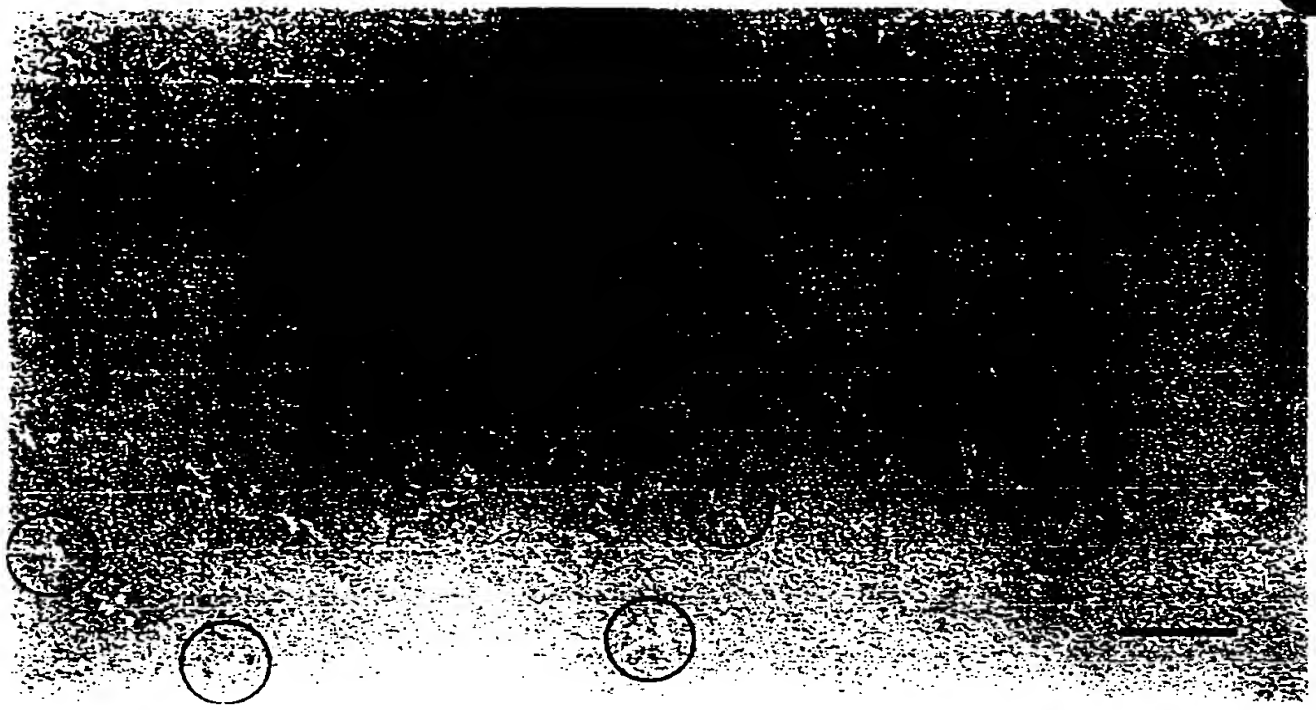


Figure 22

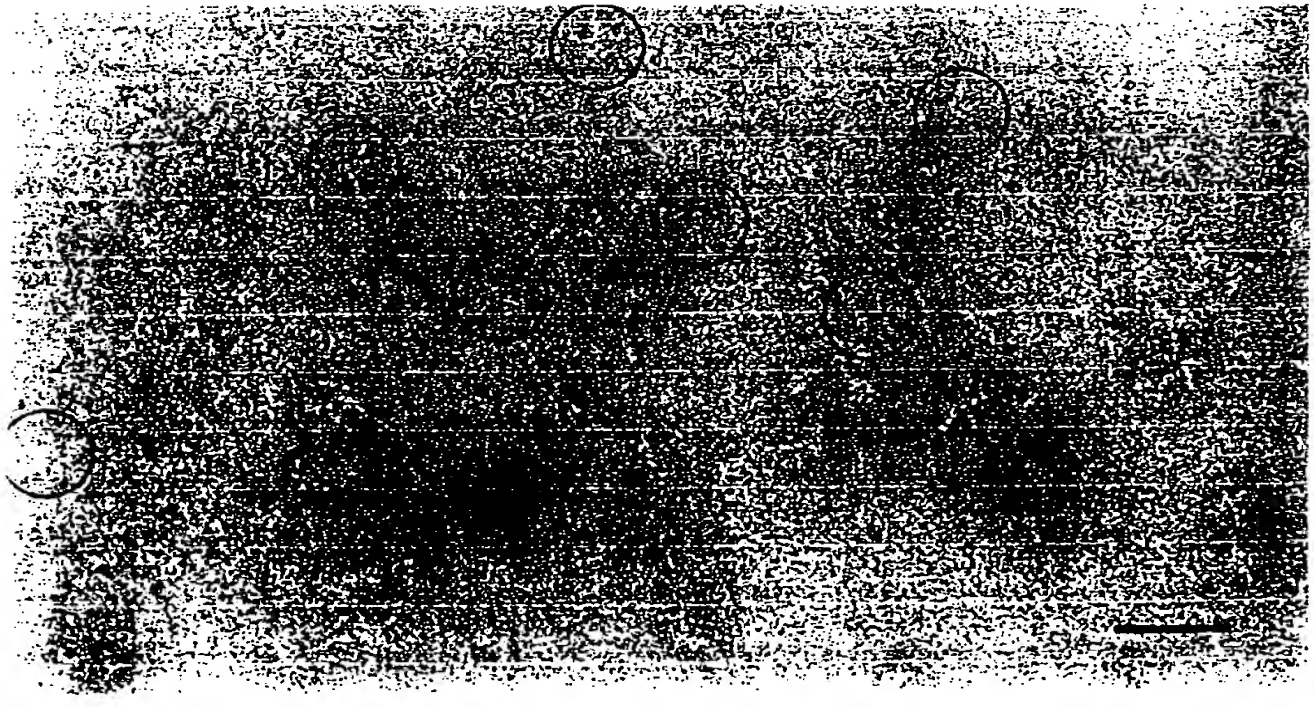


Figure 23